(19) World Intellectual Property Organization International Bureau



(43) International Publication Date 29 August 2002 (29.08.2002)

PCT

(10) International Publication Number WO 02/066501 A2

(51) International Patent Classification?: C07K 14/205, C12N 15/31, G01N 33/68, C12N 15/63, A61K 39/106, 35/74 LABIGNE, Agnès [FR/FR]; 29, rue du Bois Michel Pierre, Appt 106, F-91440 Bures sur Yvette (FR).

- (21) International Application Number: PCT/EP01/15428
- (74) Agent: ERNEST GUTMANN YVES PLASSERAUD S.A.; 3, rue Chauveau-Lagarde, F-75008 Paris (FR).

(81) Designated States (national): AE, AG, AL, AM, AT, AU,

AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,

CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,

LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ,

(22) International Filing Date:

28 December 2001 (28.12.2001)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data: 60/259,302

2 January 2001 (02.01.2001) US

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

VN, YU, ZA, ZM, ZW.

(71) Applicants (for all designated States except US): HYBRI-GENICS [FR/FR]; 3/5 Impasse Reille, F-75014 Paris (FR). INSTITUT PASTEUR [FR/FR]; 25-28, rue du Dr Roux, F-75724 Paris Cedex 15 (FR).

- (72) Inventors; and
- (75) Inventors/Applicants (for US only): LEGRAIN, Pierre [FR/FR]; 5, rue Mizon, F-75015 Paris (FR). RAIN, Jean-Christophe [FR/FR]; 32, Jardin Boeldieu, F-92800 Puteaux (FR). COLLAND, Frédéric [FR/FR]; 16, rue du Manoir, F-95380 Puiseux en France (FR). DE REUSE, Hilde [BE/FR]; 49, rue Rouelle, F-75015 Paris (FR).

Published:

 without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

BEST AVAILABLE COPY

(54) Title: PROTEIN-PROTEIN INTERACTIONS IN HELICOBACTER PYLORI

(57) Abstract: The present invention relates to protein-protein interactions of *Helicobacter pylori*. More specifically, the present invention relates to complexes of polypeptides or polynucleotides encoding the polypeptides, fragments of the polypeptides, antibodies to the complexes, Selected Interacting Domains (SID®) which are identified due to the protein-protein interactions, methods for screening drugs for agents which modulate the interaction of proteins and pharmaceutical compositions that are capable of modulating the protein-protein interactions.



PROTEIN-PROTEIN

INTERACTIONS IN Helicobacter pylori

FIELD OF THE INVENTION

5

10

15

20

25

The present invention relates to proteins that interact with Helicobacter pylori. More specifically, the present invention relates to complexes of polypeptides or polynucleotides encoding the polypeptides, fragments of the polypeptides, antibodies to the complexes, Selected Interacting Domains (SID®) which are identified due to the protein-protein interactions, methods for screening drugs for agents which modulate the interaction of proteins and pharmaceutical compositions that are capable of modulating the protein-protein interactions.

In another embodiment the present invention provides a protein-protein interaction map called a PIM® which is available in a report relating to the protein-protein interactions of *Helicobacter pylori*.

BACKGROUND AND PRIOR ART

Most biological processes involve specific protein-protein interactions. Protein-protein interactions enable two or more proteins to associate. A large number of non-covalent bonds form between the proteins when two protein surfaces are precisely matched. These bonds account for the specificity of recognition. Thus, protein-protein interactions are involved, for example, in the assembly of enzyme subunits, in antibody-antigen recognition, in the formation of biochemical complexes, in the correct folding of proteins, in the metabolism of proteins, in the transport of proteins, in the localization of proteins, in protein turnover, in first translation modifications, in the core structures of viruses and in signal transduction.

General methodologies to identify interacting proteins or to study these interactions have been developed. Among these methods are the two-hybrid system originally developed by Fields and co-workers and described, for

example, in U.S. Patent Nos. 5,283,173, 5,468,614 and 5;667,973, which are hereby incorporated by reference.

The earliest and simplest two-hybrid system, which acted as basis for development of other versions, is an *in vivo* assay between two specifically constructed proteins. The first protein, known in the art as the "bait protein" is a chimeric protein which binds to a site on DNA upstream of a reporter gene by means of a DNA-binding domain or BD. Commonly, the binding domain is the DNA-binding domain from either Gal4 or native *E. coli* LexA and the sites placed upstream of the reporter are Gal4 binding sites or LexA operators, respectively.

The second protein is also a chimeric protein known as the "prey" in the art. This second chimeric protein carries an activation domain or AD. This activation domain is typically derived from Gal4, from VP 16 or from B42.

10

15

20

25

Besides the two hybrid systems, other improved systems have been developed to detect protein-protein interactions. For example, a two-hybrid plus one system was developed that allows the use of two proteins as bait to screen available cDNA libraries to detect a third partner. This method permits the detection between proteins that are part of a larger protein complex such as the RNA polymerase II holoenzyme and the TFIIH or TFIID complexes. Therefore, this method, in general, permits the detection of ternary complex formation as well as inhibitors preventing the interaction between the two previously defined fused proteins.

Another advantage of the two-hybrid plus one system is that it allows or prevents the formation of the transcriptional activator since the third partner can be expressed from a conditional promoter such as the methionine-repressed Met25 promoter which is positively regulated in medium lacking methionine. The presence of the methionine-regulated promoter provides an excellent control to evaluate the activation or inhibition properties of the third partner due to its "on" and "off" switch for the formation of the transcriptional activator. The three-hybrid method is described, for example in Tirode et al., The Journal of Biological

10

15

20

_25

Chemistry, 272, No. 37 pp. 22995-22999 (1997) incorporated herein by reference.

Besides the two and two-hybrid plus one systems, yet another variant is that described in Vidal et al, Proc. *Natl. Sci.* **93** pgs. 10315-10320 called the reverse two-and one-hybrid systems where a collection of molecules can be screened that inhibit a specific protein-protein or protein/DNA interaction, respectively.

A summary of the available methodologies for detecting protein-protein interactions is described in Vidal and Legrain, *Nucleic Acids Research* Vol. 27, No. 4 pgs.919-929 (1999) and Legrain and Selig, FEBS Letters 480 pgs. 32-36 (2000) which references are incorporated herein by reference.

However, the above conventionally used approaches and especially the commonly used two-hybrid methods have their drawbacks. For example, it is known in the art that, more often than not, false positives and false negatives exist in the screening method. In fact, a doctrine has been developed in this field for interpreting the results and in common practice an additional technique such as co-immunoprecipitation or gradient sedimentation of the putative interactors from the appropriate cell or tissue type are generally performed. The methods used for interpreting the results are described by Brent and Finley, Jr. in *Ann. Rev. Genet.*, **31** pgs. 663-704 (1997). Thus, the data interpretation is very questionable using the conventional systems.

One method to overcome the difficulties encountered with the methods in the prior art is described in WO 99/42612, incorporated herein by reference. This method is similar to the two-hybrid system described in the prior art in that it also uses bait and prey polypeptides. However, the difference with this method is that a step of mating at least one first haploid recombinant yeast cell containing the prey polypeptide to be assayed with a second haploid recombinant yeast cell containing the bait polynucleotide is performed. Of course the person skilled in the art would appreciate that either the first recombinant yeast cell or the second

NSDOCID - WO MORESON -

WO 02/066501

5

10

15

20

25.

30

BNSDOCID: AND

PCT/EP01/15428

recombinant yeast cell also contains at least one detectable reporter gene that is activated by a polypeptide including a transcriptional activation domain.

The method described in W099/42612 permits the screening of more prey polynucleotides with a given bait polynucleotide in a single step than in the prior art systems due to the cell to cell mating strategy between haploid yeast cells. Furthermore, this method is more thorough and reproducible, as well as sensitive. Thus, the presence of false negatives and/or false positives is extremely minimal as compared to the conventional prior art methods.

One of the prokaryotic microorganisms studied by the inventors is Helicobacter pylori. Helicobacter pylori (H. pylori) is a microaerophilic, Gram negative, slow growing, spiral shaped and flagellated organism. H. pylori has been first isolated in 1983 from a gastric biopsy specimen of patient with chronic gastritis (Marshall et al., 1984, Lancet, 1:1311-1314, Unidentified curved bacilli in the stomach of patients with gastritis and peptic ulceration).

Helicobacter pylori has become identified as a primary cause of chronic gastroduodenal disorders, such as gastritis, dyspepsia, and peptic ulcers, in humans. Studies have shown (Labigne et al.) that *H. pylori* can be successfully eradicated by a treatment combining two antibiotics with a proton pump inhibitor. However, few antibiotics are active against *H. pylori* and antibiotic-resistant strains have begun to appear.

The *H. pylori* strain n° 26695 genome has been studied by Tomb et al. (Tomb et al., 1997, Nature, vol. 388, 539-547, *The complete genome sequence of the gastric pathogen Helicobacter pylori*). This strain's genome consists of a circular chromosome with a size of 1,667,867 bp, average G + C content of 39%, and 1590 predicted coding sequences (open reading frames or "ORF").

The availability of the entire genome sequence of two clinical strains, 26695 and J99 (Alm et al, 1999) (Tomb et al, 1997) has encouraged more global approaches to the functional analysis of the whole set of genes. In *H. pylori*, there is still as much as 42% of the *H. pylori* encoded proteins for which there is a need to assign biological function. Attempts to classify genes within functional

10

15

20

25

[

categories such as genes essential for viability, or conditionally essential in a given environment have been proposed by Akeriey and collaborators (Akerley et al, 1998). This concept was first applied to *H. pylori* by Chalker et al. (Chalker et al, 2001) who analyzed for essentiality a set of genes selected by bioinformatic genome prioritization.

The bacterial factors necessary for colonization of the gastric environment, and for virulence of this pathogen, are poorly understood. Examples of known virulence factors are:

- Enzymes involved in neutralizing the acid gastric pH: the multisubunit urease is a characteristic enzyme that is crucial for survival in acidic pH and for successful colonization of the gastric environment, a site that few other microbes can colonize (Labigne et al., WO 93/07273, Helicobacter pylori genes necessary for the regulation and maturation of urease, and use thereof). Genes encoding ureases have been located on a 34 kb chromosome fragment and comprise ureA, ureB, ureC, ureD, ureE, ureF, ureG, ureH and urel.
 - Bacterial flagellar proteins responsible for motility across the mucous layer (Hazell et al., 1986, J. Inf. Dis., 153, 658-663 Campylobacter pyloridis and gastritis: association with intracellular spaces and adaptation to an environment of mucus as important factors in colonization of the gastric epithelium; Leying et al., 1992, Mol. Microbiol., 6, 2863-2874 Cloning and genetic characterization of Helicobacter pylori flagellin gene): flagellar filaments biosynthesis comprises A and B flagellins and the filament cap. These two biosyntheses are regulated by flbA gene (Suerbaum et al., 2,736,360. Cloning 1995, application, patent French characterization of flbA gene of Helicobacter pylori, aflagellated strains production).
 - Two other essential toxins for virulence are VacA and CagA.

VacA is a H. pylori toxin that induces the formation of large acidic vacuoles in host epithelial cells. These large vacuoles originate from massive swelling of

membranous compartments of late stages of the endocytic pathway (de Bernard et al., 1997, Microbiology, 26(4), 665-674, Helicobacter pylori toxin VacA induces vacuole formation by acting in the cell cytosol) Proof for receptor-mediated interaction with VacA has been made by Pagliaccia et al.; m2 allele of vacA gene has always been described as inactive in the in vitro HeLa-cell assay, however, the m2 allele is associated with peptic ulcer and is prevalent in populations in which peptic ulcer and gastric-cancer have high incidence (Pagliaccia et al., Proc. Natl. Acad. Sci. U.S.A, 1998, 95(17), 10212-10217, The m2 form of the Helicobacter pylori cytotoxin has cell type-specific vacuolating activity).

10 .

15

20

25

30

CagA is one of the proteins encoded by the "cag pathogenicity island" (Spohn et al. 1997, Molecular Microbiology, 26(2), 361-372, Transcriptional analysis of the divergent cagAB genes encoded by the pathogenicity island of Helicobacter pylori) found in H. pylori strains isolated from most patients with peptic ulcer disease and adenocarcinoma. CagA is produced by 50-60% of H. pylori strains; it is a high molecular weight (120-140 kDa) superficial protein and an immunodominant antigen with unknown function. H. pylori strains that produce CagA protein have two genes cagB and cagC (36 and 101 kDa proteins, respectively). These genes are highly associated with duodenal ulcers (Blaser et al. 1996, WO 96/12825, cagB and cagC genes of Helicobacter pylori and related methods and compositions).

Other virulence factors are: several gastric tissue-specific adhesins (Boren et al., 1993, Science, **262**, 1892-1895).

Therapeutic agents are currently available that eradicate *H. pylori* infections in vitro. However, methods employing antibiotic agents result in the emergence of bacterial strains which are resistant to these agents.

Thus, it is an object of the present invention to identify protein-protein interactions for *Helicobacter pylori*.

It is another object of the present invention to identify protein-protein interactions of *Helicobacter pylori* for the development of more effective and better targeted therapeutic applications.

It is yet another object of the present invention to identify complexes of polypeptides or polynucleotides encoding the polypeptides and fragments of the polypeptides of *Helicobacter pylori*.

It is yet another object of the present invention to identify antibodies to these complexes of polypeptides or polynucleotides encoding the polypeptides and fragments of the polypeptides of *Helicobacter pylori* including polyclonal, as well as monoclonal antibodies that are used for detection.

It is still another object of the present invention to identify selected interacting domains of the polypeptides, called SID® polypeptides.

It is still another object of the present invention to identify selected interacting domains of the polynucleotides, called SID® polynucleotides.

It is another object of the present invention to generate protein-protein interactions maps called PIM®s.

It is yet another object of the present invention to classify genes of *H. pylori* into functional categories at the genomic scale such as genes essential or nonessential for viability.

It is yet another object of the present invention to identify Putative Essential Genes (PEGS) from *H. pylori*, as well as the true essential genes.

It is yet another object of the present invention to establish a large scale protein-protein interaction map of *H. pylori* using the two-hybrid system as a way to elucidate the function of yet uncharacterized proteins.

It is yet another object of the present invention to identify a superbinder phenotype in *H. pylori* with the two-hybrid system which completely inhibits specific protein-protein interactions.

25 It is yet another object of the present invention to identify oligopeptides. Their overlapping or combining derivatives that inhibit *H. pylori* growth.

10

20

20

In yet another aspect, the present invention relates to the identification of ORFs (open reading frames) having enzymatic activity, which provides a direct way to screen lead compounds that abolish enzymatic activity through the disruption of the oligomeric interaction.

It is yet another object of the present invention to provide a method for screening drugs for agents which modulate the interaction of proteins and pharmaceutical compositions that are capable of modulating the protein-protein interactions of *Helicobacter pylori*.

It is another object to administer the nucleic acids of the present invention via gene therapy.

It is yet another object of the present invention to provide protein chips or protein microarrays.

It is yet another object of he present invention to provide a report in, for example paper, electronic and/or digital forms, concerning the protein-protein interactions, the modulating compounds and the like, as well as a PIM®.

These and other objects are achieved by the present invention as evidenced by the summary of the invention, description of the preferred embodiments and the claims.

SUMMARY OF THE PRESENT INVENTION

Thus the present invention relates to a protein complex of polypeptides as described in Table 1.

Furthermore, the present invention provides SID® polynucleotides and SID® polypeptides as defined in Figure 2, as well as a PIM® for *Helicobacter pylori*.

The present invention also provides antibodies to the protein-protein complexes for *Helicobacter pylori*.

10

20

25

In another embodiment the present invention provides a method for screening drugs for agents that modulate the protein-protein interactions and pharmaceutical compositions that are capable of modulating protein-protein interactions.

In another embodiment the present invention provides protein chips or protein microarrays.

In another embodiment the present invention identifies a superbinder phenotype in H. pylori with the two-hybrid system which completely inhibits protein-protein interactions.

In another aspect the present invention provides oligopeptides, their overlapping or combining derivatives thereof that inhibit *H. pylori* growth.

In yet another embodiment, the present invention identifies ORFs having enzymatic activity which provides a direct way to screen lead compounds.

In yet another embodiment the present invention provides a report in, for example, paper, electronic and/or digital forms.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a schematic representation of the pB1 plasmid.

Fig. 2 is a schematic representation of the pB5 plasmid.

Fig. 3 is a schematic representation of the pB6 plasmid.

Fig. 4 is a schematic representation of the pB13 plasmid.

Fig. 5 is a schematic representation of the pB14 plasmid.

Fig. 6 is a schematic representation of the pB20 plasmid.

Fig. 7 is a schematic representation of the pP1 plasmid.

Fig. 8 is a schematic representation of the pP2 plasmid.

15

20

- Fig. 9 is a schematic representation of the pP3 plasmid.
- Fig. 10 is a schematic representation of the pP6 plasmid.
- Fig. 11 is a schematic representation of the pP7 plasmid.
- Fig. 12 is a schematic representation of vectors expressing the T25 fragment.
- Fig. 13 is a schematic representation of vectors expressing the T18 fragment.
- Fig. 14 is a schematic representation of various vectors of pCmAHL1, pT25 and pT18.
- Fig. 15 is a schematic representation identifying the SID®'s of Helicobacter pylori. In this figure the "Full-length prey protein" is the Open Reading Frame (ORF) or coding sequence (CDS) where the identified prey polypeptides are included. The Selected Interaction Domain (SID®) is determined by the commonly shared polypeptide domain of every selected prey fragment.
- Fig. 16 is a protein map (PIM®).
- Fig. 17 is a gel illustrating the results obtained for the disruption of the ORFs hp0099 to hp0198. This figure exemplifies first that multiple insertions of the transposon took place and second that for the majority trransposon insertion occurred at a distance ranging between 100 to 600 bp from the 5'-end of the ORF, a distance compatible with the promotion of gene replacement by allelic recombination.
- Fig. 18 is a schematic diagram of the procedure for classification of the genes as described in the present invention.
- Fig. 19 are the results of three-hybrid experiments. Growth phenotypes of diploid strains containing various plasmids were analyzed by incubating cells at various dilutions (from 1 to 10⁻⁴). Yeast growth was performed

PCT/EP01/15428

11

over 2 days at 30°C on DO-3+Met or DO-3-Met medium. Lane 1 are cells containing [p3H1-HP1230]+pP6-HP1529; Lane 2 [p3H1-HP1230-SID1529WT]+pP6-HP1529; lane 3[pH1-HP1230-SID1529(N38D-V53L)+pP6-HP1529; lane 4 [p3H1-HP1230-SID1529(V53L)]+pP6-HP1529; and lane 5 [p3H1-HP1230]+pP6-HP0875.

Fig. 20 is the pP7-centro vector.

WO 02/066501

5

10

15

20

25

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

As used herein the terms "polynucleotides", "nucleic acids" and "oligonucleotides" are used interchangeably and include, but are not limited to RNA, DNA, RNA/DNA sequences of more than one nucleotide in either single chain or duplex form. The polynucleotide sequences of the present invention may be prepared from any known method including, but not limited to, any synthetic method, any recombinant method, any ex vivo generation method and the like, as well as combinations thereof.

The term "polypeptide" means herein a polymer of amino acids having no specific length. Thus, peptides, oligopeptides and proteins are included in the definition of "polypeptide" and these terms are used interchangeably throughout the specification, as well as in the claims. The term "polypeptide" does not exclude posttranslational modifications such as polypeptides having covalent attachment of glycosyl groups, acetyl groups, phosphate groups, lipid groups and the like. Also encompassed by this definition of "polypeptide" are homologs thereof.

By the term "homologs" is meant structurally similar genes contained within a given species, orthologs are functionally equivalent genes from a given species or strain, as determined for example, in a standard complementation assay. Thus, a polypeptide of interest can be used not only as a model for identifying similar genes in given strains, but also to identify homologs and orthologs of the polypeptide of interest in other species. The orthologs, for

example, can also be identified in a conventional complementation assay. In addition or alternatively, such orthologs can be expected to exist in bacteria (or other kind of cells) in the same branch of the phylogenic tree, as set forth, for example, at ftp://ft.cme.msu.edu/pub/rdp/SSU-rRNA/SSU/Prok.phylo.

As used herein the term "prey polynucleotide" means a chimeric polynucleotide encoding a polypeptide comprising (i) a specific domain; and (ii) a polypeptide that is to be tested for interaction with a bait polypeptide. The specific domain is preferably a transcriptional activating domain.

As used herein, a "bait polynucleotide" is a chimeric polynucleotide encoding a chimeric polypeptide comprising (i) a complementary domain; and (ii) a polypeptide that is to be tested for interaction with at least one prey polypeptide. The complementary domain is preferably a DNA-binding domain that recognizes a binding site that is further detected and is contained in the host organism.

As used herein "complementary domain" is meant a functional constitution of the activity when bait and prey are interacting; for example, enzymatic activity.

As used herein "specific domain" is meant a functional interacting activation domain that may work through different mechanisms by interacting directly or indirectly through intermediary proteins with RNA polymerase II or III-associated proteins in the vicinity of the transcription start site.

As used herein the term "complementary" means that, for example, each base of a first polynucleotide is paired with the complementary base of a second polynucleotide whose orientation is reversed. The complementary bases are A and T (or A and U) or C and G.

The term "sequence identity" refers to the identity between two peptides or between two nucleic acids. Identity between sequences can be determined by comparing a position in each of the sequences which may be aligned for the purposes of comparison. When a position in the compared sequences is occupied by the same base or amino acid, then the sequences are identical at that position. A degree of sequence identity between nucleic acid sequences is a

5

10

20

25

10

15

20

25

30

function of the number of identical nucleotides at positions shared by these sequences. A degree of identity between amino acid sequences is a function of the number of identical amino acid sequences that are shared between these sequences. Since two polypeptides may each (i) comprise a sequence (i.e., a portion of a complete polynucleotide sequence) that is similar between two polynucleotides, and (ii) may further comprise a sequence that is divergent between two polynucleotides, sequence identity comparisons between two or more polynucleotides over a "comparison window" refers to the conceptual segment of at least 20 contiguous nucleotide positions wherein a polynucleotide sequence may be compared to a reference nucleotide sequence of at least 20 contiguous nucleotides and wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) of 20 percent or less compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences.

To determine the percent identity of two amino acids sequences or two nucleic acid sequences, the sequences are aligned for optimal comparison. For example, gaps can be introduced in the sequence of a first amino acid sequence or a first nucleic acid sequence for optimal alignment with the second amino acid sequence or second nucleic acid sequence. The amino acrid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, the molecules are identical at that position.

The percent identity between the two sequences is a function of the number of identical positions shared by the sequences. Hence % identity = number of identical positions / total number of overlapping positions X 100.

In this comparison the sequences can be the same length or may be different in length. Optimal alignment of sequences for determining a comparison window may be conducted by the local homology algorithm of Smith and Waterman (J. *Theor. Biol*, 91 (2) pgs. 370-380 (1981), by the homology alignment algorithm of Needleman and Wunsch, *J. Miol. Biol*, 48(3) pgs. 443-453

(1972), by the search for similarity via the method of Pearson and Lipman, PNAS, USA, 85(5) pgs. 2444-2448 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetic Computer Group, 575, Science Drive, Madison, Wisconsin) or by inspection.

5

20

25

30

The best alignment (i.e., resulting in the highest percentage of identity over the comparison window) generated by the various methods is selected.

The term "sequence identity" means that two polynucleotide sequences are identical (i.e., on a nucleotide by nucleotide basis) over the window of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A, T, C, G, U, or I) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size) and multiplying the result by 100 to yield the percentage of sequence identity. The same process can be applied to polypeptide sequences.

The percentage of sequence identity of a nucleic acid sequence or an amino acid sequence can also be calculated using BLAST software (Version 2.06 of September 1998) with the default or user defined parameter.

The term "sequence similarity" means that amino acids can be modified while retaining the same function. It is known that amino acids are classified according to the nature of their side groups and some amino acids such as the basic amino acids can be interchanged for one another while their basic function is maintained.

The term "isolated" as used herein means that a biological material such as a nucleic acid or protein has been removed from its original environment in which it is naturally present. For example, a polynucleotide present in a plant, mammal or animal is present in its natural state and is not considered to be isolated. The same polynucleotide separated from the adjacent nucleic acid

10

15

20

25

sequences in which it is naturally inserted in the genome of the plant or animal is considered as being "isolated."

The term "isolated" is not meant to exclude artificial or synthetic mixtures with other compounds, or the presence of impurities which do not interfere with the biological activity and which may be present, for example, due to incomplete purification, addition of stabilizers or mixtures with pharmaceutically acceptable excipients and the like.

"Isolated polypeptide" or "isolated protein" as used herein means a polypeptide or protein which is substantially free of those compounds that are normally associated with the polypeptide or protein in a naturally state such as other proteins or polypeptides, nucleic acids, carbohydrates, lipids and the like.

The term "purified" as used herein means at least one order of magnitude of purification is achieved, preferably two or three orders of magnitude, most preferably four or five orders of magnitude of purification of the starting material or of the natural material. Thus, the term "purified" as utilized herein does not mean that the material is 100% purified and thus excludes any other material.

The term "variants" when referring to, for example, polynucleotides encoding a polypeptide variant of a given reference polypeptide are polynucleotides that differ from the reference polypeptide but generally maintain their functional characteristics of the reference polypeptide. A variant of a polynucleotide may be a naturally occurring allelic variant or it may be a variant that is known naturally not to occur. Such non-naturally occurring variants of the reference polynucleotide can be made by, for example, mutagenesis techniques, including those mutagenesis techniques that are applied to polynucleotides, cells or organisms.

Generally, differences are limited so that the nucleotide sequences of the reference and variant are closely similar overall and, in many regions identical.

Variants of polynucleotides according to the present invention include, but are not limited to, nucleotide sequences which are at least 95% identical after

alignment to the reference polynucleotide encoding the reference polypeptide. These variants can also have 96%, 97%, 98% and 99.999% sequence identity to the reference polynucleotide.

Nucleotide changes present in a variant polynucleotide may be silent, which means that these changes do not alter the amino acid sequences encoded by the reference polynucleotide.

5

10

15

20

25

CMY -UISTONIAN

Substitutions, additions and/or deletions can involve one or more nucleic acids. Alterations can produce conservative or non-conservative amino acid substitutions, deletions and/or additions.

Variants of a prey or a SID® polypeptide encoded by a variant polynucleotide can possess a higher affinity of binding and/or a higher specificity of binding to its protein or polypeptide counterpart, against which it has been initially selected. In another context, variants can also loose their ability to bind to their protein or polypeptide counterpart.

By "anabolic pathway" is meant a reaction or series of reactions in a metabolic pathway that synthesize complex molecules from simpler ones, usually requiring the input of energy. An anabolic pathway is the opposite of a catabolic pathway.

As used herein, a "catabolic pathway" is a series of reactions in a metabolic pathway that break down complex compounds into simpler ones, usually releasing energy in the process. A catabolic pathway is the opposite of an anabolic pathway.

As used herein, "drug metabolism" is meant the study of how drugs are processed and broken down by the body. Drug metabolism can involve the study of enzymes that break down drugs, the study of how different drugs interact within the body and how diet and other ingested compounds affect the way the body processes drugs.

As used herein, "metabolism" means the sum of all of the enzymecatalyzed reactions in living cells that transform organic molecules.

10

20

25

By "secondary metabolism" is meant pathways producing specialized metabolic products that are not found in every cell.

As used herein, "SID®" means a Selected Interacting Domain and is identified as follows: for each bait polypeptide screened, selected prey polypeptides are compared. Overlapping fragments in the same ORF or CDS define the selected interacting domain.

As used herein the term "PIM®" means a protein-protein interaction map. This map is obtained from data acquired from a number of separate screens using different bait polypeptides and is designed to map out all of the interactions between the polypeptides.

The term "affinity of binding", as used herein, can be defined as the affinity constant Ka when a given SID® polypeptide of the present invention which binds to a polypeptide and is the following mathematical relationship:

[SID® /polypeptide complex]

Ka = ----
[free SID®] [free polypeptide]

wherein [free SID®], [free polypeptide] and [SID® polypeptide complex] consist of the concentrations at equilibrium respectively of the free SID® polypeptide, of the free polypeptide onto which the SID® polypeptide binds and of the complex formed between SID® polypeptide and the polypeptide onto which said SID® polypeptide specifically binds.

The affinity of a SID® polypeptide of the present invention or a variant thereof for its polypeptide counterpart can be assessed for example, on a BiacoreTM apparatus marketed by Amersham Pharmacia Biotech Company such as described by Szabo et al *Curr Opin Struct Biol* **5** pgs. 699-705 (1995) and by Edwards and Leartherbarrow, *Anal. Biochem* **246** pgs. 1-6 (1997).

10

15

20

25

30

As used herein the phrase "at least the same affinity" with respect to the binding affinity between a SID® polypeptide of the present invention to another polypeptide means that the Ka is identical or can be at least two-fold, at least three fold or at least five fold greater than the Ka value of reference.

As used herein, the term "modulating compound" means a compound that inhibits or stimulates or can act on another protein which can inhibit or stimulate the protein-protein interaction of a complex of two polypeptides or the protein-protein interaction of two polypeptides.

More specifically, the present invention comprises complexes of polypeptides or polynucleotides encoding the polypeptides composed of a bait polypeptide, or a bait polynucleotide encoding a bait polypeptide and a prey polypeptide or a prey polynucleotide encoding a prey polypeptide. The prey polypeptide or prey polynucleotide encoding the prey polypeptide is capable of interacting with a bait polypeptide of interest in various hybrid systems.

As described in the Background of the present invention there are various methods known in the art to identify prey polypeptides that interact with bait polypeptides of interest. These methods, include, but are not limited to, generic two-hybrid systems as described by Fields et al in *Nature*, 340:245-246 (1989) and more specifically in U.S. Patent Nos. 5,283,173, 5,468,614 and 5,667,973, which are hereby incorporated by reference; the reverse two-hybrid system described by Vidal et al, *supra*; the two plus one hybrid method described, for example, in Tirode et al, *supra*; the yeast forward and reverse 'n'-hybrid systems as described in Vidal and Legrain, *supra*; the method described in WO 99/42612; those methods described in Legrain et al *FEBS Letters* 480 pgs. 32-36 (2000) and the like.

The present invention is not limited to the type of method utilized to detect protein-protein interactions and therefore any method known in the art and variants thereof can be used. It is however better to use the method described in WO 99/42612 or WO 00/66722, both references incorporated herein by reference due to the methods' sensitivity, reproducibility and reliability.

10

15

20

25

30

Protein-protein interactions can also be detected using complementation Pelletier such those described by et ·al at assays as http://www.abrf.org/JBT/Articles/JBT0012/jbt0012.html, WO 00/07038 and W098/34120.

Although the above methods are described for applications in the yeast system, the present invention is not limited to detecting protein-protein interactions using yeast, but also includes similar methods that can be used in detecting protein protein interactions in, for example, mammalian systems as described, for example in Takacs et al., Proc. Nat. Acad. Sci., USA, 90 (21):10375 (1993) and Vasavada et al., Proc. Nat. Acad. Sci., USA, 88 (23):10686-90 (1991), as well as a bacterial two-hybrid system as described in Karimov et al (1998), W099/28746, WO 00/66722 and Legrain et al FEBS Letters, 480 pgs. 32-36 (2001).

The above-described methods are limited to the use of yeast, mammalian cells and *Escherichia coli* cells, however the present invention is not limited in this manner. Consequently, mammalian and typically human cells, as well as bacterial, yeast, fungus, insect, nematode and plant cells are encompassed by the present invention and may be transfected by the nucleic acid or recombinant vector as defined herein.

Examples of suitable cells include, but are not limited to, VERO cells, HELA cells such as ATCC No. CCL2, CHO cell lines such as ATCC No. CCL61, COS cells such as COS-7 cells and ATCC No. CRL 1650 cells, W138, BHK, HepG2, 3T3 such as ATCC No. CRL6361, A549, PC12, K562 cells, 293 cells, Sf9 cells such as ATCC No. CRL1711 and Cv1 cells such as ATCC No. CCL70.

Other suitable cells that can be used in the present invention include, but are not limited to, prokaryotic host cells strains such as *Escherichia coli*, (e.g., strain DH5- α , *Bacillus subtilis*, *Salmonella typhimurium*, or strains of the genera of *Pseudomonas*, *Streptomyces* and *Staphylococcus*.

Further suitable cells that can be used in the present invention include yeast cells such as those of Saccharomyces such as Saccharomyces cerevisiae.

in 15

20

25

The bait polynucleotide, as well as the prey polynucleotide can be prepared according to the methods known in the art such as those described above in the publications and patents reciting the known method per se.

The bait polynucleotide of the present invention is obtained from genomic DNA of *Helicobacter pylori*. The prey polynucleotide is obtained from genomic DNA of *Helicobacter pylori*, variants of genomic DNA of *Helicobacter pylori*, and fragments from the genome or transcriptome of *Helicobacter pylori* ranging from about 20 to 5000. The prey polynucleotide is then selected, sequenced and identified.

A genomic DNA prey library is prepared from the *Helicobacter pylori* and constructed in the specially designed prey vector pP6 as shown in Figure 10 after ligation of suitable linkers such that every genomic DNA insert is fused to a nucleotide sequence in the vector that encodes the transcription activation domain of a reporter gene. Any transcription activation domain can be used in the present invention. Examples include, but are not limited to, Gal4,YP16, B42, His and the like.

Toxic reporter genes, such as CATR, CYH2, CYH1, URA3, bacterial and fungi toxins and the like can be used in reverse two-hybrid systems.

The polypeptides encoded by the nucleotide inserts of the genomic DNA prey library thus prepared are termed "prey polypeptides in the context of the presently described selection method of the prey polynucleotides.

The bait polynucleotide can be inserted in bait plasmid as illustrated in Figure 1. The bait polynucleotide insert is fused to a polynucleotide encoding the binding domain of, for example, the Gal4 DNA binding domain and the shuttle expression vector is used to transform cells.

As stated above, any cells can be utilized in transforming the bait and prey polynucleotides of the present invention including mammalian cells, bacterial cells, yeast cells, insect cells and the like.

10

15

20

25

In an embodiment, the present invention identifies protein-protein interactions in yeast. In using known methods a prey positive clone is identified containing a vector which comprises a nucleic acid insert encoding a prey polypeptide which binds to a bait polypeptide of interest. The method in which protein-protein interactions are identified comprises the following steps:

21

- i) mating at least one first haploid recombinant yeast cell clone from a recombinant yeast cell clone library that has been transformed with a plasmid containing the prey polynucleotide to be assayed with a second haploid recombinant yeast cell clone transformed with a plasmid containing a bait polynucleotide encoding for the bait polypeptide;
- ii) cultivating diploid cell clones obtained in step i) on a selective medium; and
- iii) selecting recombinant cell clones which grow on the selective medium.

This method may further comprise the step of:

iv) characterizing the prey polynucleotide contained in each recombinant cell clone which is selected in step iii).

In yet another embodiment of the present invention, *in lieu* of yeast, *Escherichia coli is* used in a bacterial two-hybrid system, which encompasses a similar principle to that described above for yeast, but does not involve mating for characterizing the prey polynucleotide.

In yet another embodiment of the present invention, mammalian cells and a method similar to that described above for yeast for characterizing the prey polynucleotide are used.

By performing the yeast, bacterial or mammalian two-hybrid system it is possible to identify for one particular bait an interacting prey polypeptide. The prey polypeptide that has been selected by testing the library of preys in a screen

5

10

15

20

25

30

using the two-hybrid, two plus one hybrid methods and the like, encodes the polypeptide interacting with the protein of interest.

22

The present invention is also directed, in a general aspect, to a complex of polypeptides, polynucleotides encoding the polypeptides composed of a bait polypeptide or bait polynucleotide encoding the bait polypeptide and a prey polypeptide or prey polynucleotide encoding the prey polypeptide capable of interacting with the bait polypeptide of interest. These complexes are identified in Table 1, as the bait amino acid sequences and the prey amino acid sequences, as well as the bait and prey nucleic acid sequences.

In another aspect, the present invention relates to a complex of polynucleotides consisting of a first polynucleotide, or a fragment thereof, encoding a prey polypeptide that interacts with a bait polypeptide and a second polynucleotide or a fragment thereof. This fragment has at least 20 consecutive nucleotides, but can have between 20 and 5,000 consecutive nucleotides, or between 12 and 10,000 consecutive nucleotides or between 12 and 20,000 consecutive nucleotides.

The polypeptides of column 3 encoded by the polynucleotides of column 2 in Tables 2 and 7 and the polypeptides of column 5 encoded by the polynucleotides of column 3 in Table 8 according to the present invention and the complexes of the two polypeptides encoded by the sets of two polynucleotides also form part of the present invention. In yet another embodiment, the present invention relates to an isolated complex of at least two polypeptides encoded by two polynucleotides wherein said two polypeptides are associated in the complex by affinity binding and are depicted in Table 1 and Table 8.

In yet another embodiment, the present invention relates to an isolated complex comprising at least a polypeptide encoded by an ORF (HP####) of column 1 of Table 1 and a polypeptide encoded by an ORF (HP####) of column 2 of Table 1 and Table 8. The present invention is not limited to these polypeptide complexes alone but also includes the isolated complex of the two polypeptides

in which fragments and/or homologous polypeptides exhibiting at least 95% sequence identity, as well as from 96% sequence identity to 99.999% sequence identity.

Also encompassed in another embodiment of the present invention is an isolated complex in which the SID® polypeptide (see even SEQ ID Nos. from 2 to 3256 in column 3 of Table 2, even SEQ ID Nos. 6590 to 6594 in Table 7 and even SEQ ID Nos. 6596 to 6644 in Table 8.) of the prey polypeptides encoded by uneven SEQ ID Nos. 1 to 3255 in column 2 of Table 2, uneven SEQ ID Nos. 6593 in Table 7 and uneven SEQ ID Nos. 6595 to 6643 in Table 8) forming the isolated complex.

Besides the isolated complexes described above, nucleic acids coding for a Selected Interacting Domain (SID®) polypeptide or a variant thereof or any of the nucleic acids set forth in Tables 2, 7 and 8 can be inserted into an expression vector which contains the necessary elements for the transcription and translation of the inserted protein-coding sequence. Such transcription elements include a regulatory region and a promoter. Thus, the nucleic acid which may encode a marker compound of the present invention is operably linked to a promoter in the expression vector. The expression vector may also include a replication origin.

A wide variety of host/expression vector combinations are employed in expressing the nucleic acids of the present invention. Useful expression vectors that can be used include, for example, segments of chromosomal, non-chromosomal and synthetic DNA sequences. Suitable vectors include, but are not limited to, derivatives of SV40 and pcDNA and known bacterial plasmids such as col El, pCR1, pBR322, pMal-C2, pET, pGEX as described by Smith et al (1988), pM89 and derivatives thereof, plasmids such as RP4, phage DNAs such as the numerous derivatives of phage I such as NM989, as well as other phage DNA such as M13 and filamentous single stranded phage DNA; yeast plasmids such as the 2 micron plasmid or derivatives of the 2 micron plasmid, as well as centomeric and integrative yeast shuttle vectors; vectors useful in eukaryotic cells such as vectors useful in insect or mammalian cells; vectors derived from

30

5

10

15

20

25

10

20

25

30

combinations of plasmids and phage DNAs, such as plasmids that have been modified to employ phage DNA or the expression control sequences and the like.

For example in a baculovirus expression system, both non-fusion transfer vectors, such as, but not limited to pVL941 (BamHI cloning site Summers, pVL1393 (BamHI, Smal, Xbal, EcoRI, Notl, XmallI, Bg/II and Pstl cloning sites; Invitrogen) pVL1392 (Bg/II, Pstl, Notl, XmallI, EcoRI, Xball, Smal and BamHI cloning sites; Summers and Invitrogen) and pBlueBacIII (BamHI, Bg/II, Pstl, Ncol and HindIII cloning sites, with blue/white recombinant screening, Invitrogen), and fusion transfer vectors such as, but not limited to, pAc700 (BamHI and KpnI cloning sites, in which the BamHI recognition site begins with the initiation codon; Summers), pAc701 and pAc70-2 (same as pAc700, with different reading frames), pAc360 (BamHI cloning site 36 base pairs downstream of a polyhedrin initiation codon; Invitrogen (195)) and pBlueBacHisA, B, C (three different reading frames with BamHI, Bg/II, Pstl, Ncol and HindIII cloning site, an N-terminal peptide for ProBond purification and blue/white recombinant screening of plaques; Invitrogen (220) can be used.

Mammalian expression vectors contemplated for use in the invention include vectors with inducible promoters, such as the dihydrofolate reductase promoters, any expression vector with a DHFR expression cassette or a DHFR/methotrexate co- amplification vector such as pED (Pstl, Sall, Sbal, Smal) and EcoRl cloning sites, with the vector expressing both the cloned gene and DHFR; Kaufman, 1991). Alternatively a glutamine synthetase/methionine sulfoximine co-amplification vector, such as pEE14 (HindIII, Xball, Smal, Sbal, EcoRl and Bcll cloning sites in which the vector expresses glutamine synthetase and the cloned gene; Celltech). A vector that directs episomal expression under the control of the Epstein Barr Virus (EBV) or nuclear antigen (EBNA) can be used such as pREP4 (BamHI, Sfīl, Xhol, Notl, Nhel, HindIII, Nhel, Pvull and Kpnl cloning sites, constitutive RSV-LTR promoter, hygromycin selectable marker; Invitrogen) pCEP4 (BamHI, Sfīl, Xhol, Nod, Nhel, HindIII, Nhel, Pvull and Kpnl cloning sites, constitutive hCMV immediate early gene promoter, hygromycin selectable marker; Invitrogen), pMEP4 (Kpnl, Pvul, Nhel, HindIII,

15

20

25

Notl, Xhol, Sfil, BamHI cloning sites, inducible methallothionein IIa gene promoter, hygromycin selectable marker, Invitrogen), pREP8 (BamHI, Xhol, Notl, HindIII, Nhel and KpnI cloning sites, RSV-LTR promoter, histidinol selectable marker; Invitrogen), pREP9 (KpnI, Nhel, HindIII, Notl, Xhol, Sfil, BamHI cloning sites, RSV-LTR promoter, G418 selectable marker; Invitrogen), and pEBVHis (RSV-LTR promoter, hygromycin selectable marker, N-terminal peptide purifiable via ProBond resin and cleaved by enterokinase; Invitrogen).

Selectable mammalian expression vectors for use in the invention include, but are not limited to, pRc/CMV (*HindIII*, *BstXI*, *NotI*, *Sbal* and *Apal* cloning sites, G418 selection, Invitrogen), pRc/RSV (*HindII*, *Spel*, *BstXI*, *NotI*, *Xbal* cloning sites, G418 selection, Invitrogen) and the like. Vaccinia virus mammalian expression vectors (see, for example Kaufman 1991) that can be used in the present invention include, but are not limited to, pSC11 (*Smal* cloning site, TK-and β-gal selection), pMJ601 (*SaII*, *Smal*, *AfII*, *NarI*, *BspMII*, *BamHI*, *Apal*, *NheI*, *SacII*, *KpnI* and *HindIII* cloning sites; TK- and β-gal selection), pTKgptF1S (*EcoRI*, *PstI*, *SaIII*, *AccI*, *HindII*, *SbaI*, *BamHI* and *Hpa* cloning sites, TK or XPRT selection) and the like.

Yeast expression systems that can also be used in the present invention include, but are not limited to, the non-fusion pYES2 vector (Xbal, Sphl, Shol, Notl, GstXI, EcoRI, BstXI, BamHI, Sacl, Kpnl and HindIII cloning sites, Invitrogen), the fusion pYESHisA, B, C (Xbal, Sphl, Shol, Notl, BstXI, EcoRI, BamHI, Sacl, Kpnl and HindIII cloning sites, N-terminal peptide purified with ProBond resin and cleaved with enterokinase; Invitrogen), pRS vectors and the like.

Consequently, mammalian and typically human cells, as well as bacterial, yeast, fungi, insect, nematode and plant cells an used in the present invention and may be transfected by the nucleic acid or recombinant vector as defined herein.

Examples of suitable cells include, but are not limited to, VERO cells, HELA cells such as ATCC No. CCL2, CHO cell lines such as ATCC No. CCL61,

10

15

20

25

30

COS cells such as COS-7 cells and ATCC No. CRL 1650 cells, W138, BHK, HepG2, 3T3 such as ATCC No. CRL6361, A549, PC12, K562 cells, 293 cells, Sf9 cells such as ATCC No. CRL1711 and Cv1 cells such as ATCC No. CCL70.

Other suitable cells that can be used in the present invention include, but are not limited to, prokaryotic host cells strains such as *Escherichia coli*, $\{e.g., strain DH5-\alpha\}$, *Bacillus subtilis*, *Salmonella typhimurium*, or strains of the genera of *Pseudomonas*, *Streptomyces* and *Staphylococcus*.

Further suitable cells that can be used in the present invention include yeast cells such as those of Saccharomyces such as Saccharomyces cerevisiae.

Besides the specific isolated complexes, as described above, the present invention relates to and also encompasses SID® polynucleotides. As explained above, for each bait polypeptide, several prey polypeptides may be identified by comparing and selecting the intersection of every isolated fragment that are included in the same polypeptide, as set forth, in Example 5. Thus the SID® polynucleotides of the present invention are represented by the nucleic acid sequences of uneven SEQ ID Nos. 1 to 3255 in column 2 of Table 2, uneven SEQ ID Nos. 6589 to 6593 in Table 7 and uneven SEQ ID Nos. 6595 to 6643 in Table 8 encoding the SID® polypeptides of even SEQ ID Nos. 2 to 3256. of Table 2, the even SEQ ID Nos. 6590 to 6594 in Table 7 and the even SEQ ID Nos. 6596 to 6644 in Table 8.

The present invention is not limited to the SID® nucleic acid sequences as described in the above paragraph, but also includes fragments of these sequences having at least 6 consecutive nucleic acids, between 6 and 5,000 consecutive nucleic acids and between 6 and 10,000 consecutive nucleic acids and between 6 and 20,000 consecutive nucleic acids, as well as variants thereof. The fragments or variants of the SID® sequences possess at least the same affinity of binding to its protein or polypeptide counterpart, against which it has been initially selected. Moreover this variant and/or fragments of the SID® sequences alternatively can have between 95% and 99.999% sequence identity to its protein or polypeptide counterpart.

15

20

25

 \mathbb{I}^{-}

According to the present invention the variants can be created by known mutagenesis techniques either *in vitro* or *in vivo*. Such a variant can be created such that it has altered binding characteristics with respect to the target protein and more specifically that the variant binds the target sequence with either higher or lower affinity.

Polynucleotides that are complementary to the above sequences which include the polynucleotides of the SID®'s, their fragments, variants and those that have specific sequence identity are also included in the present invention.

The polynucleotide encoding the SID® polypeptide, fragment or variant thereof can also be inserted into recombinant vectors which are described in detail above.

The present invention also relates to a composition comprising the above-mentioned recombinant vectors containing the SID® polypeptides in Tables 2, 7 and 8, fragments or variants thereof, as well as recombinant host cells transformed by the vectors. The recombinant host cells that can be used in the present invention were discussed in greater detail above.

The compositions comprising the recombinant vectors can contain physiological acceptable carriers such as diluents, adjuvants, excipients and any vehicle in which this composition can be delivered therapeutically and can include, but are not limited to sterile liquids such as water and oils.

In yet another embodiment, the present invention relates to a method of selecting modulating compounds, as well as the modulating molecules or compounds themselves which may be used in a pharmaceutical composition. These modulating compounds may act as a cofactor, as an inhibitor, as antibodies, as tags, as a competitive inhibitor, as an activator or alternatively have agonistic or antagonistic activity on the protein-protein interactions.

The activity of the modulating compound does not necessarily, for example, have to be 100% activation or inhibition. Indeed, even partial activation or inhibition can be achieved that is of pharmaceutical interest.

10

15

20

25

The modulating compound can be selected according to a method which comprises:

- (a) cultivating a recombinant host cell with a modulating compound on a selective medium and a reporter gene the expression of which is toxic for said recombinant host cell wherein said recombinant host cell is transformed with two vectors:
 - (i) wherein said first vector comprises a polynucleotide encoding a first hybrid polypeptide having a DNA binding domain;
- (ii) wherein said second vector comprises a polynucleotide encoding a second hybrid polypeptide having a transcriptional activating domain that activates said toxic reporter gene when the first and second hybrid polypeptides interact;
- (b) selecting said modulating compound which inhibits or permits the growth of said recombinant host cell.

Thus, the present invention relates to a modulating compound that inhibits the protein-protein interactions of a complex of two polypeptides of Table 1 and Table 8. The present invention also relates to a modulating compound that activates the protein-protein interactions of a complex of two polypeptides of Table 1 and Table 8.

In yet another embodiment, the present invention relates to a method of selecting a modulating compound, which modulating compound inhibits the interactions of two polypeptides of Table 1. This method comprises:

(a) cultivating a recombinant host cell with a modulating compound on a selective medium and a reporter gene the expression of which is toxic for said recombinant host cell wherein said recombinant host cell is transformed with two vectors:

10.

15

20

- (i) wherein said first vector comprises a polynucleotide encoding a first hybrid polypeptide having a first domain of an enzyme;
- (ii) wherein said second vector comprises a polynucleotide encoding a second hybrid polypeptide having an enzymatic transcriptional activating domain that activates said toxic reporter gene when the first and second hybrid polypeptides interact;
- (b) selecting said modulating compound which inhibits or permits the growth of said recombinant host cell.

In the two methods described above any toxic reporter gene can be utilized including those reporter genes that can be used for negative selection including the URA3 gene, the CYH1 gene, the CYH2 gene and the like.

In yet another embodiment, the present invention provides a kit for screening a modulating compound. This kit comprises a recombinant host cell which comprises a reporter gene the expression of which is toxic for the recombinant host cell. The host cell is transformed with two vectors. The first vector comprises a polynucleotide encoding a first hybrid polypeptide having a DNA binding domain; and a second vector comprises a polynucleotide encoding a second hybrid polypeptide having a transcriptional activating domain that activates said toxic reporter gene when the first and second hybrid polypeptides interact.

In yet another embodiment a kit is provided for screening a modulating compound by providing a recombinant host cell, as described in the paragraph above, but instead of a DNA binding domain, the first vector comprises a first hybrid polypeptide containing a first domain of a protein. "The second vector comprises a second polypeptide containing a second part of a complementary domain of a protein that activates the toxic reporter gene when the first and second hybrid polypeptides interact.

In the selection methods described above, the activating domain can be p42 Gal 4, YP16 (HSV) and the DNA-binding domain can be derived from Gal4 or Lex

.15

20

25

A. The protein or enzyme can be adenylate cyclase, guanylate cyclase, DHFR and the like.

SID® in Tables 2, 7 and 8 may be used as modulating compounds.

In yet another embodiment, the present invention relates to a pharmaceutical composition comprising the modulating compounds for preventing or treating ulcers in a human or animal, most preferably in a mammal.

This pharmaceutical composition comprises a pharmaceutically acceptable amount of the modulating compound. The pharmaceutically acceptable amount can be estimated from cell culture assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes or encompasses a concentration point or range having the desired effect in an *in vitro* system. This information can thus be used to accurately determine the doses in other mammals, including humans and animals.

The therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or in experimental animals. For example, the LD50 (the dose lethal to 50% of the population) as well as the ED50 (the dose therapeutically effective in 50% of the population) can be determined using methods known in the art. The dose ratio between toxic and therapeutic effects is the therapeutic index which can be expressed as the ratio between LD50 and ED50 compounds that exhibit high therapeutic indexes.

The data obtained from the cell culture and animal studies can be used in formulating a range of dosage of such compounds which lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity.

The pharmaceutical composition can be administered via any route such as locally, orally, systemically, intravenously, intramuscularly, mucosally, using a patch and can be encapsulated in liposomes, microparticles, microcapsules, and

10

15

20

25

the like. The pharmaceutical composition can be embedded in liposomes or even encapsulated.

Any pharmaceutically acceptable carrier or adjuvant can be used in the pharmaceutical composition. The modulating compound will be preferably in a soluble form combined with a pharmaceutically acceptable carrier. The techniques for formulating and administering these compounds can be found in "Remington's Pharmaceutical Sciences" Mack Publication Co., Easton, PA, latest edition.

The mode of administration optimum dosages and galenic forms can be determined by the criteria known in the art taken into account the seriousness of the general condition of the mammal, the tolerance of the treatment and the side effects.

The present invention also relates to a method of treating or preventing ulcers in a human or mammal in need of such treatment. This method comprises administering to a mammal in need of such treatment a pharmaceutically effective amount of a modulating compound which binds to a targeted bacterial protein. In a preferred embodiment, the modulating compound is a polynucleotide which may be placed under the control of a regulatory sequence which is functional in the mammal or human.

In yet another embodiment, the present invention relates to a pharmaceutical composition comprising a SID® polypeptide, a fragment or variant thereof. The SID® polypeptide, fragment or variant thereof can be used in a pharmaceutical composition provided that it is endowed with highly specific binding properties to a bait polypeptide of interest.

The original properties of the SID® polypeptide or variants thereof interfere with the naturally occurring interaction between a first protein and a second protein within the cells of the organism. Thus, the SID® polypeptide binds specifically to either the first polypeptide or the second polypeptide.

10

15

20

25

Therefore, the SID® polypeptides of the present invention or variants thereof interfere with protein-protein interactions of *Helicotacter pylori* proteins or between *Helicobacter pylori* proteins and mammal, for example, human proteins.

Thus, the present invention relates to a pharmaceutical composition comprising a pharmaceutically acceptable amount of a SID® polypeptide or variant thereof, provided that the variant has the above-mentioned two characteristics; i.e., that it is endowed with highly specific binding properties to a bait polypeptide of interest and is devoid of biological activity of the naturally occurring protein.

In yet another embodiment, the present invention relates to a pharmaceutical composition comprising a pharmaceutically effective amount of a polynucleotide encoding a SID® polypeptide or a variant thereof wherein the polynucleotide is placed under the control of an appropriate regulatory sequence. Appropriate regulatory sequences that are used are polynucleotide sequences derived from promoter elements and the like.

Polynucleotides that can be used in the pharmaceutical composition of the present invention include the nucleotide sequence: of uneven SEQ ID Nos. 1 to 3255 in column 2 of Table 2, uneven SEQ ID Nos. 6589 to 6593 in Table 7 and uneven SEQ ID Nos. 6595 to 6643 in Table 8.

Besides the SID® polypeptides and polynucleotides, the pharmaceutical composition of the present invention can also include a recombinant expression vector comprising the polynucleotide encoding the SID® polypeptide, fragment or variant thereof.

The above described pharmaceutical compositions can be administered by any route such as orally, systemically, intravenously, intramuscularly, intradermally, mucosally, encapsulated, using a patch and the like. Any pharmaceutically acceptable carrier or adjuvant can be used in this pharmaceutical composition.

5

10

15

20

25

The SID® polypeptides as active ingredients will be preferably in a soluble form combined with a pharmaceutically acceptable carrier. The techniques for formulating and administering these compounds can be found in "Remington's Pharmaceutical Sciences" supra.

The amount of pharmaceutically acceptable SID® polypeptides can be determined as described above for the modulating compounds using cell culture and animal models.

Such compounds can be used in a pharmaceutical composition to treat or prevent ulcer.

Thus, the present invention also relates to a method of preventing or treating ulcer in a mammal said method comprising the steps of administering to a mammal in need of such treatment a pharmaceutically effective amount of:

- (1) a SID® polypeptide of even SEQ ID Nos. 2 to 3256 in column 3 of Table 2, even SEQ ID Nos. 6590 to 6594 in Table 7 and even SEQ ID Nos. 6596 to 6644 in Table 8 or variants thereof which binds to a targeted mammalian or typically human protein; or
- (2) or SID® polynucleotide encoding a SID® polypeptide of uneven SEQ ID Nos. 1 to 3255 in column 2 of Table 2, uneven SEQ ID Nos. 6589 to 6593 in Table 7 and uneven SEQ ID Nos. 6595 to 6643 in Table 8 or variants or fragments thereof wherein said polynucleotide is placed under the control of a regulatory sequence which is functional in said mammal; or
- (3) a recombinant expression vector comprising a polynucleotide encoding a SID® polypeptide which binds to a bacterial protein.

In another embodiment the present invention nucleic acids comprising a sequence which encodes the SID® proteins of Table 2 Table 7 and Table 8 and/or functional derivatives thereof are administered to modulate complex of Table 1 and Table 8 by way of gene therapy. Any of the methodologies relating to gene therapy available within the art may be

10

15

20

25

30

used in the practice of the present invention such as those described by Goldspiel et al Clin. Pharm. 12 pgs. 488-505 (1993).

Delivery of the therapeutic nucleic acid into a patient may be direct in vivo gene therapy (i.e., the patient is directly exposed to the nucleic acid or nucleic acid containing vector) or indirect ex vivo gene therapy (i.e., cells are first transformed with the nucleic acid in vitro and then transplanted into the patient).

For example for *in vivo* gene therapy, an expression vector containing the nucleic acid is administered in such a manner that it becomes intracellular; i.e., by infection using a defective or attenuated retroviral or other viral vectors as described, for example in U.S. Patent 4,980,286 or by Robbins et al, Pharmacol. *Ther.*, 80 No. 1 pgs. 35-47 (1998).

The various retroviral vectors that are known in the art are such as those described in Miller et al, *Meth. Enzymol.* 217 pgs. 581-599 (1993) which have been modified to delete those retroviral sequences which are not required for packaging of the viral genome and subsequent integration into host cell DNA. Also adenoviral vectors can be used which are advantageous due to their ability to infect non-dividing cells and such high-capacity adenoviral vectors are described in Kochanek, *Human Gene Therapy*, 10, pgs. 2451-2459 (1999). Chimeric viral vectors that can be used are those described by Reynolds et al, *Molecular Medecine Today*, pgs. 25 -31 (1999). Hybrid vectors can also be used and are described by Jacoby et al, *Gene Therapy*, 4, pgs. 1282-1283 (1997).

Direct injection of naked DNA or through the use of microparticle bombardment (e.g., Gene Gun®; Biolistic, Dupont) or by coating it with lipids can also be used in gene therapy. Cell-surface receptor s/transfecting agents or through encapsulation in liposomes, microparticles or microcapsules or by administering the nucleic acid in linkage to a peptide which is known to enter the nucleus or by administering it in linkage to a ligand predisposed to receptor-mediated endocytosis (See, Wu & Wu, J. Biol. Chem., 262 pgs. 4429-4432; (1987)) can be used to target cell types which specifically express the receptors of interest.

10 -

15

20

25

30

In another embodiment a nucleic acid ligand compound may be produced in which the ligand comprises a fusogenic viral peptide designed so as to disrupt endosomes, thus allowing the nucleic acid to avoid subsequent lysosomal degradation. The nucleic acid may be targeted *in vivo* for cell specific endocytosis and expression by targeting a specific receptor such as that described in W092/06180, W093/14188 and WO 93/20221. Alternatively the nucleic acid may be introduced intracellularly and incorporated within the host cell genome for expression by homologous recombination. See, Zijlstra et al, Nature, 342, pgs. 435-428 (1989).

In ex vivo gene a gene is transferred into cells in vitro using tissue culture and the cells are delivered to the patient by various methods such as injecting subcutaneously, application of the cells into a skin graft and the intravenous injection of recombinant blood cells such as hematopoietic stem or progenitor cells.

Cells into which a nucleic acid can be introduced for the purposes of gene therapy include, for example, epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes and blood cells. The blood cells that can be used include, for example, T-lymphocytes, B-lymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryocytes, granulocytes, hematopoietic cells or progenitor cells and the like.

In yet another embodiment the present invention relates to protein chips or protein microarrays. It is well known in the art that microarrays can contain more than 10,000 spots of a protein that can be robotically deposited on a surface of a glass slide or nylon filter. The proteins attach covalently to the slide surface, yet retain their ability to interact with other proteins or small molecules in solution. In some instances the protein samples can be made to adhere to glass slides by coating the slides with an aldehyde-containing reagent that attaches to primary amines. A process for creating microarrays is described, for example by MacBeath and Schreiber in *Science*, Volume 289, Number 5485, pgs, 1760-1763 (2000) or Service, *Science*, Vol. 289, Number 5485 pg. 1673 (2000). An

WO 02/066501 PCT/EP01/15428

5

10

15

20

25

30

apparatus for controlling, dispensing and measuring small quantities of fluid is described, for example, in U.S. Patent No. 6,112,605.

The present invention also provides a record of protein-protein interactions, PIM®'s, SID®'s and any data encompassed in the following Tables. It will be appreciated that this record can be provided in paper or electronic or digital form.

In yet another embodiment, the present invention relates to the classification of H. pylori within functional categories such as genes essential or non essential for viability using the general method described in Figure 18. In this regard, two exhaustive libraries of H. pylori ORFs were constructed in E.coli The first library contained every H. pylori (strain 26695) cloned individually (Library I) while the second one (Library II), contained these ORFs disrupted by a transposable element. These two ordered libraries are valuable tools for a large project of systematic inactivation of every ORF of the H. pylori-genome. They were used to develop a strategy to search at the genomic scale for genes essential for the viability of the bacterium grown in vitro. The inactivation strategy was applied to a series of 138 ORFs that were selected on two different criteria. Ninety six of them were previously shown to encode either proteins involved in protein-protein interaction in the two-hybrid yeast assay (Rain et al, 2001), and 42 encode H. pylori specific protein with no known function. The screening procedure led to the identification of 40 Putative Essential Genes (PEGs), of which 15 were shown to be true essential genes. The combination of both essentiality as well as the identification of interacting domains might serve as a direct pathway for the design of active compounds capable of inhibiting protein-protein interactions and possibly bacterial growth was the reasoning used behind this analysis.

Construction and validation of the two ordered libraries

Library I consisted of an individual and ordered (hp0001 to hp1590) bank of every putative ORF according to the information provided on the Webb TIGR site in 1997. Based on the 1590 ORFs identified at that time, 5' and 3'-oligonucleotides were synthesized with the characteristics described in Example 10 and in Table 3. Each ORF was cloned into a pILL570-• derivative plasmid, 3:6

kb in length. This derivative plasmid corresponds to pILL570 (Labigne et al, 1992) in which DNA from the HindIII site of the polylinker to the Aval site (position 1425 of the pBR322 bone) has been excluded by reverse PCR using plLL570 as a template and 570-1 plus 570-2 as primers (Table 4). Each ORF was cloned in such way that the 5'-end of the gene (including the ATG) was inserted immediately downstream the three transcriptional and translational stops of pILL570 (Labigne et al, 1992) to prevent toxicity of the recombinant proteins in E. coli. The library consists of 17 times 96-well plates (plate I.1 to plate XVII.1). The recombinant plasmids were transformed into DH5α E. coli cells harboring the pTCA plasmid, a plasmid that confers resistance to tetracycline, encodes the Tn3 transposase and is immune to Tn3 (Seifert et al, 1986). The presence of the two compatible plasmids pILL570-HP000X plus pTCA was checked by plasmid extraction and electrophoresis on gel individual isolated tetracycline, spectinomycin, kanamycin resistant clones. In addition, using primers 570-3 and 570-4 (corresponding to the bounderies of the cloning site on pILL570-•) the adequation between the size of the cloned PCR product and that of the corresponding ORF was confirmed. Library I consists of all the putative ORFs described on the TIGR Webb site in 1997 with the exclusion of 40 ORFs (hp01, 10, 46, 56, 94, 160, 223, 264, 289, 293, 399, 415, 435, 440, 453, 159, 464, 465, 488, 547, 607, 722, 790, 814, 846, 876, 884, 898, 968, 1007, 1069, 1205, 1248, 1304, 1358, 1394, 1452, 1460, 1497, 1511) for which either the initial gene amplification or the final cloning failed.

10

15

20

25

30

Library II consists of the random insertion of Tn3-Km into each of the recombinant plLL570-••hp000X plasmid. Process of disruption has been designed to generate multiple independent transposon insertions for each cloned ORF. Tn3-Km was shown to preferentially map into the *H. pylori* inserts due to both the intrinsic properties of Tn3 that transposes into AT rich DNA region and the requirement of maintaining intact replicative function and spectinomycin modifying enzyme (aadA). The efficiency of the whole procedure was checked for five plates. For those 5 plates, the resulting kanamycin transconjugants of 96 independent cloned ORFs were kept individually and as pools of plasmids. The 96 disrupted recombinant plasmids were extracted together and used as a

10

15

20

25

30

template for individual PCR assays using as primers the 38bp-R (Table 4) of the inverted repeats of Tn3 transposon and each of the 5'-end specific oligonucleotide used for the cloning of the ORFs. Figure 17 illustrates the results obtained for the disruption of the ORFs hp0099 to hp0198 (Plate II.2). This figure exemplifies first that multiple insertions of the transposon took place, second that for the majority trransposon insertion occurred at a distance ranging between 100 to 600 bp from the 5'-end of the ORF, a distance compatible with the promotion of gene replacement by allelic recombination.

Screening of Putative Essential Genes of H. pylori within a series of 138 selected ORFs

The ordered library of disrupted H. pylori ORFs in E. coli was used for the genomic screening of putative essential genes (PEGs), and the screening of a subset of 96 individual selected ORFs of H. pylori strain 26695 (Table 5) as genes encoding proteins demonstrating homodimeric or heterodimeric proteinprotein interactions [Rain, 2001 #14], and the screening of a subset of 42 ORFs encoding H. pylori specific predicted protein with no known function (Table 6). Included in the set of 138 ORFs were ORFs used as controls: ORFs known to be essential [groES (hp0011); holB (hp1231), dnaA (hp1529], or ORFs known to be non-essential for viability in vitro: urel, (hp0071); rdxA (hp0954); agt (hp1118) representive of various sizes. For the 138 ORFs, individual Tn3-Km disrupted recombinant plasmids were extracted from Library II, and used to transform H. pylori strain HAS141 (Janvier et al, 1999). This isolate was chosen for the initial screening due to its high natural transformation competency, two logs above that of the sequenced strain 26695, and its ability to colonize mouse stomach (Janvier et al, 1999). Kanamycin transformants were obtained for all but the hspA gene as expected, and 40 of the 138 tested ORFs, namely hp0061, 175, 377, 419, 553, 650, 739, 862, 928, 990, 1012, 1014, 1074, 1230, 1245, 1263, 1493 for the first series (Table 5), and hp0130, 231, 271, 358, 394, 659, 697, 699, 721, 726, 746, 838, 935, 947, 953, 973, 1023, 1028, 1039, 1053, 1085, 1265, 1568 (Table 6) which thus can be designated as Putative Essential Genes. Due to the presence of the two large terminal inverted repeats (38-bp in size) within Tn3-Km

15

20

25

30

which quickly reannealed during the amplification procedure, gene amplification of the disrupted allele using the respective 5' and 3' oligonucleotides of a given ORF often led to the production of a PCR product with a size similar to that of the parental allele, and thus was not helpful to confirm gene replacement of the parental by the disrupted allele. Thus, six individual kanamycin resistant transformants obtained for the 78 knock-out (KO) genes were controlled by gene amplification using the 5' and the 3' oligonucleotides of the KO-ORF respectively in pairs with the 38 bp (Table 4) of the inverted repeat of the transposon. Criteria for allelic replacement were that the sum of the size of the two PCR products be identical to that of the KO-ORF. The final identification of the disrupted ORF and of the site of insertion was done by sequencing one of the two PCR products. For ORFs with a size over 700 bp two or three different transposon insertions mapping in the middle of the ORF were commonly observed among the six analysed transformants. For a few ORFs, the 5' and the 3' oligonucleotides initially designed from the sequence of strain 26695, were unable to amplify the chromosome of the HAS141 parental strain due to intrinsic polymorphism. In these cases, the 5' and 3' oligos from ORFn+1 or ORFn-1 together with the 38 bp Unexpectedly, a few kanamycin resistant transformants were were used. obtained for hp1231 (holb), and hp1529 (dnaA). For these genes the insertion transposon mapped at the very 3' end of the genes, in contrast to the other genes where the transposable element mapped at any place but at a minimal distance of 300 bp of either end of the genes. These observations indicate that for some of the genes, known to be essential, the kanamycin resistant gene could be rescued, without allelic replacement, by integration of the whole plasmid via a single crossing-over. To estimate the frequency of this event, 260 preparations of chromosomal DNA from individual 210) or pooled (50) kanamycin resistant H. pylori transformants were spotted on nitrocellulose, denatured and hybridized with a probe consisting of the pILL570- vector. Of 260 DNA preparations tested, chromosomal DNA extracted from individual transformants of the disrupted hp1231(holB), 1514 (unknown) and 1529 (dnaA) as well as some (and not all) of the individual clones of hp0224 and hp0822 did hybridize with part of the vector confirming that a single crossing-over took place. These results underlined that

the *Tn3*-Km strategy is a powerful approach to be used as a first screen, at a genomic scale, for the identification of PEGs. The definitive assignment of a non-essential status cannot be done exclusively on the presence of kanamycin transformants, but had to be confirmed and tested for absence of vector DNA within the chromosome of transformants by hybridization.

Essentiality and functional analysis of 15 of the 40 ORFs identified as Putative Essential Genes

10

15

20

25.

According to an in-house definition, PEGs consist of ORFs that did not lead to the isolation of kanamycin transformants following the transformation of the parental isolate HAS141 with a pool of disrupted ORF. However, absence of kanamycin transformants cannot be directly associated with the identification of a true essential gene. Several explanations might account for the lack of knock out kanamycin resistant mutant, such as (i) absence of the specific gene in the tested strain, (ii) polar effect of the transposon on an essential ORF located downstream of the PEG, a property associated with miniTn3-Km (Skouloubris et al, 1998) (iii) experimental failure due to the small size of the ORF and of the bordering sequences required for allelic exchange. Thus, to confirm the essential character of a PEG (i.e., essentiality) additional experiments were achieved. For each of the 40 PEGs identified through the initial screening in strain HAS141 (Tables 5 & 6), the following criteria were used to confirm their essentiality. First, the distribution of the different ORFs of the genome by DNA/DNA hybridizations within clinical isolates to confirm their presence not only in the transformed isolate (HAS141), but also in every clinical isolate tested was studied. Second, a nonpolar mutation was introduced into the PEG cloned in E. coli following the approach depicted in the Materials and Methods section, performed by reverse PCR from plasmids of Library I. The recombinant plasmids consist, in each case, of the 0.9 kb-Kanamycin promoter-less cassette flanked respectively upstream and downstream with the 300 first and the 300 last nucleotides of the ORF to knock-out. In addition, the cassette carries a ribosome binding site and a start codon (ATG) in phase with the hundred 3'-terminal codons of the KO gene allowing the translation of the end of the gene to overcome any

WO 02/066501 PCT/EP01/15428

5

10

20

25

30

transcriptional/translational coupling effect. The resulting constructed plasmid was transformed in four different *H. pylori* genetic backgrounds: strains HAS141, N6, X47-2An and the sequenced strain 26695. Taking into account these criteria (Figure 17), the following conclusions were drawn relative to the 40 initially identified PEGs.

Strain HAS141 lacks ORFs hp0990 and hp1074. These absences accounted for the lack of mutant for these two ORFs, whereas the other 38 PEGs were found to be present in each of the 37 tested clinical isolates (Salama et al, 2000) and manuscript in preparation). The fact that no HAS141 clones resistant to kanamycin were obtained when transformed with the derivative plasmids containing the disrupted hp0990 and hp1074 ORFs confirmed that in the absence of portable homologous region integration of the plasmid does not occur. These two ORFs were not studied further since a non ubiquitous ORF has low probability to be essential and even if so, would not be a good candidate for *H. pylori* specific therapeutical drug design.

Non polar kanamycin mutants were unambiguously obtained in HAS141, N6, X47-2An as well as 26695 for ORFs hp0061, 419, 553, 650, 1263, and 1493 of the first series of genes encoding interacting protein (Table 5), and hp0130, 271, 358, 697, 699, 721, 726, 746, 838, 935, 947, 953, 973, 1023, 1028, 1039, 1053 (Table 6). Gene replacement of the parental allele by the deleted and disrupted allele was confirmed by testing the chromosome of the mutant for the disappearance of a PCR product with a size identical to that of the parental ORF and its replacement by the expected size (1.5 kb PCR product: 300 + 900+ 300 bp). When by chance, the parental ORF had a size ranging around 1.5 kb, gene replacement was confirmed by restricting the 1.5 kb PCR product with Smal to release the 0.9 kb-Km non-polar cassette.

For 15 of the 38 ubiquitous PEGs, we were unable to obtain kanamycin transformants when introducing a non polar mutation in N6, X47-2An, 26695, although the genes were found to be present in every isolates (ubiquitous). One or two very rare clones were obtained for some of the genes exclusively in HAS141. All these kanamycin resistant HAS141 transformants were positive

10

15

20

25

when tested by hybridization with the labeled pILL570-• vector used as a probe, again attesting for the presence of rare but possible single crossing-over seen under strong selective pressure. These 15 genes (hp0175, hp0231, hp0377, hp0394, hp0659, hp0739, hp0862, hp0928, hp1012, hp1014, hp1085, hp1230, hp1245, hp1265, hp1568) can thus be definitively recognized as genes essential for the viability of *H. pylori in vitro*. Among these 15 genes, 9 are known to be genes that encode proteins involved in protein-protein interactions, and 6 were selected as encoding *H. pylori* specific protein without known function. They encode proteins with properties that will be discussed and classified in regards to their potential as putative therapeutical targets.

Search for interacting proteins when using the 6 ubiquitous *H. pylori* specific essential genes as a bait in the two hybrid assay

The hp0231, hp0394, hp0659, hp1085, hp1265, and hp1568 ORFs were cloned in the pB6vector and used as individual bait for the identification of interacting proteins (Table 7).

Proteomic screens conducted for HP0231, HP1085, HP1568 did not provide data allowing assignation of a putative function and did not reveal homodimeric interaction underline the usefulness of the protein as a possible therapeutic target. Those genes remain ubiquitous, essential, *H. pylori* specific and without known function. In contrast, HP0394, HP0659 and HP1265 gave positive screens (Table 7).

Classification of twelve of the 15 ubiquitous essential genes.

The combination of both essentiality as well as the identification of interacting domains might serve as a direct pathway for the design of active compounds capable of inhibiting protein-protein interactions and possibly bacterial growth. Of the 15 ubiquitous essential genes identified by the procedure, 12 were shown to be involved in protein-protein interaction and could be classified in different categories with regards to their potential as putative therapeutic targets.

The first category consists of ubiquitous ORFs encoding proteins with heterodimeric protein-protein interactions in the two-hybrid assay where both partners are playing an essential role for the viability of *H. pylori* and at least one of the two partners is *H. pylori* specific. Four of the twelve essential ORFs answer these criteria *hp0394*, *hp0862*, *hp1230*, and *hp0659* which encode proteins with no known or putative function. Although initially annotated as *H. pylori* specific, the recent publication of the *Campylobacter* genome demonstrates for some of them the existence of homologues in this closely phylogenetically related bacteria, but no homologues have been identified in the other bacterial genomes so far sequenced.

10

20

25

30

43

The hp1230 gene encodes a protein that has been recognized via the two hybrid assay as an homodimeric protein which interacts with the predicted chromosomal replication initiator protein, DnaA, encoded by hp1529. The proteomic screen allowed the identification of a specific domain of interaction (SID) lying between AA31 and AA180 of HP1230 (SID1230) and a SID of 87 AA within the N-terminal domain of HP1529 or DnaA (AA12 to AA99) (SID1529) (Rain et al., 2001). To examine whether the HP1230/HP1529 interaction was specific and could serve as a target for screening of lead compounds with bactericidal activity, the oligonucleotide encoding SID1529 was randomly mutagenized, and selected, through the two-hybrid system, mutated sid that abolished the specific HP1230/HP1529 interaction. This allowed the demonstration of the fact that isoleucine 58 and Lysine 61 were involved in the HP1230/HP1529 interaction since a double mutant I58F/K61I within sid1529 abolished this interaction. This mutagenesis random procedure also led to the isolation of a mutated SID1529* (V53L) which confers a superbinder phenotype to HP1529 in the two-hybrid system. When overexpressed in the three-hybrid system (Tirode et al., 1997) under the control of the regulated Met25 promoter in vector p3H1 (Colland et al., 2001) (Figure 3), the superbinder SID1529* completely inhibits the HP1230/HP1529 interaction. Thus, oligopeptide -PNQLLCTTITAKYG-(SEQ ID No. 6588) or overlapping or combinatory derivatives have some potential as lead compounds to inhibit H. pylori growth.

Another example of this category of interest is the hp0862 gene. The two-hybrid screen procedure revealed interactions between the HP0862 gene product and the C-terminal domain (AA100 to AA191) of the thymidylate kinase (HP1474), an essential enzyme responsible for the first phosphorylation step in the conversion of deoxythymidine 5'-monophosphate to deoxythymidine 5'-diphosphate for the final production of dTTP. As for HP1230, the actual function of the HP0862 encoding gene is unknown, but its essential character and interaction with a known essential enzyme (Tmk) might orient further functional analysis, and encouraged the definition of more precise domain of interactions between the TmK protein and this new specific interacting protein.

The hp394 and hp659 might also enter this category. They both encode protein essential specific to *H. pylori*. The hp394 encodes a protein whose C-terminal domain (last 76 AA) interacts with the ß subunit of the acetylooenzyme A carboxylase transferase (HP950). This enzyme has an essential function in membrane lipid synthesis and catalyses the formation of malonyl-CoA, the first intermediate for fatty acid synthesis. The protein encoded by hp0659 interacts with a putative outer membrane protein HP0655 with no known function. The essential property of hp0655 has not yet been tested and thus the classification of the hp0659 gene in this first category has to be confirmed.

20

30

5

10

- The second category includes genes essential for *H. pylori* encoding predicted proteins with known functions. The characteristic of this category is that these genes essential in *H. pylori* have not been reported to be lethal in other organisms. Thus targeting the proteins encoded by these genes might be relevant of a selective drug design specifically directed against *H. pylori*. Three of the twelve essential genes displayed this characteristic: *hp0377* and *hp0175*, they both encode periplasmic proteins. *Hp0377* encodes a protein partially homologue to DsbC a thiol-disulfide interchange periplasmic protein involved in disulfide bond formation (Zapun *et al.*, 1995). So far, no other genes encoding Dsb-like proteins have been identified in the genome of *H. pylori* whereas in *€. coli*, as many as five proteins are required for disulfide bond formation in the periplasm. In *E. coli*, *dsbC* encodes a stable homodimer with both protein disulfide

15

25

30

isomerase and chaperone activities (McCarthy et al., 2000), and is not essential probably due to redundancy of the function. In contrast, in *H. pylori* we demonstrate the essential character of that gene. The HP0377 product interacts in the two-hybrid assay with the last 100 C-terminal amino acids (SID) of the homodimeric secreted cysteine containing protein encoded by hp0224. The HP0224 product is a methionine sulfoxide reductase homologue (MsrA). In *E. coli*, MsrA plays a role in response to oxidative damage by reducing the methionine sulfoxide residues (Moskovitz et al., 1995), and directly, or indirectly contributes to the maintenance of adhesins (Wizemann et al., 1996). The *H. pylori* MsrA homologue (HP0224) was identified as one of the major antigens released into the extracellular space (Cao et al., 1998). Thus, the HP0377 encoding DsbC is a good *H. pylori* specific target candidate because of the essential character unique to the bacterial species, and the accessibility of the protein within the periplasmic space.

The hp0175 gene is another representative of this category. The gene encodes a predicted peptidyl-propyl cis-trans isomerase, an enzyme that accelerates protein folding by catalyzing the cis-trans isomerization of proline imidic peptide bonds in oligopeptides. Two-hybrid screening identified HP0608, a *H. pylori* specific protein of unknown function, as interacting partner with HP0175. The essential character of the gene, documented in this study, as for HP0377, has not been reported for other microorganisms and appears unique to the species.

Finally, hp1265 is a very unique and specific target for H. pylori. This essential gene is part of a large cluster of 14 genes (hp1260 to hp1273) among which 12 encode homologues of 12 of the 14 subunits of the NADH oxidoreductase complex of E. coli. In E. coli inactivation of the genes encoding the different subunits (nuo) is not lethal for the bacterium. In H. pylori inactivation of hp1263 is not lethal, but inactivation of one of the two H. pylori specific subunit encoding gene is lethal, indicating that the HP1265 subunit which should be the subunit involved in the NADH binding has very unique properties deserving further functional investigations.

WO 02/066501 PCT/EP01/15428

- A third category, consists in ORFs that encoded conserved hypothetical proteins, distributed in almost all the sequenced bacterial genomes, for which no function has been assigned, nor the essentiality assessed. We report here on the essential character of two of them the hp0739 gene which encodes a protein that interacts with another conserved hypothetical but non essential protein (HP810), and hp1012. In the two sequenced H. pylori genomes (26695 and J99), the hp0739 gene is flanked by two genes involved in the biosynthesis of the peptidoglycan, and its involvement in this biosynthetic pathway remains to be explored. The hp1012 gene encoded a protein, which has similitude with some metallo-proteases, however the function of this specific protease is unknown. These two proteins with large distribution spectrum, so far unknown as essential genes, represent new putative targets.

10

15

20

25

30

- Finally, a fourth category, includes ORFs with known functions that were previously shown to be essential in other microorganisms. The present work allows us to extend this property to the H. pylori species, and reinforces their value as putative targets with large spectrum. The hp0928 gene is one of those; it was selected through the two-hybrid screen as an homodimer. By similarity, the assigned function was that of GTP cyclohydrolase (folE) involved in the first step of the biosynthetic pathway of tetrahydrofolate, the structure of which was shown to be a homodecameric complex form of two pentamers. inability to succeed in knocking out that gene, and its oligomeric structure supports the assigned function. The two-hybrid screening procedure delineates a domain of interaction consisting of 133 amino-acids between the FoÆ subunits. This domain might serve as a therapeutical target for the screening of lead compounds with large bacterial spectrum. The hp1014 gene (hdhA) encodes an NAD⁺-dependent oxidoreductase belonging to the short-chain dehydrogenase/reductase (SDR 1 family). The enzyme is known to require a tetrameric form to be active in E. coli (Yoshimoto et al., 1991) which was compatible with the homodimeric interaction observed in the two hybrid assay. The major interest of these two ORFs resides in their well known enzymatic activity, which provides a direct way to screen lead compounds capable of

25

abolishing the enzymatic activity through the disruption of the oligomeric interactions. The present work also classifies *hp1245* as an essential gene of this category. This gene encodes the SSB protein, the single strand binding protein, involved in DNA replication, recombination and DNA repair, and such observation is confirmatory of work previously done in other model microorganisms. HP1245 was found to interact with HP0650, a non–essential protein of unknown function, but also significantly with HP0661, a predicted ribonuclease H involved in DNA replication, a finding consistent with the HP1245 function.

In order to fully illustrate the present invention and advantages thereof, the following specific examples are given, it being understood that the same are intended only as illustrative and in nowise limitative.

EXAMPLES

- 15 <u>Example 1</u>: Preparation of a *Helicobacter pylori* genomic collection
 - 1.A. Fragment collection preparation arid transformation in E. coli
 - 1.B. Collection transformation in Saccharomyces cerevisiae
 - 1.C. Construction of bait plasmid
 - Example 2: Screening the collection with the two-hybrid in yeast system
- 20 2.A. The mating protocol
 - 2.B. The X-Gal overlay assay
 - 2.C. The luminometry assay
 - Example 3: Identification of positive clones
 - 3.A. PCR on yeast colonies
 - 3.B. Plasmid rescue from yeast by electroporation

15

20

Example 4: Detection of protein-protein interaction

Example 5: Identification of SID®

Example 6: Screening of modulating agent

Example 7: Gene therapy Example using SID® polypeptides

5 Example 8: Making of polyclonal and monoclonal antibodies

Example 9: Classification of genes of H. pylori

Example 10: Study of the interaction between two essential genes, HP1230-HP1529, by random mutagenesis.

Medium composition and standard protocols are available in Maniatis et al..

Example 1: Preparation of a Helicobacter pylori genomic collection

1.A. Collection preparation and transformation in Escherichia coli

1.A.1. Fragment of genomic DNA preparation

The *Helicobacter pylori* genomic DNA is fragmented in a nebulizer (GATC) for 1 minute, precipitated and resuspended in water.

The obtained nebulized genomic DNA is successively treated with Mung Bean Nuclease (Biolabs) (30 minutes at 30°C), T4 DNA polymerase (Biolabs) (10 minutes at 37°C) and Klenow enzyme (Pharmacia) (10 minutes at room temperature and 1 hour at 16°C).

DNA is then extracted, precipitated and resuspended in water.

1.A.2. Ligation of linkers to blunt-ended genomic DNA

Oligonucleotide PL160 (5' end phosphorylated) 1 µg /µl and PL159 2µg/µl.

10

15

20

25

Sequence of the oligo PL160: 5'-ATCCCGGACGAAGGCC-3' (SEQ ID NO. 3257)

Sequence of the oligo PL159: 5'-GGCCTTCGTCCGG-3' (SEQ ID NO. 3258)

Linkers were preincubated (5 minutes at 95°C, 10 minutes at 68°C, 15 minutes at 42°C) then cooled down at room temperature and ligated with genomic DNA inserts at 4°C overnight.

Linkers were further removed on a separation column (Chromaspin TE 400, Clontech), according to the manufacturers protocol.

1.A.3. Vector preparation

pACTIIst is successively digest with BamHI restriction enzyme (Biolabs) for 1 hour at 37°C, dephosphorylated with Calf Intestine Phosphatase (CIP) (Biolabs) and filled in with dGTP using Vent DNA polymerase (exo-) (Biolabs), extracted, precipitated and resuspended in water.

1.A.4. Ligation between vector and insert of gernomic DNA

The prepared vector is ligated overnight at 15°C with the genomic blunt ended DNA described in section 2 using T4 DNA ligase (Biolabs). The DNA is then precipitated and resuspended in water.

1.A.5. Library transformation in Escherichia coli

Transform DNA from section 1.A.4 into Electromax DH10B electrocompetent cells (Gibco BRL) with a Cell Porator apparatus (Gibe BRL). Add 1 ml SOC medium and incubate transformed cells at 37°C for 1 hour. Add 9 ml volume of SOC medium per tube and plate on LB+ampicillin medium. Scrape colonies with liquid LB medium. Aliquot and freeze at -80°C.

The obtained collection of recombinant cell clones was named HGXBHP1 (CNCM N° I-2181).

1.B. Collection transformation in Saccharomyces cerevisiae

20

The Saccharamyces cerevisiae strain (Y187 (MATα GalΔ Gal80Δ ade2-101 His3 Leu2-3, -112 Trp1-901 Ura3-52 URA3::UASGAL1-LacZ Met)) transformed with the HGXBHP1 *H. pylori* genomic DNA library.

The plasmid DNA contained in £. coli were extracted (Qiagen) from aliquoted £. coli frozen cells (1.A.5.).

Grow Saccharomyces cerevisiae yeast Y187 in YPGlu.

Yeast transformation is performed according to standard protocol (Giest et al. Yeast, 11, 355-360, 1995) using yeast carrier DNA (Clontech). This experiment leads to 10⁴ to 5 10⁴ cells/µg DNA. Spread 2 10⁴ cells on DO-Leu medium per plates. Aliquot and freeze at -80°C.

1. C. Construction of bait plasmid

The genomic amplification of the ORF is obtained by PCR using the Pfu proofreading *Taq* polymerase (Stratagene) and 200 ng of genomic DNA as the template. PCR primers are chosen in regions flanking the ORF.

5 Set up the PCR program as followed:

Check amplification on agarose gel.

Purify PCR fragments with Qiaquick column (Qiagen) according to the manufacturer's protocol.

25 Digest purified PCR fragments with adequate restriction enzymes.

Purify PCR fragments with Qiaquick column (Qiagen) according to the manufacturer's protocol.

10

15

20

Ligate digested PCR fragments into an adequately digested and dephosphorylated bait vector (pAS2 $\Delta\Delta$) according to standard protocol (Maniatis et al.).

Transform into competent bacterial cells. Grow cells, extract DNA and sequence plasmid.

Example 2: Screening the collection with the two-hybrid in yeast system

2.A. The mating protocol

We have chosen the mating two-hybrid in yeast system (first described by Legrain et al., Nature Genetics, 1997, vol. 16, 277-282, Toward a functional analysis of the yeast genome through exhaustive two-hybrid screens) for its advantages but we could also screen the Helicobacter pylori collection in the classical two-hybrid system as described in Fields et al, or in a yeast reverse two-hybrid system.

The mating procedure allows a direct selection on selective plates because the two fusion proteins are already produced in the parental cells. No replica plating is required.

This protocol is written for the use of the library transformed into the Y187 strain. Before mating, transform *S. cerevisiae* (CG 1945 strain (MATa Gal4-542 Gal180-538 ade2-101 His3*200 Leu2-3,-112 Trp1-901 Ura3-52 Lys2-801 URA3::GAL4 17mers (X3)-CyC1TATA-LacZ LYS2::GAL1UAS-GAL1TATA-HIS3 CYH^R)) according to step 1.B and spread on DO-Trp medium.

Day 1, morning: preculture

Preculture of Y187 cells carrying the bait plasmid obtained at step 1.C. in 20 ml DO-Trp medium. Grow at 30°C with vigorous agitation.

Day 1, late afternoon: culture

Measure OD_{600} nm of the DO-Trp preculture of Y187 cells carrying the bait plasmid preculture. The OD_{600} nm must lie between 0.1 and 0.5 in order to correspond to a linear measurement.

Inoculate 150 ml DO-Trp at OD₆₀₀nm 0.006/ml, grow overnight at 30°C with vigorous agitation.

Day 2 : mating

Medium and plates

5 YPGlu plates

10 50 ml tube with 30 ml DO-Leu-Trp-His

100 ml flask with 20 ml of YPGlu

75 DO-Leu-Trp-His plates

2 DO-Leu plates 2 DO-Trp plates

2 DO-Leu-Trp plates

Measure OD₆₀₀nm of the DO-Trp culture. It should be around 1.

For the mating, you must use twice as many bait cells as library cells. To get a good mating efficiency, you must collect the cells at 108 cells per cm².

Estimate the amount of bait culture (in ml) that makes up 80 OD₆₀₀nm units for the mating with the prokaryote library.

Thaw a vial containing the HGXYHP1 library slowly on ice. Add the contents of the vial to 20 ml YPGlu. Let those cells recover at 30°C, under gentle agitation for 10 minutes.

Mating

Put the 80 OD₆₀₀nm units of bait culture into a 250 ml flask.

Add the HGXYHP1 library culture to the bait culture. Transfer the mixture of diploids into 50 ml sterile tubes. Centrifuge, discard the supernatant and resuspend in YPGlu medium.

Distribute cells in 400 μ l samples in YPGlu plates with glass beads. Spread cells by shaking the plates.

Incubate plates cells-up at 30°C for 4h30min.

Collection of mated cells

Wash and rinse plates and spread collected cells on DO-Leu-Trp-His+Tet plates.

10 Day 4

Selection of clones able to grow on DO-Leu-Trp-His+-Tetracyclin: this medium allows us to isolate diploid clones presenting an interaction.

Count the His+ colonies on control plates.

The number of His+ cell clones will define which protocol is to be processed:

- 15 Upon 20 X10⁶ His+ colonies
 - if the number of His+ cell clones > 285 : then process overlay and then luminometry protocols on blue colonies (2.B and 2.C).
 - If the number of His+ cell clones < 285 : process luminometry protocol (2.C).
 - The following step leads to the selection of the strongest interaction.

2.8. The X-Gal overlay assay

The X-Gal overlay assay is performed directly on the selective medium plates after scoring the number of His+ colonies.

Material

20

Set up a waterbath. The water temperature should be 50°C.

- 0.5 M Na₂HPO₄ pH 7.5.
- 1.2% Bacto-agar.
- 2% X-Gal in DMF.
- Overlay mixture: 0.25 M Na₂HPO₄ pH7.5, 0.5% agar, 0.1% SDS, 7% DMF
 (LABOSI), 0.04% X-Gal (ICN). For each plate, 10 ml overlay mixture are needed.
 - DO-Leu-Trp-His plates.
 - Sterile toothpicks.

Experiment

Temperature of the overlay mix should be between 45 and 50°C.

Pour the overlay-mix over the plates in portions of 10 ml.

Collect them when the top layer is settled.

incubate plates overlay-up at 30°C. Note the time.

Check for blue colonies regularly. If no blue colony appears, wait for overnight incubation. Mark with a pen and number the positives.

Streak the positives colonies on fresh DO-Leu-Trp-His plates with a sterile toothpick.

2. C. The luminometry assay

Grow His+ colonies overnight at 30°C in microtiter plates containing DO-Leu-Trp-His+Tetracyclin medium with shaking. The day after, dilute 15 times overnight culture into a new microtiter plate containing the same medium. Incubate 5 hours at 30°C with shaking. Dilute samples 5 times and read OD₆₀₀nm. Dilute again to obtain between 10,000 and 75,000 yeast cells/well in 100 µl final volume.

15

10

15

Per well, add 76 μ l of One Step Yeast Lysis Buffer (Tropix), 20 μ l Sapphirell Enhancer (Tropix), 4 μ l Galacton Star (Tropix), incubate 40 minutes at 30°C. Measure the β -Gal read-out (L) using a Luminometer (Trilux, Wallach).

Calculate value of OD_{600nm}xL and select interacting preys having the highest values.

At this step of the protocol, we have isolated diploid cell clones presenting interactions. The next step is now to identify polypeptides involved in the selected interactions.

Example 3: Identification of positive clones

3.A. PCR on yeast colonies

Introduction

PCR amplification of fragments of plasmid DNA directly on yeast colonies is a quick and efficient procedure to identify sequences cloned into this plasmid. It is directly derived from a published protocol (Wang H. et al., Analytical Biochemestry, 237, 145-146, 1996). However, it is not a standardized protocol: in our hands it varies from strain to strain, it is dependent of experimental conditions (number of cells, *Taq* polymerase source, etc). This protocol should be optimized to specific local conditions.

Materials

- For 1 well, PCR mix composition is:

32.5 μl water,

5 μΙ 10X PCR buffer (Pharmacia),

1 ul dNTP 10 mM.

0.5 μι Taq polymerase (5μι /μι) (Pharmacia),

25 0.5 μι oligonucleotide ABS1 10 pmole/μι:

5'-GCGTTTGGAATCACTACAGG-3' (SEQ ID NO. 3259)

0.5 μ1 oligonucleotide ABS2 10 pmole/μ1:

5'-CACGATGCACGTTGAAGTG-3' (SEQ ID NO. 3260)

- 1 N NaOH.

5 Experiment

Grow positive colonies overnight at 30°C on a 96 well cell culture cluster (Costar), containing 150 μ l DO-Leu-Trp-His+Tetracyclin with shaking. Resuspend culture and transfer immediately 100 μ l on a Thermowell 96 (Costar).

Centrifuge 5 minutes at 4,000 rpm at room temperature.

10 Remove supernatant. Dispense 5 μl NaOH in each well, shake 1 minute.

Place the Thermowell in the thermocycler (GeneAmp 9700, Perkin Elmer) 5 minutes at 99.9°C and then 10 minutes at 4°C.

In each well, add PCR mix, shake well.

The PCR program was set up as followed:

15	94°C	3 minutes	
	94°C	30 secondes	
	53°C	1 minute 30 secondes	x 35 cycles
•	72°C	3 minutes	
	72°C	5 minutes	
20 .	15°C	æ	· · · · · · · · · · · · · · · · · · ·

The quality, the quantity and the length of the PCR fragment was checked on an agarose gel. The length of the cloned fragment was the estimated length of the PCR fragment minus 300 base pairs that corresponded to the amplified flanking plasmid sequences.

3.B. Plasmids rescue from yeast by electroporation

Introduction

The previous protocol of PCR on yeast cell may not be successful, in such a case, plasmids from yeast by electroporation can be rescued. This experiment allows the recovery of prey plasmids from yeast cells by transformation of *E. coli* with a yeast cellular extract. The prey plasmid can then be amplified and the cloned fragment can be sequenced.

Material

Plasmid rescue

10 Glass beads 425-600 μm (Sigma)

Phenol/chloroform (1/1) premixed with isoamyl alcohol (Amresco)

Extraction buffer: 2% Triton X100, 1 % SDS, 100 mM NaCl, 10 mM TrisHCl pH 8.0, 1 mM EDTA pH 8.0.

Mix ethanol/NH₄Ac: 6 volumes ethanol with 7.5 M NH₄ Acetate, 70% Ethanol and yeast cells in patches on plates.

Electroporation

SOC medium

M9 medium

Selective plates: M9-Leu+Ampicillin

2 mm electroporation cuvettes (Eurogentech)

Experiment

20

Plasmid rescue

Prepare cell patch on DO-Leu-Trp-His with cell culture of section 2.C.

. 10

Scrape the cell of each patch into an Eppendorf tube, add 300 μl of glass beads in each tube, then, add 200 μl extraction buffer and add 200 μl phenol:chloroform: isoamyl alcohol (25:24:1).

Centrifuge tubes 10 minutes at 15,000 rpm.

5 Transfer 180 μl supernatant to a sterile Eppendorf tube and add to each 500 μl ethanol/NH₄Ac, vortex.

Centrifuge tubes 15 minutes, 15,000 rpm at 4°C

Wash pellet with 200 µl 70% ethanol, remove ethanol and dry pellet.

Resuspend pellet in 10 µl water. Store extracts at -20°C.

Electroporation

Material: Electrocompetent MC1066 cells prepared according to standard protocols (Maniatis).

Add 1 μ l of yeast plasmid DNA-extract to pre-chilled Eppendorf tube, and keep on ice.

15 Mix 1 μl plasmid yeast DNA-extract sample, add 20 μl electrocompetent cells and transfer in a cold electroporation cuvette.

Set the Biorad electroporator on 200 ohms resistance, 25 μ F capacity; 2.5 kVolts. Place cuvette in the cuvette holder and electroporate.

Add 1 ml SOC into the cuvette and transfer the cell-mix into a sterile Eppendorf tube. Let cells recover for 30 minutes at 37°C, spin the cells down 1 minute, 4,000x g and pour off supernatant. Keep about 100 µl medium and use it to resuspend the cells and spread them on selective plates (e.g., M9-Leu plates).

Incubate plates for 36 hours at 37°C.

Grow one colony and extract plasmids. Check presence and size of insert through enzymatic digestion and agarose gel. Sequence insert.

20.

10

15

20

25

Example 4: Protein-protein interaction

For each bait, the previously protocol leads to the identification of prey polynucleotide sequences. In order to identify a protein-protein interaction, we need to characterize the obtained prey polypeptide sequence regarding the *Helicobacter* pylori genome.

This may be accomplish with a software program names blastwun (available on the Internet site of the University of Washington http://bioweb.pasteur.fr/seqanal/interfaces/blastwu.htm, this is a development version of software for gene and protein identification through similarity searches of protein and nucleotide sequence databases).

Blastwun program compares prey polynucleotide insert sequence (rescued from prey plasmid) with whole *Helicobacter pylori* genome (available on NCBI web site: http://www.ncbi.nlm.nih.gov—under GenBank accession number AE000511). This comparison leads to prey polynucleotide localizations in the *H. Pylori* genome, each localization having a score depending on the homology of sequence. For each prey polynucleotide, we consider the localization with the highest score and, if the insert sequence is included in and is in phase with an Open Reading Frame, we can identify one prey polypeptide interacting with one bait polypeptide.

Helicobacter pylori ORF's sequences are available on the World-Wide Web site of The Institute for Genomic Research (TIGR) at http://www.tigr.org/tdb/mbd/hpdb/hpdb/hpdb.htlm.

This web page allows several requests concerning Helicobacter pylori's genome, in particular, its ORF sequence. To get the sequences of specific ORF's, click on the ewindow named "HP#" and click search. This operation leads to a new web page presenting nucleic and peptide sequence of the specific ORF.

See Table 1 : Protein-protein interactions in Helicobacter pylori.

Example 5: Identification of SID®

15

20

25

Experiment results in step 4. sequences of each prey fragment encoding for an interacting prey polypeptide.

By comparing and selecting the intersection of every isolated fragments that are included in the same polypeptide, we define the Selected Interacting Domain (SID®) see Figure 15.

See results in Table 2.

Example 6: Screening of modulating agent

Select one specific interaction.

Transform a permeabilized yeast cell with plasmids containing bait polypeptide and prey polypeptide of the specific interaction.

Plate a top agar containing transformed permeabilized yeast cells on square boxes (that already contains agarose gel).

Apply by spotting the compounds to test on top agar as soon as it is solidified. Incubate overnight at 30°C.

Analyse results : select lead compounds that prevent transformed permeabilized yeast cells from growing.

Example 7: Gene therapy Example using SID® polypeptides

An expression vector containing the SID® polynucleotide is made in the manner described in U.S. Patent 4,980,286. It is then administered to patients to treat *H. pylori* infections.

Example 8: Making of polyclonal and monoclonal antibodies

The protein-protein complex of Table 1 was injected into mice and polyclonal and monoclonal antibodies were made following the procedure set forth in Sambrook et al *supra*.

More specifically mice are immunized with an immunogen comprising complexes conjugated to keyhole limpet hemocyanin using glutaraldehyde or

10

15

20

25

30

EDC as is well known in the art. The complexes can also be stabilized by crosslinking as described in WO 00/37483. The immunogen is then mixed with an adjuvant. Each mouse receives four injections of 10 μg to 100 μg of immunogen, and after the fourth injection, blood samples are taken from the mice to determine if the serum contains antibodies to the immunogen. Serum titer is determined by ELISA or RIA. Mice with sera indicating the presence of antibody to the immunogen are selected for hybridoma production.

Spleens are removed from immune mice and single-cell suspension is prepared (Harlow et al 1988). Cell fusions are performed essentially as described by Kohler et al. Briefly, P365.3 myeloma cells (ATTC Rockville, Md) or NS-1 myeloma cells are fused with spleen cells using polyethylene glycol as described by Harlow et al. Cells are plated at a density of 2 x 10⁵ cells/well in 96-well tissue culture plates. Individual wells are examined for growth and the supernatants of wells with growth are tested for the presence of Table 1 complex-specific antibodies by ELISA or RIA using the Table 1 complex as a target protein. Cells in positive wells are expanded and subcloned to establish and confirm monoclonality.

Clones with the desired specificities are expanded and grown as ascites in mice or in a hollow fiber system to produce sufficient quantities of antibodies for characterization and assay development. Antibodies are tested for binding to bait polypeptide (from column 1 of Table 1) alone or to prey polypeptide (from column 2 of Table 1) alone, to determine which are specific for the Table 1 complex as opposed to those that bind to the individual proteins.

Monoclonal antibodies against each of the complexes set forth in Table 1 are prepared in a similar manner by mixing specified proteins together, immunizing an animal, fusing spleen cells with myeloma cells and isolating clones which produce antibodies specific for he protein complex, but not for individual proteins.

Example 9: Classification of genes of *H. pylori* within function categories at the genomic scale using 2 exhaustive libraries in *E. coli*

10

15

20

1. Bacterial strains, growth and storage conditions.

Escherichia coli strains DH5α (BRL) HB101 (Boyer and Roulland-Dussoix, 1969) and NS2114 (Rif^R) (Seifert et al., 1986) were used as hosts for plasmid cloning and disruption experiments and were grown at 37°C in L-broth (10 g of tryptone, 5 g of yeast extract and 5 g of NaCl per liter, pH 7.0) or on L-agar plates (1.5% agar) at 37°C. Antibiotics were used at the following final concentrations (µg/ml) unless indicated in the text: spectinomycin:100 (Upjohn Laboratories, Paris, France), tetracycline: 8 (Sigma Chemicals, Saint-Quentin Fallavier, France), kanamycin: 25 (Serva, Frankfurt, Germany), rifampicine: 100 ug (Sigma Chemicals). Independent recombinant £. coli were saved by storing up to 96 clones individually in 96-well microtitre plates; clones were inoculated into L-broth supplemented with 8 μg/ml tetracycline, 100 μg/ml spectinomycin and 7% DMSO (Sigma) and stored at -80°C. H. pylori strain 26695 (Tomb et al., 1997), HAS141 (Janvier et al., 1999), N6 (Ferrero et al., 1992), X47-2an (GUY et al., 1999) were routinely cultured on 10% horse blood agar medium (Blood Agar Base no. 2; Oxoid, Lyon, France) or in Brucella broth supplemented with 10 % Fecal Calf Serum (Gibco). Solid and liquid media contained supplements at the following final concentrations: 10 µg vancomycin (Dakota Pharmaceuticals, Creteil, France), 2.5 IU polymyxin (Pfizer Laboratories, Orsay, France), 5 μg trimethoprim (Sigma) and 4 µg amphotericin B (Bristol-Myers Squibb, Paris, France)/ml. Plates were incubated at 37°C under microaerobic conditions in an anaerobic jar with a carbon dioxide generator (CampyGen, Oxoid) without catalyst. H. pylori that had undergone chromosomal allelic exchange were selected on medium supplemented with 25 µg kanamycin.

25

30

Production of amplicons corresponding to each of the 1590 ORFs originally identified by TIGR in strain 26695: 1621 pairs of forward and reverse oligonucleotides targeting the 1590 ORFs of the genome of strain 26695, as assigned on the Webb site in 1997, were designed and synthesized by Eurogentec (Bel S.A., Seraing, Belgium). Pairs (sense and antisense, Table 3) of oligonucleotides were designed in order to allow full length amplification of each of the ORFs, with the exception of ORFs with a size over 3 kb that were split into

two or three PCR products. Every forward and reverse 21 bp-oligonucleotide was tagged respectively at its 5'extremity with a CAUCAUCAU (Seq ID No.3261) and a CUACUACUA (SEQ ID No. 3262) sequence. Genomic DNA of *Hp* strain 26695, prepared from cesium chloride extraction (Labigne-Roussel *et al.*, 1988), was used as a template for PCR. Seventeen times 96 amplicons were produced by polymerase chain reactions (PCR) using a PCR-express thermal cycler through 40 cycles consisting of a denaturation step of 94°C for 2 mn, a primer annealing step of 50°C for 30 sec. and an extension step at 72°C for 2 mn, under a 96-well format. The amplicons were controlled for size and quality (single band) on agarose gel.

Systematic UDG cloning of the ORFs of H. pylori strain 26695

5

10

15

20

25

30

The cloning of the 96 amplicons was performed using the ligation-independent method described by Rashtchian (Rashtchian, 1995). First the linear plLL570derivative vector was prepared by gene amplification using #570-1 and #570-2 (Table 4) as primers and the pILL570 plasmid (Labigne et al., 1992) as a template. Three microliters of individual HP0001 to HP1590 PCR products were mixed together with 2 µl of plLL570-• derivative vector (75 ng), 14 µl of 1XPCR buffer, 1 µl of uracil DNA glycosylase (UDG) in a 2000-µl 96-well disposable plate. The plates were incubated at 37°C for 30 mn allowing the enzymatic reaction as well as the hybridization between protruding and complementary extension hybridization to occur. Competent DH5 α cells (100 μ l) harboring the pTCA plasmid (Seifert et al., 1986) were added to each well, and the 96-well plate was further incubated for 45 mn on ice. One ml of prewarmed L-broth was added to each well, and the plate was then incubated for 90 mn at 37°C. Finally, a selective antibiotic cocktail containing spectinomycin, tetracycline was added to each well to positively select and enrich in pILL570- derivative recombinant plasmid transformed DH5α(pTCA) cells; plates were then incubated for another 13 hours at 37°C under agitation. Individual transformant colonies were isolated by spotting 10 µl of liquid culture from each well on square agar plates containing tetracycline and spectinomycin using a 96-well inoculator designed to deliver a 10 μl liquid volume; cloning of the PCR product was confirmed by mini-preparation recombinant plasmid restricted with *Clal-Aval*. They were stored in DMSO (7%) at -80°C under a 96-well format as "library I" consisting of plate 1.1 to plate XVII.1.

5

10

15.

20

25

30

Systematic disruption of the recombinant plasmids by transposon mutagenesis in E. coli. Transposon mutagenesis of individual E. coli clones was performed using the mini-Tn3-Km transposon as previously described by Jenks et al. (Jenks et al., in press). All manipulations were performed in a 96-well format and four independent transposon mutageneses were carried out in parallel so as to saturate the mutagenesis disrupting process with independent events. Briefly, the stored microtitre plates containing the individual E. coli DH5a clones that harbored the pTCA plus the recombinant plLL570- derivative plasmids were thawed and used to inoculate fresh plates. Plasmid plLL553 harboring the mini-Tn3-Km transposon (Seifert et al., 1986) (Labigne, 1997) (a low copy autotransferable plasmid pOX38 derivative) was transferred into these £. coli DH5a clones by conjugation. Transconjugates harboring all three plasmids (recombinant pILL570- derivative, pTCA and pILL553), were selected by spotting 10 µl of the mating mixture on L-agar containing 25 µg/ml kanamycin, 8 μg/ml tetracycline and 100 μg/ml spectinomycin. Cointegrates were transferred by conjugation into E. coli NS2114SmRif carrying the cre gene. Positive . selection of resolved forms of the cointegrates was obtained by growth on L-agar containing 100 μg/ml rifampicin (Sigma), 625 μg/ml kanamycin, 625 μg/ml spectinomycin and 625 µg/ml streptomycin. A pool of each TnKm disrupted recombinant plasmids was stored as individual stock of disrupted ORFs at -80°C in DMSO (7%), designated "library II" consisting of plate I.2 to plate XVII.2.

DNA preparation and standard molecular biology techniques. The alkaline lysis procedure (Sambrook et al., 1989) was used for small-scale preparation and MIDI Qiagen (Qiagen, Courtaboeuf, France) columns were used for large-scale plasmid preparation. Whole cell genomic DNA from individual generated *H. pylori* mutants was extracted using the QIAamp Tissue Kit (Qiagen) according to the

10

15

manufacturer's instructions. Standard procedures for DNA/DNA hybridization were prepared on nitrocellulose membranes (Schleicher and Schuell,) according to the procedure of Sambrook et al. (Sambrook et al., 1989). They were hybridized under standard conditions with [α - 32 P]-deoxyribonucleotide probes labeled by random priming using the MegaPrime DNA system (Amersham) according to the manufacturer's instructions.

Transformation of *H. pylori*. *H. pylori* strains were naturally transformed with circular plasmid DNA ($\sim 2~\mu g$ per transformation). Briefly, bacteria were inoculated as 1 cm patches and grown for 5 h before addition of 10 μl supercoiled plasmid DNA. Each disrupted plasmid consisting either of a pool of disrupted plasmids when originating from library II or of a single recombinant plasmid for the non polar mutation construction was added to 4 independently prepared patches of *H. pylori*. After further incubation for 18 h, the bacteria from each individual patch were harvested and plated directly onto a single plate of selective medium (kanamycin, 25 $\mu g/m l$). Six individual kanamycin transformants were then subcultured. Chromosomal DNA was extracted using QiAmp kit extraction, and the constructed mutant characterized by several PCR controls and/or hybridization as described in the result section.

20

25

30

Introduction of a non polar mutation in a selected ORF (HP000X)

For a given cloned ORF (HP000X) present in Library I, the recombinant plasmid was prepared and used as a template for reverse PCR performed with two oligonucleotides. Oligonucleotide HP000X-1 consists of 24 nucleotides complementary to an intragenic sequence located 300 bp downstream the 5'-end of the gene, and HP000X-2 consists of 24 nucleotides complementary to an intragenic sequence located 300 bp upstream of the 3'-end of the gene. All the HP00X-1 and HP000X-2 oligos were tagged respectively at their 5'-end with a CGGGGTACC (SEQ ID No. 3261) (KpnI) sequence and at their 3'-end with a CGCGGATCC (SEQ ID No. 3262) (BamHI) sequence (Table 4). Following reverse amplification with high fidelity Taq polymerase (Boerhinger) from the given cloned ORF, 5 µI of PCR product were restricted with DpnI in order to

10

eliminate the template molecule, then restricted with *Kpnl* and *8amHl* and directly ligated to the promoterless non polar *Kpnl-BamHl* kanamycin cassette (0.9 kb) previously described (Skouloubris et al., 1998). Transformants were selected on spectinomycin containing plates. Recombinant plasmids were then purified, controlled, and introduced by natural transformation into *H. pylori* cells.

Example 10 – Study of the interaction between two essential genes, HP1230-HP1529, by random mutagenesis.

- 1. Preparation of mutagenized SID1529 collection
- A. Collection preparation and transformation in Escherichia coli
 - i. A Random mutagenesis of SID1529 by PCR

Mutagenized SID1529 was obtained by PCR using the Taq polymerase (Stratagene) and 200 ng of Helicobacter pylori genomic DNA and the following oligonucleotides:

15 5'-ATTTGCGGCCGCAATCTTGGCGCTAGTCAAACAA-3' (SEQ ID No. 3263)

5'-CCGGGATCCTCAAGATTGGGCGTTAATTTGGAT-3' (SEQ ID No. 3264)

The PCR program was set up as follows:

20

94° 1'

45° 1' x 30 cycles

75° 1'

10

The PCR conditions were as follows:

KCl (50 mM), Tris pH 9.0 (10 mM), MgCl₂ (7 mM), MnCl₂ (0.2 mM)

The amplification was checked by agarose gel electrophoresis.

B. Digestion of mutagenized SID1529 and pP7-centro vector

The PCR fragments were purified with Qiaquick column (Qiagen) according to the manufacturer's protocol and digested (Notl-BamHI). The vector (pP7-centro) (see, Figure 20) was digested (Notl-BamHI) and dephosphorylated according to standard protocol (Sambrook et al.).

- C. Library transformation in Escherichia coli
- The method followed in this section is the same as the one described in Example 1.A.5 above.
 - 2. Collection transformation in Saccharomyces cerevisiae
- The method followed in this section is the same as the one described in Example 1.B above.
 - 3. Construction of HP1230 bait plasmid

15

20

The genomic amplification of the HP1230 ORF was obtained by PCR using the Pfu proofreading Taq polymerase (Stratagene) and 200 ng of Helicobacter pylori genomic DNA as template.

5 The PCR program was set up as follows:

94°	45"	
94°	45"	
48°	45"	x 30 cycles
72°	6'	
72°	10'	

The amplification was checked by agarose gel electrophoresis.

The PCR fragments were purified with Qiaquick column (Qiagen) according to the manufacturer's protocol. The digested PCR fragments were ligated into an adequately digested (BamHI-PstI) and dephosphorylated bait vector (pB1) according to standard protocol (Sambrook *et al.*) and were transformed into competent bacterial cells. The cells were grown, the DNA extracted and the plasmid was sequenced.

4. Screening the mutagenized SID1529 collection with the HP1230 bait protein using two-hybrid in yeast

The method followed in this section is the same as the one described in Example 2 above, with the exception that DO Leu-Trp-His + Tet plates were replaced by DOLeu-Trp-His + Tet + 40 mM 3-AT plates.

5. Identification of positive clones

The method followed in this section is the same as the one described in Example 3 above.

WO 02/066501 PCT/EP01/15428

6. The SID 1529* (V53L) inhibits the interaction between HP1529 and HP1230

5

10

15

20

25

30

In the three-hybrid system, the HP1529 protein is expressed fused to the GAL4 Activation Domain (AD) in the pP6 plasmid, whereas HP1230 is introduced in the p3H1 vector in fusion with the DNA-binding domain (DBD) of GAL4. In addition, this vector contains the Met25 promoter which allow expression of a third partner in medium lacking methionine. After transformation of Y187 and CG1945 yeast by the pP6-HP1529 and p3H1-HP1230 vectors, respectively, both strains were mated. The resulting diploid strain was grown on a minimal medium lacking leucine and tryptophan to select for both plasmids (DO-2) and on DO-2 without histidine to select for interaction (DO-3). As a positive control, this strain was observed to grow on the selective medium for dilutions ranging from 1 to 10⁻⁴ (Figure 19, lane 1). This result shows an interaction between HP1230 and HP1529 proteins, as previously identified using library screening (Rain *et al.*, 2001).

Two different plasmids were used for this study: (i) the pP6 vector which contain the GAL4 activation domain (AD) (Rain *et al.*, 2001). One of the HP1529 fragments (nucleotides 1-1374) obtained by screening the HP1230 protein was selected and used as prey in the pP6 vector fused to GAL4 AD; (ii) the p3H1 vector which contains the DNA-binding domain (DBD) of GAL4 and a methionine-regulated Met25 promoter (Tirode *et al.*, 1997, J. Biol. Chem. 272: 22995-22999). The HP1230 encoding sequence of 540 bp was sub-cloned from pB1-HP1230 into the *BamHI/Pst*1 sites of p3H1 as fusion protein with GAL4-DBD giving p3H1-HP1230. In addition, the WT SID1529 or SID1529* (N38D-V53L) or SID1529* (V53L) were sub-cloned from pP7-centro (Notl-BamHI) to the *Notl/Bgl*II sites of p3H1-HP1230 under the control of the Met25 promoter. Expression from the Met25 promoter is obtained in the absence of methionine. As negative control, we used a prey encoding the HP0875 protein. All PCR fragments and in frame fusions were checked by sequencing.

The pP6 and p3H1 derived-vectors were used to transform the Y187 and CG1945 yeast strains, respectively. Both strains were mated in YPD buffer (Yeast Peptone Dextrose; Bio 101, Inc) for 4 hours at 30°C and the resulting

WO 02/066501 PCT/EP01/15428

diploid strain was selected on a minimal medium lacking leucine and tryptophane (DO-2). The interaction between proteins was observed in plates containing DO-2 deleted in histidine (DO-3) without methionine.

To assay whether The different versions of SID1529 can modulate this interaction, this protein was cloned in the p3H1-HP1230 vector under the control of the Met25 promoter. In the presence of the WT SID1529, growth was observed on DO3-Met medium thus showing that the WT SID1529 had little or no effect on the HP1230-HP1529 interaction (Figure 19, lane 2). In contrast, cells transformed with pP6-HP1529 and p3H1-HP1230-SID1529*(N38D-V53L) or p3H1-HP1230-SID1529* (V53L) were almost unable to grow on the selective medium (Figure 19, lanes 3-4). The growth of both strains in selective medium and in the presence of methionine (DO-3 + Met) was not affected, thus showing that the effect of SID1529* (N38D-V53L) or SID1529* (V53L) is a specific inhibition of the HP1230-HP1529 interaction (Figure 18, lanes 3-4). Taken together, these results clearly demonstrate that substitution of valine to leucine at position 53 of SID1529 led to complete inhibition of the HP1230-HP1529 interaction and confirm that SID1529 derivatived might have some potential as lead compounds to inhibit Helicobacter pylori growth.

Example 11: Modulating compounds/PIM screening

The following results obtained from these Examples, as well as the teachings in the specification are set forth in the Tables below.

While the invention has been described in terms of the various preferred embodiments, the skilled artisan will appreciate that various modifications, substitutions, omissions and changes may be made without departing from the scope thereof. Accordingly, it is intended that the present invention be limited by the scope of the following claims, including equivalents thereof,

NCUUCIU- MU USUUSEUTO I

5

10

15

20

25

35

REFERENCES

Akerley, B.J., Rubin, E.J., Camilli, A., Lampe, D.J., Robertson, H.M., and Mekalanos, J.J. (1998) Systematic identification of essential genes by *in vitro mariner* mutagenesis. *Proc Natl Acad Sci USA* **95**: 8927-8932.

Alm, R.A., Ling, L.S., Moir, D.T., King, B.L., Brown, E.D., Doig, P.C., *et al.* (1999) Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori [published erratum appears in Nature 1999 Feb 25:397(6721):719]. *Nature* **397**: 176-180.

- Bijlsma, J.J., Vandenbroucke-Grauls, C.M., Phadnis, S.H., and Kusters, J.G. (1999) Identification of virulence genes of Helicobacter pylori by random insertion mutagenesis. *Infect Immun* 67: 2433-2440.

 Blaser, M.J. (1993) *Helicobacter pylori*: microbiology of a 'slow' bacterial infection. *Trends Microbiol* 1: 255-260.
- Boyer, H.W., and Roulland-Dussoix, D. (1969) A complementation analysis of the restriction and modification of DNA in *Escherichia coli. J Mol Biol* 41: 459-472. Cao, P., McClain, M.S., Forsyth, M.H., and Cover, T.L. (1998) Extracellular release of antigenic proteins by *Helicobacter pylori*. *Infect Immun* 66: 2984-2986. Chalker, A.F., Minehart, H.W., Hughes, N.J., Koretke, K.K., Lonetto, M.A.,
- Brinkman, K.K., et al. (2001) Systematic identification of selective essential genes in *Helicobacter pylori* by genome prioritization and allelic replacement mutagenesis. *J Bacteriol* **183**: 1259-1268.
 - Chevalier, C., Thiberge, J.-M., Ferrero, R.L., and Labigne, A. (1999) Essential role of *Helicobacter pylori* g-glutamyltranspeptidase for the colonization of the gastric mucosa of mice. *Mol Microbiol* 31: 1359-1372.
 - Colland, F., Rain, J.-C., Gounon, P., Labigne, A., Legrain, P., and De Reuse, H. (2001) Identification of the *Helicobacter pyllori* anti-s²⁸ factor. *Molecular Microbiology*: in press.
- Ferrero, R.L., Cussac, V., Courcoux, P., and Labigne, A. (1992) Construction of isogenic urease-negative mutants of *Helicobacter pylori* by allelic exchange. *J Bacteriol* **174**: 4212-4217.
 - GUY, B., C. HESSLER, S. FOURAGE, B. ROKBI, M.-J. QUENTIN MILLET (1999). Comparison between targeted and untargeted systemic immunizations with adjuvanted urease to cure *Helicobacter pylori* infection in mice. Vaccine 17: 1130-1135.
 - Haas, R., Meyer, T.F., and van Putten, J.P. (1993) Aflagellated mutants of Helicobacter pylori generated by genetic transformation of naturally competent strains using transposon shuttle mutagenesis. *Mol Microbiol* 8: 753-760. Janvier, B., Grignon, B., Audibert, C., Pezennec, L., and Fauchère, J.L. (1999)
- Phenotypic changes of *Helicobacter pylori* components during an experimental infection in mice. **24**: 27-33.
 - Jenks, P.J., Chevalier, C., Ecobichon, C., and Labigne, A. (in press) Identification of non-essential *Helicobacter pylori* genes using random mutagenesis and loop amplification (RMLA). Res *Microbiol*.

- Labigne, A. (1997) Random mutagenesis of the *H. pylori* genome. In *Helicobacter pylori protocols*. Mobley, C.L.C.a.H.M.T. (ed) Totowa, N. J.: Humana Press, pp. 153-163.
- Labigne, A., Courcoux, P., and Tompkins, L. (1992) Cloning of Campylobacter jejuni genes required for leucine biosynthesis, and construction of leu-negative mutant of C. jejuni by shuttle transposon mutagenesis. *Research in Microbiology* **143**: 15-26.

Labigne-Roussel, A., Courcoux, P., and Tompkins, L. (1988) Gene disruption and replacement as a feasible approach for mutagenesis of *Campylobacter jejuni*. J. 1704, 1708

Bacteriol 170: 1704-1708.

McCarthy, M.A., Haebel, P.W., Torronen, A., Rybin, V., Baker, E.N., and Metcalf, P. (2000) Crystal structure of the protein disulfide bond isomerase, DsbC, from Escherichia coli. Nat Struct Biol 7: 196-199.

Moskovitz, J., Rahman, M.A., Stassman, J., Yancey, S.O., Kushner, S.R., Brot,

N., and Weissbach, H. (1995) Escherichia coli peptide methionine sulfoxide reductase gene: regulation of expression oand role in protecting against-oxidative damage. J Bacteriol 177: 502-507.

Odenbreit, S., Till, M., Hofreuter, D., Faller, G., and Haas, R. (1999) Genetic and functional characterization of the alpAB gene locus essential for the adhesion of

Helicobacter pylori to human gastric tissue. *Mol Microbiol* **31**: 1537-1548.

Ogura, K., Maeda, S., Nakao, M., Watanabe, T., Tada, M., Kyutoku, T., *et al.*(2000) Virulence factors of *Helicobacter pylori* responsible for gastric diseases in monoglian gerbil. *J Exp Med* **192**: 1601-1610.

Parsonnet, J., Friedman, G.D., Vandersteed, D.P., Chang, Y., Vogelman, J.H.,

- Orentreich, N., and Sibley, R.K. (1991) *Helicobacter pylori* infection and the risk of gastric carcinoma. *N Engl J* **325**: 1127-1131.

 Parsonnet, J., Hansen, S., Rodriguez, L., Gelb, A.B., Warnke, R.A., Jellum, E., et al. (1994) *Helicobacter pylori* infection and gastric lymphoma. *N Engl J Med* **330**: 1267-1271.
- Rain, J.-C., Selig, L., de Reuse, H., Battaglia, V., Reverdy, C., Simon, S., et al. (2001) The protein-protein interaction map of *Helicobacter pylori*. *Nature* **409**: 211-215.
 - Rashtchian, A. (1995) Novel methods for cloning and engineering genes using the polymerase chain reaction. *Current Opinion in Biotechnology* 6: 30-36.
- Salama, N., Guillemin, K., McDaniel, T.K., Sherlock, G., Tompkins, L., and Falkow, S. (2000) A whole-genome microarray reveals genetic diversity among Helicobacter pylori strains. Proc Natl Acad Sci USA 97: 14668-14673.
 Sambrook, J., Fritsch, E.F., and Maniatis, T. (1989) Molecular cloning: a laboratory manual. Cold Spring Harbor, N. Y.: Cold Spring Harbor Laboratory Press.
 - Seifert, H.S., Chen, E.Y., So, M., and Heffron, F. (1986) Shuttle mutagenesis: a method of transposon mutagenesis for Saccharomyces cerevisae. Proc Natl Acad Sci USA 83: 735-739.
- Skouloubris, S., Thiberge, J.M., Labigne, A., and De Reuse, H. (1998) The Helicobacter pylori Urel protein is not involved in urease activity but is essential for bacterial survival in vivo. *Infection & Immunity* 66: 4517-4521.

- Tirode, F., Malaguti, C., Romero, F., Attar, R., Camonis, J., and Egly, J.M. (1997) A conditionally expressed thirt partner stabilizes or prevents the formation of a transcriptional activator in a three-hybrid system. *J Biol Chem* **272**: 22995-22999. Tomb, J.-F., White, O., Kerlavage, A.R., Clayton, R.A., Sutton, G.G.,
- Fleischmann, R.D., et al. (1997) The complete genome sequence of the gastric pathogen Helicobacter pylori. Nature 388: 539-547.
 Wizemann, T.M., Moskovitz, J., Pearce, B.J., Cundell, D., Arvidson, C.G., So, M., et al. (1996) Peptide methionine sulfoxide reductase contributes to the maintenance of adhesins in three major pathogens. Proc Natl Acad Sci USA 93:
 - Yoshimoto, T., Higashi, H., Kanatani, A., Lin, X.S., Nagai, H., Oyama, H., et al. (1991) Cloning and sequencing of the 7 alpha-hydroxysteroid dehydrogenase gene from Escherichia coli HB101 and characterization of the expressed enzyme. J Bacteriol 173: 2173-2179.
- Zapun, A., Missiakas, D., Raina, S., and Creighton, T.E. (1995) Structural and functional characterization of DsbC, a protein involved in disulfide bond formation in *Escherichia coli*. *Biochemistry* 34: 5075-5089.

TABLE 1
Complexes of interacting proteins

1-Bait ORF	2-Prey ORF						
HP0338	HP0132	HP1542	HP1430	HP0336	HP1479	HP0547	HP0802
HP0338	HP0337	HP1542	HP1542	HP0336	HP1541	HP0662	HP0662
HP0339	HP0006	HP0452	HP0155	HP0697	HP0012	HP0662	HP1168
HP0339	HP0116	HP0452	HP1409	HP0697	HP0048	HP0661	HP0432
HP0339	HP0178	HP0452	HP1523	HP0697	HP0558	HP0661	HP0605
HP0339	HP0252	HP0336	HP0056	HP0697	HP0599	HP0661	HP0609
HP0339	HP0267	HP0336	HP0066	HP0697	HP0696	HP0661	HP0876
HP0339	HP0298	HP0336	HP0100	HP0697	HP0864	HP0661	HP1245
HP0339	HP0488	HP0336	HP0112	HP0697	HP1037	HP1492	HP0172
HP0339	HP0544	HP0336	HP0116	HP0697	HP1038	HP1492	HP0351
HP0339	HP0578	HP0336	HP0145	HP0697	HP1299	HP1492	HP0464
HP0339	HP0613	HP0336	HP0154	HP0697	HP1576	HP1492	HP0593
HP0339	HP0626	HP0336	HP0192	HP1423	HP0697	HP1492	HP1041
HP0339	HP0705	HP0336	HP0230	HP1423	HP0775	HP1492	HP1286
HP0339	HP0736	HP0336	HP0281	HP1423	HP1024	HP1492	HP1533
HP0339	HP0922	HP0336	HP0306	HP1423	HP1198	HP0667	HP0620
HP0339	HP0961	HP0336	HP0364	HP1423	HP1222	HP0667	HP0770
HP0339	HP1084	HP0336	HP0405	HP1423	HP1421	HP0667	HP1430
HP0339	HP1092	HP0336	HP0470	HP1423	HP1529	HP0667	HP1571
HP0339	HP1156	HP0336	HP0476	HP0691	HP0692	HP1073	HP0552
HP0339	HP1207	HP0336	HP0540	HP0691	HP1362	HP1073	HP0973
HP0339	HP1241	HP0336	HP0592	HP0224	HP0224	HP1073	HP1309
HP0339	HP1333	HP0336	HP0605	HP0224	HP0919	HP1073	HP1409
HP0339	HP1373	HP0336	HP0621	HP0224	HP1374	HP1198	HP0088
HP0339	HP1513	HP0336	HP0626	HP0224	HP1409	HP1198	HP0268
HP1427	HP0025	HP0336	HP0660	HP0692	HP0197	HP1198	HP0293
HP1427	HP0116	HP0336	HP0665	HP0692	HP0584	HP1198	HP0452
HP1427	HP0229	HP0336	HP0680	HP0692	HP0887	HP1198	HP0705
HP1427	HP0289	HP0336	HP0701	HP0071	HP0288	HP1198	HP0775
HP1427	HP0317	HP0336	HP0717	HP0071	HP0378	HP1198	HP0965
HP1427	HP0373	HP0336	HP0760	HP0071	1HP1165	HP1198	HP1032
HP1427	HP0810	HP0336	HP0774	HP0071	HP1450	HP1198	HP1114
HP1427	HP0896	HP0336	HP0775	HP0071	HP1503	HP1198	HP1124
HP1427	HP0913	HP0336	HP0779	HP0071	HP1503	HP1198]HP1198
HP1427	HP0944	HP0336	HP0786	HP0714	HP0116	HP1198	HP1274
HP1427	HP1120	HP0336	HP0794	HP0714	HP0289	HP1198	HP1378
HP1427	HP1157	HP0336	HP0795	HP0714	HP0527	HP1198	HP1411
HP1427	HP1157	HP0336	HP0850	HP0714	HP0528	HP1198	HP1541
HP1427	HP1157	HP0336	HP0858	HP0714	HP0552	HP1076	4HP0033
HP1427	HP1243	HP0336	HP0903	HP0714	HP0714]HP1076	HP0275
HP1427	HP1342	HP0336	HP0919	HP0714	HP0958	HP1076	HP0304
HP0218	HP0527	HP0336	HP0929	HP0714	HP1138	HP1076	HP0319
HP1301	HP0030	HP0336	HP0996	HP0714	HP1300	HP1076	HP0449
HP1301	HP0705	HP0336	HP1026	HP0714	HP1446	HP1076	HP0753
HP1301	HP0887	HP0336	HP1037	HP0428	HP0284	HP1076	HP0841
HP1301	HP1409	HP0336	HP1132	HP0428	HP0705	HP1076	HP1544
HP1542	HP0289	JHP0336	HP1236	HP0428]HP1350	HP1076	HP1563

HP1542	HP0289	HP0336	HP1241	HP0428	HP1409	HP1196	HP1409
HP1542	HP0289	HP0336	HP1266	HP1518	HP0116	HP1196	HP1514
HP1542	HP0601	HP0336	HP1274	HP1518	HP0705	HP1529	HP1230
1-Bait ORF	2-Prey ORF	1-Bait ORF	2-Prey ORF	1-Bait ORF	2-Prey ORF	1-Bait ORF	2-Prey ORF
HP1542	HP0609	HP0336	HP1325	HP1518	HP1065	HP0071	HP0278
HP1542	HP0610	HP0336	HP1332	HP1518	HP1489	HP0071	HP0570
HP1542	HP0610	HP0336	HP1434	HP0547	HP0299	HP0071	HP0775
HP1542	HP0740	HP0336	HP1452	HP0547	HP0601	HP0071	HP1340
HP1542	HP1273	HP0336	HP1452	HP0547	HP0687	HP0071	HP1409
HP0316	HP0621	HP0687	HP1503	HP0072	HP1489	HP0411	HP0304
HP0316	HP0895	HP0687	HP1506	HP0765	HP0764	HP0411	HP0464
HP0316	HP1350	HP0687	HP0174	HP0765	HP1024	HP0411	HP1019
HP1448	HP0107	HP0687	HP0687	HP0072	HP1489	HP0411	HP1326
HP0431	HP0547	HP0687	HP0759	HP0642	HP0642	HP0411	HP1453
HP0431	HP0705	HP0687	HP0942	HP1173	HP0528	HP0411	HP1470
HP0674	HP0033	HP0687	HP1185	HP1173	HP0595	HP0887	HP0610
HP0674	HP0862	HP0687	HP1212	HP1173	HP0610	HP0887	HP0887
HP0553	HP0553	HP0687	HP1510	HP1173	HP0816	HP0887	HP1157
HP0311	HP0312	HP0525	HP0389	HP1173	HP1553	HP0887	HP1464
HP1077	HP0304	HP0525	HP0513	HP1293	HP1198	HP1198	HP1032
HP1077	HP1472	HP0525	HP0525	HP1051	HP0435	HP1198	HP1218
HP0798	HP0798	HP0525	HP0550	HP1051	HP1513	HP1065	HP0918
HP0436	<u> </u>	HP0525	HP1409	HP1291	HP0278	HP1198	HP0264
HP0436	HP0072	HP0525	HP1411	HP1291	HP1283	HP1198	HP0371
HP0436	HP0858	HP0525	HP1451	HP1291	HP1409	HP1198	HP0615
HP0436	HP0887	HP0887	HP0459	HP1291	HP1553	HP1198	HP0655
HP0436		HP0887	HP0610	HP0084	HP0392	HP1198	HP0793
HP0436	HP1513	HP0887	HP0699	HP0084	HP0950	HP1198	HP1002
HP0071		HP0887	HP0887	HP0134	HP1012	HP1198	HP1048
HP0071	HP1550	HP0887	HP1157	HP0325	HP0246	HP1198	HP1069
HP1402	HP0420	HP0887	HP1460	HP0325	HP0278	HP0868	HP0088
HP1402	HP0621	HP0887	HP1464	HP0325	HP0338	HP0868	HP0327
HP1402	HP0657	HP0088	HP0011	HP0325	HP0399	HP0868	HP0869
HP1402	HP1355	HP0088	HP0088	HP0325	HP0449	HP0868	HP1142
HP0071	HP1409	HP0088	HP0221	HP0325	HP1321	HP0748	HP0048
HP0775			HP0437		HP1409	HP0748	HP0100
HP0775		HP0088	HP0464	HP0419	HP0321	HP0748	HP0695
HP0775	HP0231	HP0088	HP0792	HP0419	HP0419	HP0748	HP0736
HP0775	HP0285	HP0088	HP0974	HP0419	HP0862	HP0748	HP0748
HP0775	HP0378	HP0088	HP0988	HP0893	HP0862	HP0289	HP0289
HP0775	HP0621	HP0088	HP1045	HP0410	HP1080	HP0289	HP0289
HP0775	HP0645	HP0088	HP1096	HP0410	HP1198	HP0289	HP0610
HP0775	HP0705	HP0088	HP1198	HP1067	HP0392	HP0289	HP0887
HP0775	HP0775	HP0088	HP1535	HP0650	HP0012	HP0289	HP0922
		HP1298	HP0012	HP0650	HP0272	HP0289	HP1038
HP0775		HP1298	HP0278	HP0650	HP0317	HP0289	HP1542
HP0775		HP1298	HP0449	HP0650	HP1026	HP0289	HP0289
HP0775		HP1298	HP0522	HP0650	HP1245	HP0289	HP0289
HP0775 HP0775		HP1298 HP1298	HP0528	HP0650	HP1547	HP0289	HP0610
		HP1298	HP0696	HP0776	HP0067	HP0289	HP1355
HP1489	UL 1409	11730	HP0705	HP0776	HP0278	HP0383	HP0547

Brichoole ...

HP1086	HP0019	HP1298	HP0770	HP0776	HP1378	HP0507	HP0172
HP1086	HP0278	HP1298		HP0776	HP1409	HP0507	HP1409
HP1086	HP1409	HP1298		HP0897	HP0422	HP0507	HP1489
HP0071	HP0189	HP1298		HP0897	HP1362	HP1158	HP1158
HP0071	HP1072	HP1298		HP0895	HP0316	HP1158	HP1329
			2-Prey ORF				
HP0071	HP1165	HP0072 ·	HP0017	HP0895	HP0426	HP1158	HP1409
HP0071	HP1486	HP0072		HP0895	HP0894	HP1158	HP1527
HP0071	HP1503	HP0072	HP0156	HP0895	HP0895	HP0068	HP0070
HP0687	HP0705	HP0072	HP0216	HP0895	HP1409	HP0068	HP0118
HP0687	HP0889	HP0072	HP0437	HP0653	HP0247	HP0069	HP0067
HP0687	HP1072	HP0072	HP0610	HP0653	HP0653	HP0066	HP0066
HP0687	HP1329	HP0072		HP0653	HP1012	HP0187	HP0020
HP0687	HP1487	HP0072	HP1138	HP0653	HP1409	HP0187	HP0231
HP0187	HP0254	HP1033	HP0379	HP1238	HP1488	HP0870	HP0748
HP0187	HP0705	HP0064	HP0063	HP1444	HP0010	HP0870	HP1157
HP0187	HP0862	HP1032	HP0643	HP1444	HP0088	HP0870	HP1243
HP0187	HP1414	HP1032	HP0818	HP1444	HP0099	HP0199	HP0278
HP0187	HP1513	HP1032	HP1122	HP1444	HP0392	HP0199	HP0356
HP0958	HP0353	HP1032	HP1198	HP1444	HP0760	HP0199	HP0449
HP0958	HP0522	HP1032	HP1316	HP1444	1HP1116	HP0199	HP0891
HP0958	HP0582	HP0062	HP0062	HP1444	HP1332	HP0199	HP1198
HP0958	HP0714	HP0062	HP0103	HP1074	HP0347	HP0199	HP1313
HP0958	HP0884	HP0062	HP0170	HP1074	HP0593	HPC199	HP1314
HP0958	HP1428	HP0062	HP1156	HP1074	HP1278	HP0875	HP0874
HP0958	HP1462	HP0062	HP1409	HP1074	HP1316	HP0510	HP0347
HP0067	HP0069	HP0184	HP0123	HP1074	HP1399	HP0510	HP0510
HP0145	HP0116	HP0184	HP0238	HP1074	HP1493	HP1464	HP0132
HP0145	HP0281	HP0184	HP0354	HP1074	HP1497	HP1464	HP0740
HP0145	HP0468	HP0184	HP0609	HP0515	HP1409	HP1464	HP1198
HP0145	HP0887	HP0184	HP0655	HP0515	HP1537	HP1464	HP1464
HP0145	HP1274	HP0184	HP0705	HP0515	HP1561	HP1464	HP1510
HP0620	HP0620	HP0184	HP0793	HP1444	HP0088	HP0070	HP0068
HP0620	HP1409	HP0184	HP1409	HP1444	HP0392	HP0070	HP0070
HP0595	HP0025	HP0879	HP0033	HP1444	HP0422	HP0377	HP0033
HP0595	HP0060	HP0879	HP0066	HP1444	HP0655	HP0377	HP0145
HP0595	HP0595	HP0879	HP0252	HP1444	HP1332	HP0377	HP0183
HP0595	HP0870	HP0879	HP0401	HP1444	HP1493	HP0377	HP0194
HP0595	HP1052	HP0879	HP0407	HP1238	HP1238	HP0377	HP0224
HP0595	HP1430	HP0879	HP0421	HP1048	HP1198	HP0377	HP0285
HP0621	HP0609	HP0879	HP0626	HP0990	HP0085	HP0377	HP0399
HP0621	HP0610	HP0879	HP0649	HP0990	HP0116	HP0377	HP0486
HP0621	HP0862	HP0879	HP0703	HP0990	HP0321	HP0377	HP0854
HP1150	HP1451	HP0879	HP1248	HP0990	HP0663	HP0377	HP1409
HP0181	HP0807	HP0879	HP1274	HP0990	HP0727	HP0075	HP0075
HP1391	HP1041	HP0879	HP1379	HP0990	HP0909]HP0073	HP0067
HP0061	HP0066	HP0879	HP1422	HP0990	HP1213	HP0073	HP0232
HP0061	HP0978	HP0879	HP0012	HP0990]HP1327	HP0073	HP0705
HP0061	HP1409	HP0879	HP0116	HP0990	JHP1333	HP0762	HP0272
HP1390	HP0118	HP0879	HP0178	HP0990	HP1345	HP0762	HP0506
HP1390	HP0120	HP0879	HP0275	HP1046]HP0162	HP0762	HP0655

HP1390	HP0154	HP0879	HP0281	HP1046	HP0182	HP0762	HP1409
HP1390	HP0325	HP0879	HP0321	HP1046	HP0220	HP0156	HP0156
HP1390	HP0351	HP0879	HP0483	HP1046	HP0509	HP0452	HP0109
HP1390	HP0528	HP0879	HP0578	HP1046	HP0583	HP0452	HP0155
HP1390	HP0751	HP0879	HP0639	HP1046	HP0746	HP0452	HP0278
HP1390	HP0809	HP0879	HP0666	HP1046	HP0750	HP0452	HP0705
HP1390	HP0816	HP0879	HP0699	HP1046	HP0760	HP0452	HP1282
1-Bait ORF	2-Prey ORF	1-Bait ORF	2-Prey ORF				2-Prey ORF
HP1390	HP1012	HP0879	HP0735	HP1046	HP1024	HP0452	HP1409
HP1390	HP1081	HP0879	HP0821	HP1046	HP1197	HP1072	HP0096
HP1390	HP1188	HP0879	HP1012	HP1046	HP1312	HP1072	HP0792
HP1390	HP1379	HP0879	HP1160	HP1046	HP1464	HP1072	HP1321
HP1390	HP1486	HP0879	HP1299	HP1046	HP1488	HP1072	HP1409
HP1390	HP1513	HP0879	HP1374	HP1045	HP0325	HP1072	HP0050
HP0838	HP1409	HP0879	HP1459	HP1045	HP0750	HP1072	HP0231
HP1033	HP0599	HP0879	HP1513	HP1045	HP1205	HP1072	HP0263
HP1033	HP1513	HP0879	HP1567	HP0870	HP0317	HP1072	HP0705
HP1033	HP0651	HP1238	HP1238	HP0870	HP0488	HP1072	HP0836
HP1033	HP1105	HP1238	HP0655	HP0870	HP0595	HP1072	HP1430
HP0602	HP1402	HP1015	HP1521	HP0962	HP0617	HP1255	HP0687
HP0608	HP0175	HP0167	HP1035	HP0962	HP0621	HP1255	HP0969
HP0608	HP0589	HP1014	HP1014	HP0962	HP0655	HP1255	HP0969
HP0608	HP0626	HP1014	HP1409	HP0962	HP0750	HP1255	HP1072
HP0608	HP0919	HP0047	HP0047	HP0962	HP0996	HP1255	HP1077
HP0232	HP0605	HP0047	HP0048	HP0962	HP1019	HP1255	HP1114
HP0849	HP0056	HP0047	HP0695	HP0962	HP1024	HP1255	HP1290
HP0849	HP0066	HP1497	HP1074 .	HP0962	HP1025	HP1255	HP1550
HP0849	HP0109	HP1496	HP0769	HP0962	HP1188	HP0978	HP0979
HP0849	HP0116	HP0045	HP0045	HP0962	HP1274	HP0978	HP1583
HP0849	HP0132	HP0045	HP1409	HP0962	HP1353	HP0753	HP0030
HP0849	HP0197	HP0601	HP0547	HP0962	HP1379	HP0753	HP0033
HP0849	HP0213	HP0601	HP0753	HP0962	HP1409	HP0753	HP0115
HP0849	HP0354	HP0601	HP1154	HP0962	HP1478	HP0753	HP0197
HP0849	HP0370	HP0601	HP1377	HP0194	HP0592	HP0753	HP0492
HP0849	HP0373	HP0601	HP1409	HP0194	HP1377	HP0753	HP0747
HP0849	HP0417	HP1259	HP0006	HP0194	HP1488	HP0753	HP1035
HP0849	HP0452	HP1259	HP0025	HP0194	HP1489	HP0753	HP1098
HP0849	HP0466	HP1259	HP0025	HP0042	HP0017	HP0753	HP1274
HP0849	HP0476	HP1259	HP0026	HP0042	HP0051	HP0753	HP1454
HP0849	HP0512	HP1259	HP0033	HP0042	HP0054	HP0753	HP1485
HP0849	HP0539	HP1259	HP0212	HP0042	HP0278	HP0753	HP1523
HP0849	HP0569	HP1259	HP0231	HP0042	HP0381	HP0979	HP0977
HP0849	HP0570	HP1259	HP0252	HP0042	HP0419	HP0979	HP0979
HP0849	HP0583	HP1259	HP0280	HP0042	HP0723	HP0979	HP1278
HP0849	HP0593	HP1259	HP0317	HP0042	HP1133	HP0614	HP0614
HP0849	HP0618	HP1259	HP0354	HP0042	HP1318	HP0739	HP0016
HP0849	HP0621	HP1259	HP0405	HP0042	HP1392	HP0739	HP0379
HP0849	HP0717	HP1259	HP0585	HP1493	HP0033	HP0739	HP0453
HP0849	HP0760	HP1259	HP0615	HP1493	HP0043	HP0739	HP0527
	HP0971			HP1493	HP0051	HP0739	HP0547
HP0849	HP1037	HP1259	HP0705	HP1493	HP0116	HP0739	HP0621

HP0849	HP1041	HP1259	HP0779	HP1493	HP0281	HP0739	HP0655
		HP1259	HP0792	HP1493	HP0435	HP0739	HP0687
		HP1259	HP0830	HP1493	HP0483	HP0739	HP0810
HP0849		HP1259	HP0862 1	HP1493	HP0501	HP0739	HP1056
HP0849		HP1259	HP0965	HP1493	HP0669	HP0739	HP1157
HP0849		HP1259	HP1012	HP1493	HP0841	HP0739	HP1279
HP0849		HP1259	HP1232	HP1493	HP0977	HP0739	HP1357
HP0849		HP1259	HP1259	HP1493	HP1002	HP1025	HP0668
HP0849		HP1259		HP1493	HP1025	HP1025	HP1025
	2-Prey ORF		2-Prey ORF				
HP0849		HP1259	HP1342	HP1493	HP1138	HP1025	HP1114
HP0849		HP1259	HP1411	HP1493	HP1198	HP1145	HP0182
HP0849	HP1393	HP1259	HP1422	HP1493	HP1350	HP1145	HP0289
HP0849	HP1400	HP1259	HP1430	HP1493	HP1411	HP1145	HP0400
HP0849	HP1452	HP0962	HP0030	HP1493	HP1533	HP1145	HP0550
HP0849	HP1489	HP0962	HP0088	HP0862	HP0607	HP1145	HP0621
HP0849	HP1493	HP0962	HP0111	HP0862	HP0621	HP1145	HP0669
HP0849	HP1553	HP0962	HP0244	HP0862	HP0791	HP1145	HP0690
HP1015	HP0299	HP0962	HP0285	HP0862	HP1474	HP1145	HP0705
HP1015	HP0547	HP0962	HP0410	HP0402	HP0825	HP1145	HP1010
HP1015	HP0607	HP0962	HP0426	HP0402	HP1130	HP0177	HP1409
HP1015	HP0687	HP0962	HP0490	HP0402	HP1234	HP0177	HP1508
HP1015	HP1435	HP0962	HP0528	HP0402	HP1478	HP0177	HP1550
HP1015	HP1490	HP0962	HP0537	HP1255	HP0607	HP0291	HP0279
HP0291	HP0291	HP1114	HP0919	HP1236	HP1148	HP0016	HP0791
HP0291	HP1409	HP0481	HP0281	HP1236	HP1263	HP0016	HP0969
HP0291	HP1541	HP0481	HP0298	HP0909	HP0587	HP0016	HP1017
HP0291	HP1550	HP0481	HP0416	HP0909	HP0607	HP0016	HP1183
HP0874	HP0875	HP0481	HP0421	HP0909	HP1081	HP0016	HP1267
HP1382	HP0025	HP0481	HP0494	HP0909	HP1521	HP0016	HP1450
HP1382	HP0182	HP0481	HP0645	HP0909	HP1561	HP0016	HP1490
HP1382	HP0269	HP0481	HP0736	HP1478	HP1478	HP1559	HP0010
HP1382	HP0317	HP0481	HP0741	HP1231	HP1247	HP1559	HP0056
HP1382	HP0705	HP0481	HP0779	HP0262	HP0355	HP1559	HP0087
HP1382	HP0896	HP0481	HP0971	HP0262	HP1318	HP1559	HP0116
HP1382	HP1142	HP0481	HP1000	HP1230	HP1230	HP1559	HP0116
HP1382	HP1182	HP0481	HP1025	HP1230	HP1529	HP1559	HP0116
HP1382	HP1237	HP0481	HP1266	HP0263	HP0056	HP1559	HP0120
HP1382	HP1243	HP0481	HP1406	HP0263	HP0486]HP1559	HP0132
HP1382	HP1342	HP0481	HP1435	HP0263	HP0605	HP1559	HP0145
HP0150	HP1037	HP0481	HP1513	HP0263	HP0779	HP1559	HP0355
HP0150	HP1067	HP1118	HP0822	HP0263	HP0792	HP1559	HP0364
HP0150	HP1198	HP0149	HP0103	HP0263	HP1238	HP1559	1HP0379
HP0150	HP1371	HP0149	HP0196	HP0263	HP1325	HP1559	HP0406
HP0150	HP1409	HP0149	HP0331	HP0263	HP1332	HP1559	HP0466
HP0150	HP0449	HP0149	HP0527	HP0263	HP1489	HP1559	HP0488
HP0294	HP0100	HP0149	HP0547	HP0263	HP1513	HP1559	HP0589
HP0294	HP0289	HP0149	HP0693	HP0224	HP0250]HP1559	HP0606
HP0294	HP0377	HP0149	HP0775	HP0224	HP0920	HP1559	HP0615
HP0294	HP0399	HP0149	HP1034	HP0224	HP1076	THP1559	HP0621
HP0294	HP1318	HP0149	HP1079	HP0224]HP1198]HP1559	HP0660

HD1400	LUDO4 40	(1)D4445	1100400	U Datat		
						HP0663
						HP0669
						HP0680
						HP0710
				 		HP0780
						HP0795
				HP0632		HP0817
			HP0261	HP0655	HP1559	HP0858
		HP0791		HP0750 .		HP0929
		HP0969	HP0261	HP0887		HP1026
				HP1019	HP1559	HP1041
		2-Prey ORF	1-Bait ORF	2-Prey ORF	1-Bait ORF	2-Prey ORF
		HP1072	HP0261	HP1124	HP1559	HP1075
		HP1222	HP0261	HP1274	HP1559	HP1116
	HP0028	HP1450	HP0261	HP1350	HP1559	HP1143
HP0919	HP0028	HP1470	HP0261	HP1489	HP1559	HP1187
HP0969	HP0028	HP1503	HP0261	HP1513	HP1559	HP1207
HP1024	HP0028	HP1550	HP0261	HP1517	HP1559	HP1236
HP1116	HP0821	HP0705	HP0261	HP1543	HP1559	HP1266
HP1409	HP0821	HP0821	HP0902	HP0588	HP1559	HP1274
HP0096	HP0821	HP1114	HP0902	HP0887	HP1559	HP1325
HP0116	HP0821	HP1409	HP0902	HP1409	HP1559	HP1393
HP0569	HP0389	HP0696	HP0016	HP0016		HP1434
HP0621	HP0389	HP1262		HP0038		HP1452
HP1012	HP0389	HP1400				HP1453
HP1205	HP0268	HP1198				HP1470
HP1373	HP1236	HP0026	HP0016			HP1472
HP0651	HP1236	HP0347				HP1479
HP0705	HP1236	HP0355	HP0016			HP1489
HP1493	HP1246	HP0326	HP1489			HP0134
HP1399	HP1246					HP0928
HP1541	HP1246	HP0886				HP1409
HP0996	HP1246					HP0514
HP1041	HP1246	HP1244				HP0010
HP1081	HP1246					HP0317
HP1241 .	HP0035					HP0753
HP1256						HP1157
HP1321						HP1329
HP0083						HP1409
						HP0002
						HP1200
						HP1409
						HP1451
						HP0377
						HP1409
						HP0242
						HP0050
						HP0355
						HP0792
						HP1409
HP0152	HP0276	HP1489 1	HP1482	HENAUD 1	MPUZAK	HPIAIN '
	HP0255 HP0352 HP0488 HP0919 HP0969 HP1024 HP1116 HP1409 HP0096 HP0116 HP0569 HP0621 HP1012 HP1205 HP1373 HP0651 HP1373 HP0651 HP0705 HP1493 HP1399 HP1541 HP0996 HP1041 HP1081 HP1081 HP1081 HP1081 HP1081 HP1081 HP1083 HP0083 HP0085	HP0651 HP0149 HP0725 HP0149 HP0822 HP0028 HP0033 HP0028 HP0024 HP0028 HP0944 HP0028 HP1318 HP0028 HP1529 HP0028 HP0100 HP0028 HP01529 HP0028 HP0352 HP0028 HP0352 HP0028 HP0948 HP0028 HP0969 HP0028 HP1116 HP0821 HP116 HP0821 HP1016 HP0821 HP01096 HP0821 HP01016 HP0821 HP0116 HP0821 HP0116 HP0821 HP0116 HP0821 HP0169 HP0389 HP1024 HP0389 HP1024 HP0389 HP1048 HP1246 HP1373 HP1236 HP0705 HP1236 HP1373 HP1246 HP1399 HP1246 HP1399 HP1246 HP1541 HP1246 HP1541 HP1246 HP1041 HP1245 HP0045 HP0399 HP1430 HP1244 HP1523 HP1244	HP0651 HP0149 HP1248 HP0725 HP0149 HP1332 HP0822 HP0028 HP0214 HP0033 HP0028 HP0527 HP0695 HP0028 HP0547 HP0944 HP0028 HP0607 HP1318 HP0028 HP0699 HP0100 HP0028 HP0969 HP0100 HP0028 HP1041 2-Prey ORF H-Bait ORF 2-Prey ORF HP0255 HP0028 HP1072 HP0352 HP0028 HP1470 HP0959 HP0028 HP1503 HP0919 HP0028 HP1503 HP1091 HP0821 HP0821 HP0969 HP0821 HP0821 HP1409 HP0821 HP1409 HP0569 HP0821 HP1409 HP0569 <td>HP0651 HP0149 HP1248 HP0109 HP0725 HP0149 HP1332 HP0261 HP0822 HP0028 HP0214 HP0261 HP0033 HP0028 HP0527 HP0261 HP0224 HP0028 HP0527 HP0261 HP0695 HP0028 HP0547 HP0261 HP0944 HP0028 HP0607 HP0261 HP1318 HP0028 HP0697 HP0261 HP1318 HP0028 HP0969 HP0261 HP1529 HP0028 HP0969 HP0261 HP1529 HP0028 HP041 HP0261 HP0100 HP0028 HP1041 HP0261 HP0101 HP0028 HP1072 HP0261 HP0352 HP0028 HP1222 HP0261 HP0352 HP0028 HP1470 HP0261 HP0999 HP0028 HP1503 HP0261 HP0969 HP0028 HP1503 HP0261 HP1040 HP0821 HP0705 <</td> <td> HP0651</td> <td> HP0651</td>	HP0651 HP0149 HP1248 HP0109 HP0725 HP0149 HP1332 HP0261 HP0822 HP0028 HP0214 HP0261 HP0033 HP0028 HP0527 HP0261 HP0224 HP0028 HP0527 HP0261 HP0695 HP0028 HP0547 HP0261 HP0944 HP0028 HP0607 HP0261 HP1318 HP0028 HP0697 HP0261 HP1318 HP0028 HP0969 HP0261 HP1529 HP0028 HP0969 HP0261 HP1529 HP0028 HP041 HP0261 HP0100 HP0028 HP1041 HP0261 HP0101 HP0028 HP1072 HP0261 HP0352 HP0028 HP1222 HP0261 HP0352 HP0028 HP1470 HP0261 HP0999 HP0028 HP1503 HP0261 HP0969 HP0028 HP1503 HP0261 HP1040 HP0821 HP0705 <	HP0651	HP0651

HP0712	1100070	41100010					
	HP0278	HP0340	HP0096	HP1482]HP0645	HP1338	HP1338
HP0712 HP0712	HP0281	HP0340	HP0231]HP1482	HP0760	HP1338	HP1409
	HP0662	HP0340	HP0340	HP1482	HP1115	HP1338	HP1523
HP0712 HP0712	HP0714	HP0340	HP0695	HP1482	HP1369	HP0249	HP0012
	HP0736	HP0340	HP0730]HP0073	HP0073]HP0249	HP0099
HP0712	HP0836	HP0340	HP0821	HP0073	HP0232	HP0249	HP0174
HP0712	HP0850	HP0340	HP0834	HP0073	HP0259	HP0249	HP0214
HP0712	HP1160	HP0340	HP1088	HP1449	HP0615	HP0249	HP0415
HP0712	HP1470	HP0340	HP1138	HP1449	HP1019	HP0249	HP0527
HP0712	HP1489	HP0340	HP1198	HP1449	HP1332	HP0249	HP0547
HP0712	HP1513	HP0340	HP1274	HP1202	HP1068	HP0249	HP0610
HP0100	HP0123	HP0340	HP1362	HP1322	HP0013	HP0249	HP0787
HP0100	HP0132	HP0950	HP0030	HP1322	HP0649	HP0249	HP0922
1-Bait ORF		1-Bait ORF	2-Prey ORF	1-Bait-ORF	2-Prey ORF		2-Prey O
HP0100	HP0278	HP0950	HP0116	HP1322	HP1488	HP0249	HP0969
HP0100	HP0585	HP0950	HP0192	HP0113	HP1041	HP0249	HP1041
HP0100	HP0617	HP0950	HP0304	HP1200	HP1037	HP0249	HP1154
HP0100	HP0707	HP0950	HP0394	HP1200	HP1199	HP0249	HP1157
HP0100	HP0710	HP0950	HP0884	HP1563	HP0785	HP0249	HP1377
HP0100	HP0726	HP0950	HP1025	HP1563	HP1080	HP0249	HP1409
HP0100	HP0830	HP0950	HP1198	HP0800	HP0433	HP0249	HP1487
HP0100	HP0852	HP0950	HP1438	HP0800	HP0687	HP0249	HP1503
HP0100	HP0898	HP1247	HP1231	HP0800	HP0800	HP0249	HP1543
HP0100	HP0919	HP1247	HP1353	HP0800	HP0801	HP0591	HP0582
HP0100	HP1050	HP0951	HP0116	HP0800	HP0924	HP0591	HP0610
HP0100	HP1157	HP0951	HP1409	HP0800	HP1267	HP0591	HP0663
HP0100	HP1379	HP0951	HP1411	HP0800	HP1460	HP0368	HP0409
HP0100	HP1411	HP1489	HP0001	HP0353	HP0353	HP0368	HP0435
HP0100	HP1458	HP1489	HP0351	HP0353	HP0406	HP0368	HP0897
HP0105	HP0105	HP1489	HP0540	HP0353	HP1420	HP0368	HP1293
HP0105	HP1409	HP1489	HP0705	HP0801	HP0152	HP0368	HP1356
HP0837	HP0705	HP1489	HP0797	HP0801	HP0800	HP0368	HP1410
	HP0836	HP1489	HP0841	HP0801	HP1513	HP0005	HP0088
HP1246	HP0121	HP1489		HP0806	HP1198		HP0116
HP0005	HP0175			HP1414	HP0522		HP0983
HP0005	HP0278	HP1537					HP1119
HP0005	HP0317						HP1195
HP0005	HP0583	1.15					HP1205
HP0005	HP0615	150 4 0 0 0					HP1241
HP0005	HP0640	1.150.4.5.5.5					HP1393
HP0005	HP0657	1.150.4.5.5.5			11000		HP1430
HP0005							
HP0005	HP0714					1	HP1510
HP0005		15.45.5					HP1553
HP0005							HP0706
							HP0010
							HP0066
							HP0109
							HP0197
							HP0244
		15444					HP0247
 L	L	!·		11.1227	1703	HP0137	HP0289

LIB0247	LID1400	LID1444	U/D0704	1104004	1104470	1100407	() ID0400
	HP1409	HP1411				HP0137	1HP0422
HP0247	HP1572	HP1411	HP0809	HP0134	HP1012	HP0137	HP0452
HP1411	HP0027	HP1411	HP1198	HP1223	HP0332	HP0137	HP0592
HP1411	HP0397	HP1411	HP1287	HP1223	HP0514	HP0137	HP0609
HP1411	HP1411	HP1411	HP1411	HP1223	HP0746	HP0137	HP0610
HP1411	HP0701	HP1411	HP1530	HP1223	HP0775	HP0137	HP0621
HP1411	HP0809	HP0935	HP0072	HP1223	HP1409	HP0137	HP0626
HP1411	HP1422	HP0935	HP0528	HP1102	HP0231	HP0137	HP0635
HP1411	HP1530	HP0935	HP0657	HP1102	HP0540	HP0137	HP0853
HP0482	HP0145	HP1530	HP1411	HP1102	HP0775	HP0137	HP0900
HP0482	HP0482	HP0797	HP0289	HP0495	HP0821	HP0137	HP0908
HP0482	HP1409	HP0797	HP0887	HP0495	HP1205	HP0137	HP0996
HP0241	HP0134	HP0797	HP1349	HP0132	HP0304	HP0137	HP1114
HP0241	HP0289	HP0933	HP0025	HP0132	HP0679	HP0137	HP1143
HP0241	HP0317	HP0933	HP0052	HP1464	HP1464	HP0137	HP1332
	2-Prey ORF			· · · · · · · · · · · · · · · · · · ·	2-Prey ORF		2-Prey ORF
HP0241	HP0500	HP0933	HP0123	HP1464	HP1433	HP0137	HP1393
HP0241	HP0610	HP0933	HP0197	HP1464	HP1157	HP0137	HP1406
HP0241	HP0745	HP0933	HP0231	HP1464	HP0816	HP0137	HP1553
HP0241	HP0973	HP0933	HP0278	HP1464	HP0610	HP0372	HP0347
HP0241	HP1048	HP0933	HP0528	HP1464	HP0489	HP0372	HP0372
HP0241	HP1157	HP0933	HP0532	HP1464	HP0346	HP0010	HP0605
HP0241	HP1177	HP0933	HP0610	HP1464	HP0232	HP0010	HP0655
HP0241	HP1370	HP0933	HP0775	HP1464	HP0088	HP0010	HP1026
HP0241	HP1454	HP0933	HP0825	HP0011	HP0011	HP0010	HP1124
HP1570	HP0060	HP0933	HP0900	HP0011	HP1409	HP0010	HP1216
HP1570	HP0806	HP0933	HP1198	HP0496	HP0547	HP0371	HP0056
HP0448	HP0303	HP0933	HP1213	HP0136	HP0109	HP0371	HP0289
HP0448	HP0416	HP0933	HP1248	HP0136	HP0156	HP0371	HP0289
HP0819	HP0522	HP0938	HP0109	HP0136	HP0244	HP0371	HP0371
HP1537 HP1537	HP0088	HP0938	HP0268	HP0136	HP0247	HP0371	HP0527
HP1537	HP0621 HP0655	HP0938	HP0401	HP0136	HP0295	HP0371	HP0528
HP1537	HP0660	HP0938 HP0938	HP0501 HP0705	HP0136	HP0303	HP0371	HP0609
HP1537	HP0705	HP0938	HP0846	HP0136	HP0325	HP0371	HP0609
				HP0136	HP0399	HP0371	HP0609
HP1537	HP0822	HP1414					HP0610
HP1537	HP0841	HP1414		HP0136 HP0136	HP0760	HP0371	HP0610
HP1537	HP1114	HP1414	HP0281		HP0779	HP0371	HP0752
HP1122	HP0051	HP0406		HP0136	HP0795	HP0371	HP0908
HP1122	HP0680	HP0287		HP0406	HP0119	HP0975	HP0658
HP1122	HP0850	HP0287		HP0406 HP0406		HP0975	HP0941
HP1122	HP1032	HP0287				HP0975	HP1150
HP1122	HP1393	HP0287		HP0406 HP0406		HP0975 HP0975	HP1344
HP0634	HP0071	HP0287			`	וחרטשוט	HP1513
HP0634	HP0278	HP0287		HP0406	HP0353		
HP0634	HP0281	HP0287			HP0399	-1	
HP0634	HP0285	HP0287	HP0488		HP0509		•
HP0634	HP0381	HP0287	HP0550		HP0514		
HP0634	HP0480	HP0287	HP0605	HP0406	HP0527		
HP0634	HP0592	HP0287		HP0406	HP0555		
0007	111 0002	111 0201	1.1. 0000	HP0406	HP0593		

HP0634	HP0609	HP0287	HP0792	HP0406	HP0621
HP0634	HP0645	HP0287	HP0977	HP0406	HP0655
HP0634	HP0655	HP0287	HP1045	HP0406	HP0795
HP0634	HP1177	HP0287	HP1069	HP0406	HP0797
HP0634	HP1394	HP0287	HP1116	HP0406	HP1024
HP0634	HP1489	HP0287	HP1216	HP0406	HP1030
HP0634	HP1513	HP0287	HP1274	HP0406	HP1048
HP0634	HP1540	HP0287	HP1430	HP0406	HP1069
HP0830	HP0736	HP0287	HP1470	HP0406	HP1114
HP0830	HP0975	HP0287	HP1479	HP0406	HP1188
HP0830	HP1012	HP0287	HP1489	HP0406	HP1195
HP0830	HP1411	HP0287	HP1556	HP0406	HP1274
HP0830	HP1430	HP0975	HP0036	HP0406	HP1341
HP0830	HP1489	HP0975	HP0449	HP0406	HP1430
HP0406	HP0109	HP0975	HP0528	HP0406	HP1489
HP0406	HP0118	HP0975	HP0552		·

TABLE 2 SID®s Sequences

1-Bail	2-SID nucleic sequence	Csequence	13 SID profes segmente	Spilence	Γ
ORF					
	SEO ID#	Sequence	SEO ID#	Sequence	Γ
HP0338		1TGAAGAGGATGGGAATGAAAGTATTGCCTATGATTTTTCAAGCGCTAAGGAGTTGCTAGAATTGTGCCAAAAACACC	2	EEDGNESIAYDFSSAKELLELCOKHOK	×
		AAAAAAGCATCGCTGAAATCGTGCGTTTGAGAGAAAACGCCCTGAAAAACCCCCTGATGCATGC		SIAEIVRLRENALKNHPDATMYKIYHAM	Ž
		TATCATGCGATGCTTGAGTGTTATGATAATGGGGCTAATTCTAAAGAAAG		LECYDNGANSKERYLPGSLKVTRLAPS	PS
		CGATTGGCCCCAAGCATTAAAACGCGCGTAGAAAAACACCCCACAAGCGGGAAAGACCCCCTTAGCCTTGATTGA	8	IKTRLEKHPTSGKDPLALIDYISLYARA	3
		CATTICGCTTTACGCTCGCGCCCATTGCTGAAGAAACGCTAGCGGAGGCAAGGTGGTAACCGCCCCCACTAATGGG	(5	AEENASGGKVVTAPTNGACAVVPSVL	ر
		GCGTGCGCGTGGTGCCAAGCGTGCTTTTATACGCTAAAAACCATTTGTTTG	 -	LYAKNHLFENLSQKAINDFLL1'SAAIGY	<u></u>
		GATITITIACTCACTAGTGCGGCGATTGGCTATCTTTACAAGAAAAACGCTTCCTTGAGTGGCGCAGAAGCCGGGTG		LYKKNASLSGAEAGCQAEIGVASSMAA	ş
		TCAGGCTGAAATTGGCGTGGCAAGCTCTATGGCTGCGGGGGGTTAGCTCATTTGTGCCAAGCGACGCAACA	_	GGLAHLCQATTQQVLIASEIAMEHHLG	0
		GGTTTTGATCGCTAGTGAAATCGCTATGGAACACCCATTTAGGATTGACATGCGATCCGGTGGGGGGGCTTGGTGCTGA		LTCDPVGGLVQIPCIERNVLG/AIKAISAS	S
		ATCCCTTGCATTGAACGCAATGTTTTAGGGGCGATTAAAGCGATCAGCGCTTCTAAACTAGCCTTAGAAGATGAATAC		KLALEDEYKPKVSLDEVIATMYATGKD	_
		AAGCCTAAAGTGAGTCTGGATGAAGTGATCGCTACAATGTATGCGACCGGAAAAGACATGAAAGAGACATGAAAAGA		MNEKYKETSLGGLAKTLKC	
		GACTTCGTTAGGGGGGTTAGCCAAAACCTTAAAATGCTAAGGGATGAATCTAATCTTTAGGGGGCTTTAGGTTTCTAA	-		_
		AGAAAGTAAAAAGGTTTGTTTTTATCAAATATCAATAAGCCTTATCTGCTTTGATATTCTTAAAAAATTTTAAAAAATAG			
		GGTTTTAAAGCGTTCCTTCA			
HP0338		3 GAGAGCAAGCGGTTAAAATCGTGGAAAAACGCTTGAAAAAGAGGGCCATGAAATTGAGCGATTTTAACGAAGAAGAA		4 EOAVKIVEKRLKKEGMKLSDFNEEELKI	호
		TTGAAAATCATGTTTGAAGCGGAAGAGAAAAGGCTTTTAGAACAAATCCAAACTAAGCATTTTAAAGAAGTTTGGGGAA		MFEAEEKRLLEQIQTKHFKEVNEKGD	_
		AAGGGCGACAATGAGCAAGGAAAATAGCGTAATTTCTGGTTTAATGAATTTTTTTAGCGAAAAGAATGAACGCTGGCT		NEGGK	
		GTTAGCCCACAGGCACACGAGAGAGGGTTTGTGATCGTGGCGTGGCTTTTTCGGTTTAAAAGCATTGCGTTTTCTATTC			_
4		TGATCACTTTGTTGGTGATTTGG			_
HP0339	43	STGCGCGTGTTAGAAACGATTGTTGCTTTAAGAGAGTATCGTAAAAGTTTGGAAGAAAGCGTGGGGGTTTGTGCCGACT		6 RVLETIVALREYRKSLEESVGFVPTMG	G
		ATGGGGGCTTTACACAAAGGGCATCAAAGCTTGATAGAAAGGAGTTTGAAAGAAA		ALHKGHOSLIERSLKENSHTIVSVFVNP	چ
_		1111GTCAATCCCACGCAATTGGGGCTAACGAAGATTTTAACGCTTACCCTCGCCCTTTAGAAAAGGATTTGGCTTT		TOFGANEDFNAYPRPLEKDLALCEKLG	<u>ග</u>
		ATGTGAAAAATTAGGCGTTAATGCGGTGTTTGTGCCTAAAATTGGCGAAATGTATCCCTATGAAGCAGGGAACGCC		VNAVFVPKIGEMYPYEAEQRLKLYAPK	¥
		TGAAACTCTATGCTCCTAAATTTTTATCTAGCTCTTTAGAGGGAG		FLSSSLEG	

HP0339	7 ATTTACCCCCTAAAGCCAAAGTCTATTCCAGCAAGAATAAAAACGCCCCAAGAAGCCCATGAAGCGATCAGGCCCACT TCTATTATTTTAGAGCCAAAGCCTTTAAAAGGACTACCTTAAAGCCTGAAGAATTAAGGAATTAAGGAAATTACAAAC GCTTTTTAGCTCTCCAAATGCAAAGCCTTTTTGAAAGCCTAAAGCCTGGTTGTGGCTTGCGAAAAAGGCGAGTTT AAAAGCGAGTGGGAAAAGCTCCTTTTTTGAAAAAATTTTAAAAATTTTAGGCATTGCGAAAAAGGCGAGTTT AAAAAAAAAA	8 LPPKAKVYSSKNKNAQEAHEAIRPTSII LEPNALKDYLKPEELRLYTLIYKRFLAS GMGDALFESGSVVVACEKGEFKASGR KLLFDGYYKILGNDDKDKLLPNLKEND PIKLEKLESNAHVTEPPARYSEASLIKV LESLGIGRPSTYAPTISLLQNRDYIKVE KKQISALESAFKVIEILEKHFEEIVDSKF SASLEEELDNIAQNKADYQQVLKDFYY PFMDKIEAGKKNIISQKVHEKTGQSCP KCGGELVKKNSRYGEFIACNNYPKCK YVKQTESANDEADQELCEKCGGEMV QKFSRNGAFLACNNYPECKNTKSLKN TPNAKETIEGVKCPECGGDIALKRSKK GSFYGCNNYPKCNFLSNIHKPINKRCE KCHYLMSERIYRKKAHECIKCKERVF LEEDNG
нР0339	9TAGGGGTATGGCTACACACCGAATTGCAAGACGCTATCTCATTGTGCAGAAGAGTGAATATTTTGACATCACCCT TTTAAAATGCGTGGCTACACGCGAATTGCAAAATAGAAGACGCTAACTTGTTGAGCATGGTTAAATTAGGCGAAATCTT TGGCGTTAAATTTGGCTTGAGCGATCACACGATTGGCTCTTTTGCCCCATTTTAGCCACCACTTTAGGAGCGAGC	10 SGIATHTELODAISLCRRVNNFDITLLK CVSAYPSKIEDANLLSMYKLGEIFGVKF GLSDHTIGSLCPILATTLGASMIEKHFIL NKSLQTPDSAFSMDFNGFKSMVEAIK QSVLALGEEEPRINPKTLEKRRFFARS LFVIKDIGKGEALTENNIKALRPNLGLH PKFYKEILGGKASKFL
HP0339	11 TGTCTTTGTGCAGGGCTGAAGATGGGGGCGTTTTTTGTCATAGATTACCAGACGAGTTTGTGCAGGGATTG AAAAATCCAGCGCTCACCAAGCAATTAAGGCAGTTGATCAGAGATGGGGCTGTGAGGTTGCAGAACTTCTG AAAAATCCCAGGCTTCACCACCCAAGCAATTAAGGCAATAAAACAGCAACTCTTTTGCGTGAAGGTTGCAAACTTCTG CCATTCCCTTATCCTACCAACCCAAC	12 SLCRAEEDGAFFVIDYQTSLARGELKN PGFTQAGELROLINDGAVRLOTSAIPL SYYLDILGNKTATLLRESLKNNAÓPSÓ PNAÓPPÓONGPSNÓALANLEOSLGIL GKLLDLSOQYASOGVIRPLVVDVGKEG IGITDSMLLVAÓNIVLALGÖVDLSKIQÓ NNNEOLYENIMKVMLLGAGGTNGAYN GVSVGDIATGMÖNFSSÖTGLIGANSTV SELNALIKSGISLDRETLGLGSFIEKNIC SGASSCFSGNÓLIYKKGLDRTINIINTVL GGFESSASSLYKISYIPNLFSLKÖY
нР0339	13 TCAAATCGCTCTATAAGGGCGCGAACGATTACATTGACATGTTTAAAGGCGCGCACTTTATTCGTGCTGATAACCAGT TCGCTTCTTTAGAAGGCGTTAAAAGGGTTAAATCTCAAGGCGTTTTTTATTCACTGCGTTTTTTAATCACTTTTTAAACGCTTTTTTAATCAGGCGGCAAGCGTTTTTTAATCAGAAGAACGCGTTTTGAACCGGGCAAGCGTTTTTTAGAACGAAC	14 KSLYKGANDYIDMFKOTHTLFVHNGFA SLEALKRIKSÖVKNAFLITCPFSNRLLS GQALDLERTKEAGLSVSVATÖGLSSNI SLSLLDELRAFLLTHNMPLLELAKIALLG ATRHGAKALALNNGEIEAWKRADLSVF GFNEKFTKEÖAILÖF

84

HP0339	15/A1/GGCGAAAGCTATGTAGCAACGGGCAATATTTATGACACGCTCGTGCAATTCAGATACGGCACACAGAAGTTGAA	16 GESYVATGNIYDTLVQFRYGTTEVEPA
_	CACCAAGGAAGTATTGGAATAAAAAAGTAGAGTTTAGGGCTAAAAGATGTGTTTTTGGTTTTGATTTGAAGGGGATTAGAT	LATSWDISPUGLYY I FHLKKGVYFHQT
	AAAGCTAAACGATATTATAGCCCGGGGGCTAAAAGCTATAAGTATTGGGAAGGCATGGCCATGTCTCATATTAA	IRYYSPGAKSYKYWEGMGMSHIIKSIFA
	GAGCATTGAAGCTTTAGATGACTATACCATTAGATTCACACTTAATGGGCCAGAAGCCCCGTTTTTAGCGAATTTGGG	LDDYTIRFTLNGPEAPFLANLGMDFLSI
	CATGGACTITITGAGCATTTTGAGGATTACGCTGATTACCTGGCTCAAAATAAAAAAGACGAGTTGGCTAA	LSKDYADYLAONNKKDELAKKPIGTGP
_	AAAACCTATTGGGACAGGGCCTTTCAAATTCTTTTTGTGGAATAAAGATGAAAAAATCATTCTTTTAAAAAATCAAGAT	FKFFLWNKDEKIILLKNODYWGPKAYL
	TATTGGGGGCCTAAAGCGTATTTGGATAAGGTGGTGCGCACCATTCCTAATTCTTCCACTCGCGCTTTAGCGTT	DKVVVRTIPNSSTRALALRTGEIMLMT
	GCGCGCGGCGAAATCATGCTCATGACTGGGCCTAATCTCAATGAAGTGGAAGAAAAAAAA	GPNLNEVEQLEKVPNIVVDKSAGLLAS
	TGGTGGACAAAAGTGCTGGGTTGTTGGCGAGTTGGCTTTCGTTGAACACACAAAAAAAGTATTTGACAACCCTTTG	WLSLNTQKKYFDNPLVRLAINHAINAD
	GTGCGTTTGGCTATCAATCATGCGATCAATGCAGATGATTACAAAGGGTTTATGAAGGCTTTGCTCAAAAAATG	DYIKVLYEGFAQKMVNPFPPTIWGYNY
	GTCAATCCTTTCCCGCCCACCATATGGGGTTATAACTACAATATCAAACCCTATGAATACGATTTGAAAAAGGCTAAG	NIKPYEYDLKKAKELLKQAGYPNGF
HP0339	17 TACCCACACAAACACAAAGGGGCAATTACCCAAAAGGCGGAGTGAGGGCTAAACGAACG	18 PTOTOAQLPKSRVRLNEREIYDLDYAIV
	GCGATCGTCAAAGCGAAAGATTTAAAACCAAGCTTTACCACAGGCGGGACGCAAAAGAGAAACGGACATGAACGAAG	KAKDLKPSFTTGGTOKRTDMNEEOIKS
	AGCAGATTAAAAGCATTGCTGAAAATTTTGATCCTAAAAAGATATTTGGTAGCGGAGGGTTTGAAGATTTACCGATCA	IAENFDPKKIFGSGGFEDLFIILHDGOVI
		AGNHRIOGMLNFTPKSRFSYERAIKEY
	TCTTACGAGAGAGGGATCAAGAATACTATCACATAGACTTAAAACCGGACGAGGGTTGTTAGTGAGAGTGCCACACAA	YHIDLKPDELLVRVPHKRLNINTEINNLA
	GCGCCTAAACAACACCGAGATCAACAATTTAGCGGCTTCATCCAATCAAGGACGCTTCAATAGCGAAAGCGATCACG	ASSNGGRFNSESDHAIAVL SHYEAKLK
	CTATAGCGGTTTTAAGCCACTATGAAGCCAGTTAAAAGAATTAGACCAAAAATTAGACGCTGATAGCATCTACTCAT	ELDOKLDADSIYSLKNIVAKIVLNFDKAT
_	TAAAAAACATTGTTGCTAAAAATTTGAATTTTGATAAGGCTACGCATCCTAATGTAACCGATAGTAATTTAGCGTTGCT	HPNVTDSNLALLMFNMPRTKTQGIELL
	GATGTTTAACATGCCACGAACCAAAGGCAAGGGATAGAATTACTCAACCGCTGGAAAAAAAA	NRWKKEFSNDIKSYEKVKKMFVDNAG
	I I AAAAGCI AI GAAAAAAGTAAAAAAAATGI I I GAAAAATGI TOO GAAAA GAAACTTI AAAAAGCI AI GAAAAAAAAAAAAAAAAAAAAAAAAA	SFHNLIHDLNFPKVSLNAYLSDIMDRSF
	CCCTAAGGTGAGTTTAAACGCTTATTTAAGCGATATTATGGATCGCAGTTTTGCGAATTTAAAGAATTACCAAAGCAC	ANLKNYQSTSESLKDLSEKI:YKTSSLE
	GAGCGAGAGCCIGAAAGATTIGAGCGAAAAATTCTATAAAACGAGTTCGTTAGAGATGTTTGAAAAGAGCGATCAAA	MFEKSDQSTSDISEILGGAI\ARFARFDD
	GCACGACTTGATTTGATGATTTGAGGAGGAGGGATCGCACGATTTGCACGATTTGATGATCCGAGCAAAGCGTT ATTTGAAGCCCTTAAGAAG	PSKALFEALRSDNIK
-		
HP0339	19 IATTIAGEOTTAGEOATOTAATATAGEOTTGGAAAACTTAGEOAACCAAAAGCGATGAAAAAGATGGCAACAGCATTTTCA	20 ISVVKELVKNLATKSDEKDENGNSISFS
	CATCACTCAACTTATTAATGCTTTCGGGAAAGACCACAATGATCCTAATGGGCTTGTGGGTTGTGGGATTAGCAATGTTTTTTG	ILAUSINI LAAAN INLI GUMINLU I PII UL NAFGKUHNDBNGI VARI AFIFCKSTNG
	CAAATCAACCAATGGTGAATTTCAATGGCTTTTTGATAATAAGCAAGGGATCGCTTAGATTTTTCAAAAACGATTATT	EFGWLFDNKATÖRLDFSKTIIGVDGSS
	GGCGTTGATGGGTCAAGTTTCTTAGACAATAATGATGTTTCGCCCTTTATTTGTTTTACCTTTTCGCTCGTATCCAAG	FLDNNDVSPFICFYLFARIOEAMDGRR
	AGGCAATGGATGGGTAGATTTGTCTTAGATATTGATGAAGCTTGGAAATATTTAGGCGATCCAAAGGTCGCTTATT	FVLDIDEAWKYLGDPKVAYI*VRDMLKT
	TTGTAAGAGACATGCTAAAAACTGCAAGGAAAAGAAACGCTATTGTCAGACTTGCGACTCAAAGCATCACTGATCTTT	ARKRNAIVRLATOSITDLLACPIADTIRE
	IGGCTTGCCCTATTGCTGATACGATTAGAGAACAATGCCCTACAAGATTTTTTGAGAAACGATGGGGGGCAATCTTT	QCPTKIFLRNDGGNLSDYQRLANVTEK
	CLIGATIACCAAAGAIIGGCIAAIGIIACAGAAAAGAAIIIGAAAICAICACTAAGGGACIAGAIAGGA	EFEIITKGLDR

HP0339	21 TCAGGTCGGATCGCATTTAGACATCGCCCCTACGATTATTGAATTAGTCGCCCCTAAAGGCTTTCAATTCGTGAGTTTTTTCTAACAATTAGTCGCCCCTAAAGGCCTTTCAATTCGTGAGTTCGTCGATTCGTGAGTTCGTCGAAGCCAATGCGTCGAAGCCAAGCCCTAAAGCAAGAGCCTTTGAAGCAAGAGCCTTAGTTTTTTTT	22 QVGSHLDIAPTIIELVAPKGFGFVSFGK PLFSNNTTNPPSHPNYALGYEAIATKD YFYNPSLGLRYLNESPKEPKDKGNDKI EASKFYQQLESLKALSYYLLYHGANLK D
НР0339	23 TGGAAAATCAACGCTTATCAACACTATTCTAGGCATTAGATCAGACTATAATTTTAAAGCACAAAACAATAATATTCCAACACAAAACATAATATTCCAAAATCAACGAATAATATTCCAAAAAAAA	24 GKSTLINTILGIRSDYNFKAQNNNIPYH DNVIPQRKQLGVVSNLFNYPPRLNAND LFKFYQFFHKNCTPNLFEKNLLNKTYE HLSDGQKQRLKIDLALSHHPQLIIMDEP ETSLEQNALIRLSNLISLRNTQQLTSIIA THDLI
HP0339	25 TGAAACTTITAGCGCTCTCTTTAGGTAAAGCCCCTTTGAGGTTTTGAATTTAGAGGGGTATTTTTAACCAGCTTTCTAA TGCGGCCTGGAGCGGTAACAAGCCCTATGAATTAGAATGGAATGAAGTGGAAGTGGCTTTAAAAATGCGAGC CATTTCCCTAGCATTGATTCATAGATAAATTCCACGCTATTTGATGCAATTAATCCCTGAGTTTGATAATACCGCT TATTGGATAGCTCAAAAACGCGCTTTGGGGCGTATTTAGGGACTGGAGTTTCTCCTGGGGCTAGTTAT GTGAATTTTAACGCAGGGGCTTTGGGGGGTTTTAGGGACTGGGGGCGTATTTCTTCGTGGGGCTATGGGAGTGGATTGCATGGGGAGCGTAGTTAA AAATTGTTTGCTAGGGGGGGGGG	26 KLLALSLGKAPLRSLNLEGIFNÖLSNAA WSGNKPYELEWLRMNEVALKMRDHF PSIDFIDKFPRYLMOLIPEFDNIRLLDSS KTRFGAYLGTGGYTÖMPGASYVNFNA GAMCYCMNEGRISSSVYVGAGYDIGG GASVLGVLSGGNNNPISIGKNCLLGAN SVTGISLGDGCIVDAGVAILAGSVIEIEE NEFKKLLEVNSALEKHANNLYKGKELS GKNGVHFRSNSÖNGKLIAFRSVKKIEL NÖNLH
HP0339	27 CCTTITAAACCATGCTAAAAAACTCAAAGCTTGAATGGGGTGGAGATTGTAGGGTTGGAGCATTTGGATAAAGTGATTTTAAACCATGCAAGTGATTTTAGATCAAGCCCCCATAGGCAAAACCCCAGGAGAGCCCTTACACGGGGAGTGATGGAATCAGGATTTTAGATCAAGGAGCCCATTTTAGATCAAGGAGGCAAAAGGAAGCCCAGAAGCCATTTTAGATGTTAAAGGAGGGAAATCAGGAGTGCGGTGCGAGAAATGAAGGAGGGGAAATGCCATTGCCGATGCCGATGCGAGGGGAAATGCCATTGCCGATGCCGATGCGATAGGAATGCCATTGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCGATGTGCCGATGCCGATGCCGATGCCGATGCCGATGGGGGGGG	28 LLNHAKKTÖSLNGVEIVĞLEHLDİKVIYL DÖAPIGKTPRSNPATYTĞVMDEIRILFA EQKEAKILĞYSASRFSFNVKĞRCEKC ĞĞDĞDİKIEMHFLPDVLVQCDSCKĞAK YNPQTLEIKVKĞKSIADVLNIMSVEEAY EFFAKFPKIAVKLKTLMDVĞLĞYITLĞ NATTLSĞĞEAQRİKLAKELSKKDTĞKT LYILDEPTTĞLHFEDVNHLLQVLHSLVA LĞNSMLVIEHNLDİIKNAÖYIID

	SECOND SECTION OF TAXABLE AND A SECOND SECTION OF THE SECTION OF T	30 LFTPGPVAINEEMRTSFSQPMIPHRTK
HP0339	CALENTIA DE LA COMPANA DE LA C	DFEKIFOSVRENLKKMTGLEEVLLLSSS 97
	TAAGCAGCGGGACAGGGGCTATGGAAGCGAGCGTGATTTCCTTGTGAAAAAGAGCCTATGAATGCG	GTGAMEASVISLCGRELLFVNAGRFGE 03 RFGKIAKAHSIKAHELVYEWDTPAQVD 10
	GGCAAGTTTGGCGAAAGGTTGGCAAGATTTAAAGCCTTTAAAGCCCAACCCTAACATTGATGCGTTTTGCATTCAAGCATG	EILSVLKANPNIDAFCIQACESSGGLRH
	CEACTOTAGEGGGGTTAGGACTAGGCGTGTGGAAAAATCGCTCAAGCGATCAAGAAACTAACCCGAATGTTTTG	PVEKIAGAIKETNPNVFVIVDAITALGVE
	TAATTGTAGATGCTATCACCGCTTTAGGGGTTGAGCCTTTAGAAATAACGCATGTTGATGCGCTCATTGGAGGGGGT	PLEITHVDALIGGSQKAFMLPPAMSLVA
	CAAAAAGCGTTCATGCTGCCTCCTGCGATGAGCCTAGTCGCATTGAGCCAGAATGCAATTGAGCGTATAGAAGAAC	LSQNAIERIEERNVGFYFNLKSELKNG DNNTTSVTADII HTI GI ORVEEI VONI
	GCAATGTGGGGTTTTATTTCAATTTAAAGGGGGAATTGAAAAACCAAAGGAATAACGCCACAGGGTACACCGCTCTATAAAGGAATAAACGAAAGGAATAAAAAAAA	GGEFAI YRETKKAAI ATOKAVI ALGLKI
	TTTTACACACTTTAGGGTTGCAACGCTATTTTGGTTTTAGGTTTAAAGATTTTCCCTAAAAAGACACTTGAA	FPKSPSLSMTTIVNEHAKELRNLLKEKY
	GCATGACAACGATTGTTAATGAGCATGCCAAAGAATTGAGAAACCTTTTAAAAGAAAATACCAGGTGCAATTTGCGG	QVQFAGGQEPYKDALIRINHMGIIPVYK
	GCGGTCAAGAGCCTTATAAAGATGCGCTCATTCGTATCAACCACATGGGGATCATTCCTGTTTATAAAAGCGCTTAC	SAYALNALELALNIJLDLREFDGVANAL
3000	21 CONTRACT TO CARABATGA BACCTTAGGC CCA ACTTATAGGT CA ABATA ACTTAGAT TATTGA AT TATAGGGGGG	32 ASLONETLGOLIGONNLDDLLNINSGVM
HF0338	TCATGAATGCAATCCAAAATATTATCAGTAAAAACTAAGCATTTTTGGTAATTTTGTTACCCCATCCAT	NAIGNISKKESITGNEV I PSIIETTEANG
	CTACCTTGCTAAGCAGTCTTTAAAAAAGCATGCTAGACGATAAAAGGGCTTTTGAALIIIAIUGGIGGGIAIAIGAAAGGTT	SVVI KOLTNPPTSLOKDIGVVANDLLNE
	TTCTGAATTAAGTTCTATTTTAAGCGTGGTTTTAAAAGATATTAATCAAAAAAGCTAGAAAGCTAGAAAGCTTAGAAAGAA	FLGQDVIKKLESQGLVSNIINNIISQGGL
	GIGGIAGCGAACGACIIGIIGAACGAGIIIIIAGGACGAGGGGGGTTTATAATCAAGGGGTTTGCCGCC	SGVYNGGLGSVLPPSLQNALKENDLG
	PARIATION PARI	TLLSPRGLHDFWQKGYFNFLSNGYVF
	AGGGTATTTTAACTTTTTAAGCAATGGCTATGTTTTTGTCAATAACAGCTCTTTTAG	VNNSSF
00000	31 PRITICE AND THE CONTINUE CO	34 VEMORFGAFFGGKTETFLGLSGAGDL
HP0558	TECTITITA ACCOCCIANTICIAL TITITATO TA GO CANA TATO TATO CA CANA CANA CANA CANA CANA CANA CANA	FLTANSILSRNYRVGLGLAUNKPLEVVL
	GTGGTTTTAGAAGAATTGGGCGAAGTGGCTGAAGGGGTGAAAACGACCAACGCCATTGTGGAAATCGCTAGAAAAT	EELGEVAEGVKTTNAIVEIARKYGIYTPI
	ACGGCATTTATACGCCCATTGCGAGCGAATTAGCCTTGCTTTTAAAGGGTAAGAGTGTGTGCTAGAG	ASELALLENGINGVEL
0000011	ASIATTACTCCAAAGGCTAGGGCTTGAGATCATGCTGCGCTCCAAGCTCCATGCTCCCTAGCGTTTCTTTAAAAACGA	36 LLQRLGLEIMLCAPSSMLPSVSLKTTH
ECC071	CGCACAACGTTGAAGAAGCGATAGCATTTGCAGACATTTTAATGAGTTTGAGGACCCAAACCGAAACGGCACAATACG	NVEEAIAFADILMSLK I GTEKTIN I TIFA ST KOYGNAYCITOOBI KAHAKINKEVIIL
	CCCATTTTTGCGAGCTTGAAAGATTATGGCAACGCTTGTTATTGATATCATATAGAAAGCGGGGGGTGTTAGAAGGG	HPGPVHRDIDIESAVLEDERSKVLEGV
	AAAGAGGIGATIATI ACACCCCAGGCCCGGIGCATAGGGGGTGTTGGGGGTGTTTGGTTTTGCTATAGATTTTGCTATTGATTG	KNGVAMRMAVLEFLLLD
	GTCAAACTTAAAAAATGCTTTTTGGCGTTTTTTAAAAAATGGGTTTGGTTATAAAACGGCACAAAAACCCCTAATTTGA	
	TTAAGTTTTGATTTACTTTATCTCATTTTATGATGAAACTAAAAAAATTTCGTTATAATCTAAAAAAAA	
	AAAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	
	CTTTGCAAGCGTTTGATTATAAAATTGAAGTTTCAGCGGAGTCCTTTTCTAAAGTTGGCTTTAATAAAAAAAGATTGA	
	I AI AGCI AGGGGGGAI I AI CCI ACAGAGAGAG	

·V	V	

HP0339	で <u> </u>	37 GCGTGGATAAAGACGGCTTTTTAGTTACTCTTAATGGCTTTTAGGGTGCTTTCTCGTTCGGGCTTGAACGAAAAGGA GGGATCATGCTCAAAAAGGAATTGAAGTTGATGACCTTTAGGGATTAGGGATAATGAGGCCCA AATTCAAGCAGCCCTGACGCTGAAATTGAAGTTGAAAATGGGCAAAAAAAA	38 VDKDGFLVTLNGFRVLSRSGLNEKGG, MLMPDAEIEVDQNGGITFRDNEAQIQA GALALVSFSEPKNLKKIGQNLYTYQGE GVHQVSDSGALRQYMLEKSNVNAVRK; MSALIEINRFLDMYSKVLKTHQDDMNA EAINKLAAKA
НР 0339	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	39 CTTTAATGCAAGCAGGGATTTTAGGGGGGCTTAGCCAATGAAAAGCCAATTTGGCTTACATTACAAAAGCAAAGCAAAGCCCCTAAT GGTAGCGATTCCCAACAAGGCTTACCAAGGCTTAGCGGGCTTATTACACTAAAAACGGCGCTAATGGCATA CCCAAGCGCCCTTGAAAGCATTACCCGGTGGGGCGACAATGGATCAGGCCAATACACCTACCACCCCAG CTCGGCAGTCATTATTTAGCCGATAGCCATCATTGCTAATGGACTCACCGCTTCTATGATTTTTTAGCGGCATAGCAAAA TTTCGCCAATAAAGCCGCTAAACTGACGCACTTCAAGCTATAGCCAGATGCAAGATGCAAGAACAAAAA TTTCGCCAATAAAGCCGTAAGCGGATTTCATCACCAATTGGCGAAGAGCCCCCTATTTGGATTTAACACAACAAAA GCTTGCTCAGTAACACGAACTAGGGGCAATTGATGGTGCTAATCATCAAACAAA	40 LMQAGILGGLANEKQFGFTYNKAPNG SDSQQGYQSFSGPGYYTKNGANGTT QAPLKALPAGATIGSGNGQYTYHPSSA VYYLADSIIANGITASMIFSGMQNFANK AAKLTGTSSYSOMQDAINYGESLLSNT VAYGDFITKWVAPYLDLNNKGLNFPS YGGQLNGANHQTPQLTPQQAQQEQK VINNQLEQATNAPTPAGINRILANPYSP
HP0339	41.66 6.6 CA TTA	41 GGCGTTGTTCAAAAGCATGGCAACAAGAATCAAGAGAGTTTGAAGCAATTTGAAGTTTATCAAAGTGGGG GGATTTCAAGGAATGAAAAAATCCAATATTTTTATAACGAGATTTTGAAAAACCCCTATGGCTCAAGAGAAGAGGG CATTAGCCCTGGAGTTTGGCACTATTATAGAACAAAAGCTTTTTGATAGGGAGCATTTGAATAGCGAAGTGATGGCAT TTATTGATAAGCATTATAAAAATCATGTTTTCCATATCGCTTCAGCGGCCTTGCATAGCGAATTGCAAGTGTTGTGCG AGTTTTAGGGGATCATTAAAGAGTGTTTTAAGGGCGTTGAAGGGGGGTCC	42 ALFOKHGNKNOESLKOFEVYHYGSGG ISRNEKIQYFYNEILKTPIAGEEVDALAL EFGTIIEOKLFDREHLNSEVMAFIDKHY KNHVFHIASAALHSELÖVLCEFLGIIKYF KSVEGS
HP0338	44 A A A A A A A A A A A A A A A A A A	43] AAAACAACAAAAAGGAATACCCATGGATATTCGCAACGAATTTTTACAATTTTTCAAAATAAAGGGCATGCCGTTTAT CCTAGCATGCCTTTAGTGCCTAATGACGCTACCTTGCTTTTTACCAATGCCGGCATGGTGCAATTTATAAAGATTTTT ACCGGGATTGTGCCACGCCCTAGCATTCCTAGAGCGGCAAGCTCGCAATTGTGCATGCGCAGGCGGCAGCAT AACGATTTGGAAAATGTCGGTTATACCGCAAGGCCACACGCTTTTTGAAATGCTAGGGAATTTCTTGGGGATTTTGGAAAAGAAGAAGAACTTTTGGAAATGCTTTTTGGGGATTTTTTTT	44 KOOKGIPMDIRNEFLOFFONKGHAVYP SMPLVPNDATLLFTNAGMVOFKDIFTGI VPRPSIPRAASSQLCMRAGGKHNDLE NVGYTARHHTLFEMLGNFSFGDYFKE EALFAWEFVT
666	GACACA GACACA ATGGA ATTTA GCCCC TAACC	13 I CARAGARA CARARAGE LAGGACCOTARATAGCCAAGGCGTTTTTTTAACGCCAGGCGGATTTTTG GACACTGATGCACTATTGAAACAGCGCTTTGGAATTAGAAAATTACAAGCCTTTAGAAAACACATAAAAAGGGC ATGGAACAAGAACGCTTAATAGAAGAGCGCTTTTTGCAAGAGCCATTGCCCTTATTTGAGCGCGTTAAG AATTTAGAACAGCTTCAAACGCTTTAGAAGCCTTTTTTACAAGAGCCCTTTTTTAGAAGACCCTTAATTGAGCGCGTTAAG GCCCCTTTTCTTAGAAGAGCCTTCAAACGCTTTAGAAGCCCTTTTCTTACTTA	46 KEIKKÁNSTLNSÖRRFFNASÖIRLMDT DALLKOSALELEKLÖALEKHIKKGMEÖ ERLIEESÖTLFLÖEHCPYLSGYKNLEE ASNALEVGEONNALFLLKEPKLARLLS RLÖLMSALNALCÖÖVLENÖAHN

PCT/EP01/15428

			•
66 66 66 66 66 66 66 66 66 66 66 66 66	47 GGATCAAGTGAGT GAGAAATTTCTAGG GTGGTGCTTACCG TGTGGCGATGAG GTGGGTTTAGTGA GATTTAAGGGTA AACGTTCATCA TAGAAACGCCGA CATGACTTCATTCA TATGGCCTTGTTC TCACAAGCGGTGC AATTAGTCGTGGAT GATTTTGGAGCGGTGCA	47 IGGATCAAGTGGGCTGTTGCACACGATTGAATTGAGCTCTGATGATGTGTTTGGAGGCCATTAAAGGTCAGGTGAGGTGAGATCAAGGTCAAAGGCCATTAAAGGTCAGGTGAGGCGATTTCTAGCCTAAAGGCCTTTAAAGGCCTTGAAAGGCCTTGTGCCAAATGGCTACCGGCGTGGGGGGGG	48 DQVSGLLHTIELSSDDVFEAI (DQVREE) SSALRSVLEEVKPDLAKDIVCINGVNLT 9 GGGALIKGLDKYLSDMVKLP/YVGDEF9 LLAVAKGTGEAIQDLDLLSRVGFSE 10
HP0339	49 GGGATGTGG GATAAATTC1 CCTTTATAGA AGAAGACAT TTTAAAGCC1 TCCTTTGCC GCGTTATCGC CTCTGGTTTT CAAAACGCTA TAGAATGCA1 CGCAAAATGA GAAGTTTAAAA	49 GGGATGTGGATTTGTCAAACAGAGTGGCTTTGGAAGAATTTTAGCCCTAAAACCATGGCTTTTAAGCTTTTAGCGCG GATAAATTCTTTAACAGTGCGCAAGCGGCATTATTATGGGGCAAAAAGCGTTGAAGCGTTTAAAAAAACCACC GATAAATTCTTTAACAGTGCGCAAGCTAAATTATTATTGCAGCCTTAAAAAGCGTTGAATCATCA GAAAAATCTTTAAGGGTTGGGTGAAAATCGCCTCACCTTGCTTATTGCAAAAGCCTTGCATAAATCATCA AGAAGACATTACAATCCATGCGTTATTGAACCAAACTAAAAAAAA	50 DVDLSNRVALEEILALKPSLLSFSADKF FNSAQAGIIMGQKERVEALKNHPLYRV LRVGKITLTLLFCSLKAWINHGEDITIHA LLNQTKDALLQKALKLYALLKFLELNVS IASSFSKIGNLFGRELESFCVKIQPKNT RALNSEKLYLKLFQKGVIARISCEFVCF EVFSLNEKDFEKIALVLEEILNKA
HP1427	51 AAAGTGGAG AAGCGGGCA CCAGCCAGG AAGAATTAA TTAATGAAGC AGATAAAGGC	51 AAAGTGGAGCGGTATATCCACTGAAAATTACGCAAAAATCAATAAAGCCTATCAAATCATCCAAAAGGCTTTTGGAGC AAGCGGGCAAGAATTACTCCTGCCTTAAGCGACACCAAGGAACTTTTTGAATTAAATGAAAAAAAA	52 KWSGISTENYAKINKAYQIIQKÜFGASG QDIPALSDTKELNFEIKGKKNDISVQPG ERWKFPWTNGKFVSVKWVNGKYEIK EDIKVSNNAQELLKQASTILTTI NEACP WLSNGGAGNVAGGNSLWAGIDKGDG SACGIFKNEISAIQDMIK

—PC1	/EP01/	15428
------	--------	-------

02/066501	10 7 8		PCT/E
54 NKLKAGELIDEKKAGEIKNELEKESYAISSSSINKKSKKSPTPPPFMTSTLOGSASSSSILGESTAINGSASSSSILGESTTAMSIAGKLYEGVATPGGVAGGINTYMRTDSLNIAKEALEEARNKILKDDYGVITYMRTDSLNIAKEALEEARNKILKDDYGVITYMKAGAREALESKUNKNAGEAHEALESPAILESVANKNAGEAHEALESVANKNAGERGEKANGAGERGEKANGAGARGERGEKANGAGAGARGERGEKANGAGAGARGERGERGAGAGAGAGAGAGAGAGAGAGAGAGAG	56 EYNKINAISÖSLÖNTLENKNNDLKIEND YÖHLLTÖASTINTLOSÖCPGIDGGNGK PWGINASGNACNIFGNTFNAITSMIDSA KKAAADARRTAPESPNÖPSAFNNADF NKNLNÖVSSVINÖTISYLKGÖNLATIYN TLÖKTPÖSKGFÖSLVSKSSYSYSLNET ÖYSEFÖTTTKEFGHNPFRSVGLINSÖS NNGAMNGVGVÖLGYK	58 LGSĞNAWĞTĞGSASVTFNSQTSLILN QANIVSSQTDGIFSMLGDEGINKVFNQ AĞLANILGEVAVÖSINKAĞGLĞULIVNT LGSNSVIGĞYLTPEQKNÖTLSÖLLĞON NFDNLMNDSGLNT	60 FÖITNNAEGLLNÖAANIMÖVLNTÖCPL VASTNINENTPGGGOPWGLSTSGNAC TO SIFÖDEFSÖVTSMIKNAQEIIAÖSKIVSE TO NAQNO
53 GCAACAAACTCAAAGCCCAAGAACTCATTGATGAAAAAAAA	55 TGAATACAACAAATCAATGCGATTTCTCAATCGCTCCAAAACCCCTTAGAAATAAAACAATGATGATGATGATGAATTGAAATTGAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAAATTGAAAGCCCAAGGCAATGCCCAGGCATAGACGGAAGCCCAATGCCCAATGCCCAATGCCCAATGACGGGAAGCGGAAGATGCCAATGCCAATGCCAATGCCAATGACGCGATAGACGCATCACATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGCCAATGACTACACAGTTAGCATGACTAAAAAAGCCGCCGAGATGCCCGAAGTGCCCCAGAAGTCCCAAAGCCCAAGTGCCTTAACAACGCTGAATAAAAAAACCTTAAATGAAAAAGTTTCAAAAAAAGCTTCAAAAAAGCCTTCAAAAAAGCCCTCAAAAGAATTTAATGACAAAGGTTTGGTGAGCCGAATTGAAAAAGCCTTCAAAAAAAA	57 CTTTAGGGAGCGGGAACGCATGGGGGACTGGGGGGGCGCGCGTAACTTTTAACAGGCCAAACTTGGCTCATTCT CAATCAGGCTAATATCGTAAGCTCGCAAACCGATGGGATCTTTAGCATGCTGGGTCAAGAGGGGTATTAATAAGGTTT TCAATCAAGCCGGGCTCGCTAATATTTTGGGCGAAGTGGCGGTGCAATCCATCAACAAAGCCGGGGGATTAGGGGAA TTTGATAGTAAATACGCTAGGGAGTAATAGCGTGATTGGGGGGTATTAACGCCTGAACAAAAAAATCAAACCCTAA GCCAGCTTTTAGGGGAGAATAACTTTGATAATCTCATGAACGATAGCGGTTTGAATAGGG	solatticacatcaataacecteaacacaccecteaacacceccaaacatcateatcatcataatacecaatcatcatcataacacatcataaccecaataaccecaataccecaataaccaataaccaataaccaataaccaataaccaataaccaataaccaataaccaataaccaataaccaacaa
HP1427	HP1427	HP1427	HP1427

W	O	02/0	6

	PCT/EP01/15428
64 GLGLNLPNISSTRPTKAN'RESFFNTLO AEINGAHFIEVFSGSASMGLEALSRGA KSAVFFEONKSAYKTLENISI-FKNRLK KEMEIQTFLDDAFKLLPTI.CLKNGVLNII YLDPPFETSGFLGIYEKCI-QALERLLKR FNPKNLLVVFEHESMHEMPKSLVTLAII KQKKFGKTTLTYFQ	66 GQDTTTITCNSYYEPGHGGPISTANYA KINQAYQIIQKALTANGANI3DGVPVLS NTTTKLDFTINGDKRTGGKPNTPEKFP WSDGKYIHTQWINTIVTPTETNINTENN AQELKQASIIITTLNEACP UFQNGGRS YWQGISGNGTMCGMFKNEISAIQGMIA NAQEAVAQSKIVSENAQNONNLDTGK PFNPYTDASFAQSMLKNAQAQAEILNQL AEQVVKNFEKIPTAF 61
63 GGGATTAGGCTTGAATTTGCCTAACATTTCTAGCACGCGCCCCACCAAAGCGATCGTAAGAGTCGTTTTTAACA CCTTGCAAGCAGAATTAATGGAGCGCATTTATAGAAGTGTTTTCAGGCAGCGCTTCTATGGGTTTAGAAGTTTGA CCTTGCAAGCAGAAATTAATGGAGCGCATTTTTGAACATAAGGCGCTTTTAGAAAATTTTCCCTTT TAAAAAACGCTTGAAAAAAGGAAATTGAAACCTTTTTAGATGATGGCTTTTCAGCCTTTTGAAAAATTGCCCACGCTGTGTT TTAAAAATGGCGTTTTGAATATTATTTTTTTGAACCTTTTTGAACAAGTGTTTTGGGCTTTTTTTT	65 AGGACAAGATACGACCATCACTTGCAATTCGTATTATGAGCCAGGGACATGGTGGGCCTATATCCACTGCAATTTTATGAATTGAGCCTATATGCACTGCAATTTTAAGCAAATTTTAAGCAAAATCAATGCAAATACACCCCCCCC
НР1427	HP1427
	63 GGGATTAGGCTTGAALTTTCTAGCACGCGCCCCACCAAGGCGATCGTAAGAGGTCGTTTTTTAACA CCTTGCAAGCAGAACTAACATTTTTTGAACAACAACAAAGCGGCTTCTATGGGTTTTAGAGACTTTTGA CCTTGCAAGCAGAAATTAATGAACAACAACAACAAGCGCTTTTAGAAATTTTCCTTTT GTAGGGGGGCTAAAAGGAAATGGAAACCAACATTTTTGAACAGCGCTTTTAGAAATTTTCCTTTT AAAAAACCGCTTTGAAAAAGAAATGGAATTCAAACCTTTTTGAACAGTGGGTTTTTGCCCACGCTGTGTTT AAAAAATGGCGTTTTGAAAAAGAAATGGAACCTTTTTTTT

C	٠,	
c		١

68 TNNGLCFGGNLDLYNEMVGSIKTLSG ISKNIFGGNNNTTSONLSNOLSELNTAB ISVYLTYMNSFLNANNOAGGIFONNTNG OAYGNGVTAQQIAYILKOASITMGPSCT DSGAAAFLDAALAQHVFNSANAGND LSAKEFTSLVQNIVNNSQNALTLANNA NISNSTGYQVSYGGHIDQARSTQ	70 GIDVSTGEFKGADIHSQTTQSMENIKAI LKEAGLGMDSVVKTTILLKSLDDFAVV NGIYGSYFTEPYPARATFQVAKLPKDA LVEIEAIAIK	72 AETRAKGFVMÍVVLHSHLENALKÖLKEL IDLTERDIRDIKLAKHTEIFERNHÖKGLA IQAFEKEKANIDVOMI.SLKNÖFPÖKEM SELLDEKTSĎFLNOMRESLFVLKEKNLI YSRMAFAVSEFYSSLIQQIIPHDTČDYK GSRHVGSHFLRVOA	74 TTÖSPNSTVMGALNTVLÖRVSNFÖÖSI ONAFÖNGESNIGAWANNAIYNTNGSOS GEMTPNNNÖÖLRIOLRANFYÖLINTIN ÖÖVPTDMNALINÖSÖĞTÖÖTSGSAS	76 NSSSGGLSISGNAGLÖNIL 78 INIAGPTTGLITLSSQTVIDALGYGVSNTT- VGNQLEGISNILNOIGKRKDFYSSRQIS D SISQQIIGLKGSSDPLKAHSSQITAKLLS- NTGSAFDQGIALSTNIISSINSLNPSNNTFF QEVKKQLQNTAQSMTELLQQIEH 01
67 CTACTAACAATGGCCTTTGTTTCCAAGGTAACCTGGATCTTTATAACGAAATGGTTGGCTCTATCAAAACTTTGAGTC AAAACATCAGCAAGAACATCTTTCAAGGCAACAACACCACGAGCCAAAACCTCCCAACCAGCTCAGTGAGCTT AAACACCGCTAGCGTTTATTTGACTTACATGACTCCTTCTTAAACCAACC	69 AGGCATTGATGTAGCACCGGCGAGTTTAAAGGCGCAGACATTCATT	71 GGCTGAAACAAGAGGATTIGTTATGGTCGTTTTACATTCTCATTTAGAAAGGCGCGCTAAAACAAGAGAGAG	73 CAACCACACATCTCCTAACAGCACGGTGATGGGACCTTTAAACACCGTGTTGCAAATGTCAGCAATTTCCAACAA AGCATTCAAAACGCTTTTCAAAACCAAGAAGTAATATCCAAGCTTGGGCGAATGCGATTTATAACACTATGGGAGT CAGTCGCAAGAGATGACACCTAACAATAACCAAGATTTACGCATTCCAATTGGGCGAATTTTACCAGCTCATCAAT CAGTCGCAAGAGATGACGAATAACCAAGATTTACGCATCCAATTGAGGCGGATTTTTACCAGCTCATCAAT ACCATTAACCAGCAAGTGCCTACAGACATGAATGCTTTAATTAA	75 GCAATAGCTCTTCAGGGGGTTTGAGCGTCAGCGGGAACGCCCAATTGCAAATATTTTÄA 77 CGATCAACATTGCAGGGCCTACTACCGGCCTTATCACTTTAAGCTCTCAAACCGTCATTGAGCTTTAGGCTATGGC 77 CGATCAACACTGTTGCAACCAATAGAGGGCCTTTTTAATATTCTTAAATCAAATTGCAAATTGGCAAAAGAAAG
HP1427	HP1427	HP1427	HP1427	HP1427 HP1427

HP1427	PIAACCACAACCCAAACCATGAACGGGAAAAGGGTAACCACCACGATGAGTGGTTCAAAAGTGGTTGGT	88 86
	GGACATAATAGCCAAATATTGGTTAAGTCAATCTGTGGATTTAGACCCATACGACCCTATTAAAGTTGTAGTTTCTTT CACCCACAACCTGAAAATGGTAAAGAGACTACAAAATTTAAGAACCAAAGATGGGATTGAGAACATTTATGCGACA CACCCACAACCTGAAAATGGTAAAGAGACTACAAAATTTTTAAAAAGACCACAAGGATTGAGGACTTTATGTCTAGC CTCTATAACACATTGGGTAGGGGTTATGTGGGAAAAATATGGCAAGGACACAAAGACATTAAAAAGACATAAGAATGAAT	CTTT SQSVDLDPYDPIKVVDFFHPQPENGKE SACA TTKFKNYKDRIENIYATLYNTLGRGYVD FAGC KFFKKEATMRDFMSSDKFVERYRYTR GAAT KENMARTQALKOIMNIDFDFIGYIEVLG FOAC YWKDNPKDNILPDKEVSIFVFGNEPSS GGTA TFDLKNHLLIWGKGFRQYAICYGGQLIA NKNKTYRIDLISCRPDNFGSEVWAKFTGI KESVDSOI POAI TRINDSJYTFI

02/066501	10> 10> 10 m	PCT/EP01
BB QTLLPTAQTLLNHAKKTQSLNGVEIVG SELLDKVIYLDQAPIGKTPRSNPATYTG'S MDEIRILFAEGKEAKILGYSASRFSFNVGKGRCEKCQGDGDIKIEMHFLPDVLV CQCDSCKGAKYNPQTLEIKVKGKSIADV LNMSVEEAYEFFAKFPKIAVKLKTLMD VGLGYITLGQNATTLSGGEAQRIKLAK ELSKKDTGKTLYLDEPTTGLHFEDVNH	90 YKASLTTNAAHLHIGKGGINLSNGASG RTLLVENLTRAAHLHIGKGGINLSNGASG RTLLVENLTRAGTOTKNGTATFNN DISLGRFVNLKVDAHTANFKGIDTGNG GFNTLDFSGVTGKVNINKLITASTNVAV KNFNINELVNKTNGSVGEYTHFSEDI GSGSRINTVRLETGTRSIFSGGVKFKS GEKLVIDEFYYSPWNYFDARNIKWVEIT RKFASSTPENPWGTSKLMFNNLTLGO NAVMDYSGFSNLTIQGDFINNQGTINY LVRGGQVATLNVGNAAAMFFSNINVDS ATGFYQPLMKINSAQDLIKNKEHVLLKA KIIGYGNVSLGTNSISNVKILGGFKERLA LYNNNNRMDICVVRNTDDIKACGTAIG NGSMVNNPDNYKYLIGKAWKNIGISKT ANGSKISVYYLGKSTPTEKGGNTTNLP TNTTSNVRSANNALAQNAPFAQPSAT	92 DKGLKKVFKDSKKDACGFIYEISEFMK AYTALLKKÖDRYVYLLRYLPSRYWASI LTTALYKRYPDFDALKKLLVSYYYQTWI AGGTITRIKOTSINIKNWKSNKSVETIKE LILNSIDSYNTFDQYLYNLWDSSSVYHS KWVRPVLALANYFMADEEKPHFIAMD AETÖVEHILPÖTPKRĞSÖWNADFDKE KREEWVNNIANLTLLKRKKNAHALNGD FDEKRKIYGGKÖTSKVISCYDITKELYS NYRKWNEKSLĞRÄYKSLYNTITPVLHI EGĞEDÖFEDÖFÖLE
	68	91 CCGATAAGGGATTAAAAAGGTGTTCAAAGACAGCAAAAAGGCCCTTGCGGGTTCATCTTGAGATCAGCGATTC ATGAAGCCTATTAACGACTGCCATTGCTAAAAAAACAGGCCGATACGTCTATTTGAGGTTCTCCCCCTCTAGGTATTGG GCCAGCATTTTAACGACTGCCCTTTATGCAAAAACGATACGCTTTGAAAAAGCTTTTGGTGCTCTTATTAAAAAGCGTTAATAAAAAGCGTTAAAAGC AATAAGAGCTTGGATTGCAGGAGGCTCAAATACGAACCAGTATCAACAATATTGAAAAGC AATAAGAGCGTTGGATTGCAGGAGGCTTAAATTGAATAGCAACCAGTTTATAACAACTTACAAAAAGC AATAAGAGCGTTGAAACCATCAAAGAGCTTAATTGAATAGCATCTTAAACACCTTTATACCCCTTATAAAGCAAATAATACAATAAAAAAGAAGAGAAAAGAAAG
HP1301	HP1301	HP1301

11,045,40	43/ACAAAAAAAAACGCCACGCCAAAAAAAAAAAAAAAAAA	94 EKNASFVTNNLNIQGAFNNNATOKIEV	2/0
TF1347	CONTRACTOR AND A TANGET OF THE TANGE OF THE	LQNLVIASNASLSTGIYGLEVGGALNN)60 ŽŽ
	TOATTATTATTATTATTATTATTATTATATATTATTATTA	GAIHFNLENTQTPTPLICAEGIINLNTTC	550 E
	ATTANCETOR AND AND AND AND AND AND AND AND AND AND	TPFMNVNNSMANNTTYTLLKSSRYIDY 1	01))
	A PROPERTY GATTER ATTACATA COCCOA COCCOA COCT TO CONTROL OF THE CANTOT C	NINPNSLOSYLNLYTLININGNHIEEKNG	KNG
	CAACGGGAACCACCATAGAGGAAAAAAACGGCGATTGACTTATTTGGGCCAACGGGTTTTGTTGCAAGATAAGGGG	ALTYLGQRVLLQDKGLLLSVALPNSNN	SNN
	TTATTGTTAAGCGTTGCCCAACTCAAACAACGCTTCTCAAAACAACAACATTTTAAGCCTTTCTGTAAACAACAACATTTTAAGCCTTTCTGTAAACAACAACAACAACAACAACAACAACAACAACAACAA	ASQNNILSLSVLYNQVKMSCGDKAMD	AMO MO
	AAGTTAAAATGTCTTGCGGCGATAAGCGATGGATTTTACCCCCCTACCTA	FTPPTLQDYIVGIQGQS/ALNQIEAVGG	ည
	GGCAAAGCGCGCTCAATCAAATTGAAGCTGTTGGGGGGAACGCTATCAAGTGGCTTTCAACATTGATGGAGAC	NAIKWLSTLMMETKENPFFAPIYLKNH	Ē
	TAAAGAAACCCGTTTTTGCGCCGATTTATTAAAAAACCACTC		1
2,7,0	os Carcattaatre TTTCCaataaCGCCCCCCCCACGATTATGCGAGCTTGATTGCGAGCTTGATTGCCACCTTCACTTTTTTTT	96 TINVSNNATINDYASLIASNGSHLNFNG	FNG
HF1542	TAYAGGGGGGTTAAATTCAAATTCAAGGAATATTAAGGGGGGGTTTGAATAATTCCTCTATCGTGTTTAAAGGGGGGGG	AVNFNSANITTSLNNSS VFKGAVSLGG	166
	CANADA CONTROL ANTITA A	QFNLSNNSSLDFQGSS/AITSNTAFNFY	NFY
	COLOR TO A TAXA TAXA TAXA TAXA TAXA TAXA TAXA	DNAFSOSPITFHOALDIKAPLSLGGNLI	SNLL
	Geter I AA I LOTAL GATTER CONTINUE	NPNNSSVI DI KNSOLVEGDOGSLNIAN	NAN
	AGI I I GGGAGGCAACCI II I AAACCCI IAACAACAGCAGGCAGGCAGGAGGAGGAGGAGGAACAGCAACAGAGGAG	VALIDATION	24
	TCAAGGGAGTTTGAATATCGCTAACATTGATTTACTAAGCGATCTAAATGATAAAAAAICGIGIGIGIAIAACAICAIC	IDEL SULFINDININA TRIFLAADININSI	- i
	CAAGGGGACATGAATAGTAATTGGTATGAGCGTATCAGCTTCTTTGGCATGCACATCAATGACGGGATTTATGATGC	JERISFFGMHINDGIYDAK,NO. YSF INFL	Ę
	TAAAAACCAAACTTATAGTTTCACTAACCCCCTAAAAATCACGAGAGAGA	NNALKITESFKDNQLSVTLSQIPGIKNTL	N I
	ACCEPTAGE CTCTCTAGA TECCEGGETATTAGA ACCECTE TAGA CATTER A CATTER A CATACAGA A CATTER A CATACAGA A CATTER A CATACAGA A CATTER A CATACAGA A CATTER A CATACAGA A CATTER A CATACAGA A CATTER A CATACAGA A CATTER A CATACAGA A CATTER A CATACAGA A CATTER A CATACAGA A CATTER A CATACAGA A CATTER A CATACAGA A	YNIGSEIFNYQKVYNNANGVYSYSDDA	DOA DOA
	CATTACT ACCOUNT OF THE PROPERTY OF THE PROPERT	QGVFYLTSNVKGYYNPIVQSYQASGSN	GSN
	COLTATION OF THE TANK OF THE T	NTTKNNNLTSESSIISQTYNAQGNPISA	PISA
	CONTRACTOR CON	LHIYNKGYNFNNIKALG()MALKLYPEIK	픴
	THE CALLY CONTACT AND CONTACT	THE STATE OF THE INSURAL INSURAL INC.	H IX
	TTCAACAATATCAAAGCGTTAGGGCAAATGGCTCTCAAACTCTACCCTGAAATCAAAAAGGTATTAGGGAAATGATTTT	DNDWK	į
	TCGCCCTCA	SACOLE.	

•
•
_
•

02/066501	PC'
98 LEVGNRVGSGAGTHTGTATLNLNANI/© 98 LEVGNRVGSGAGTHTGTATLNLNANI/© SLSGDVCSSLASVGIGANCSTSGPSYGS FKGTTNATNTAFSNASGSFTFEENATI-SGAKWNGGTYTFNKEFSATNNTAFSS GSFNFKGVSSFNGGTFTFNNQTNPTNNAQ ATFONSSFNGGTFTFNNQTNPTNNAQ ATFONSSFNGGTFTFNNQTNPTNNAQ ATFONSSFNGGTFTNNATHWANIACHTICNASFNNATHNASGGTTSNLLNHANIACHTGSCANTLNHANIACHTGSCANTHRASLSNPQSFAQGLWD IITYNGYTGALKTGELSNPQSFAQGLWD IITYNGYTGALKTGETSSHNSIIIQALESGTYTPPPVINGSKFÜLSAHNSIIIQALESGTYTPPPVINGSKFÜLSAHNSIIIQALESGTYTPPPVINGSKFÜLSAHNSIIIQALESGTYTPPPVINGSKFÜLSAHNSIIIQALESGTYTPPPVINGSKFÜLSAHNSIIIQALESGTYTPPPVINGSKFÜLSAHNSIIIQALESGTYTPPPVINGSKFÜLSGANLIFNGVIGNINGNAGIYSSSMTFSTQ SALNGHCGPWPYYQCTGTTNGTYS GSALNGHCGPWPYYQCTGTTNGTYS AYHVYITANILRSGNRICTGGAANLIFNG VDSINIANAGIYSSSMTFSTQ SMÖNSONLNGLNSNGKLSVYGTFTN EAKÖGKFIFNAGGAVFENTNFNGGSY	100 AMDEGLKILDTVKVKATQAAQDGGTTE SRKAIQSDIVRLIGGLDNIGNTTTYNGG ALLSGOFTNKEFQVGAYSNQSIKASIG STTSDKIGQVRATGALTASGDISLTFK QVDGVNDVTLESVKVSSSAGTGIGVLA EVINKNSNRTGVKAYASVITTSDVAVÓ SGSLSNLTLNGIHLGNIADIKKNDSDGR LVAAINAVTSETGVEAVTDÖKGRLNILR SIDGRGIEIKTDSVSNGPSALTMVNGG QDLTKGSTNYGRLSLTRLDAKSINV
97 ITTAGAAGTGGGTAATCGTGGGGATGGGGAGCTGGCACGCCGCCACTTTAAACTTGAACTTTGAATTCCAATATCCAATATCAATGCAAGTGTATTAAAGGGAGTTATAAAGGGATTTGCAATTCCAATATCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTCCAATTTGCAAGTGTTTTAAAGGGATTTTGCATTTGCATTTGCATTTGCATTTGCAATTCCAATTCCATTAAAGGGAGCTTAATTCCAATTCCATTAAAGGGAGCTTAATTGCAAGGGGCAATTTGCATTTTAAAGGGACTTTAATTTAAAGGGAGTTTAATTTAAAGGGAGTTTAATTTAAAGGGAGTTTAATTTTAATTTTAAAGGGAGTTTTAATTTAAAGGGAGTTTTAATTTAAAGGGAGTTTTAATTTAATAA	99 GGCTATGGATGAGCAGTTAAAAATCTTAGACACCGTTAAAGGTTAAAGGTCAAGCGGCTCAAGCGGCTCAAGCGGCAAGTA CAGAATCTCGTAAAGCGATTCAATCTGACATCGTTTGATTCAAGGTTTAGACAATATCGGTAATACCAATGTT ATAACGGCCAAGCGTTATTGTCTGGTCAATTCACCAACAAGGATTCCAAGTAGCGCTTATTCTAACCAAGCATTA ATAACGGCCAAGCGTTATTGTCTGGTCAATTCACCAACAGGATTACCACAGGCGTTATTCTAACCAAGCATTA AAGCTTCTATCGGCTCTACCACTTCCGATAAAATCGGTCGTATCGCTACAGGTGCGTTAATCACCGCTTCT GGAGATATTAGCCTTGACTTTTAAACAAGTGGTTAACAGAACTCTAACCGAACAGCGTTAAAATTGGGG GCGTTATCACCACGAGCGTTTTAGCAGAAGTGATTAACAGAACTTTAACCGAATTGGCGG AATATCGCAGATTTAACGGAGCTCAGAGCGATTAGTCGCAGTAATTTAACCGTTACTTCAGAAACCGG CGTGGAAGCTTTATAACGGATCAAAAAGGGCGTTGAATTTGACCAGTAATTAACAGAATCAAAAACCGG CGTGGAAGCTTTAACGGATCAAAAAGGGCGCTTGAATTTGACGAGTTAAAATGGCGTTAAAATCAAAAACCGG CGTGGAAGCTTTAACGGATCAAAAAGGGCGCTTGAATTTGCCAGTTAACAAAACCGG CGTGGAAGCTTTCTCTCACACCCTAAAAACGATCAAATGCCGGCTTAACAAAACCGG GGAAGCTTTCTCTCACACCCTTAACAAAAGGGCCTTAACAATGCCGATTAACAAAAAGGCTCTAACTAC GGAAGCTTTCTCTCACACCCTTAACACAAGAGCCTTAACTACTAACTA
HP1542	HP1542

P	C{1}	[/]	EP	01	/1	54	2	8

SGAILV COTSWISS SGENACIO SIGGSIT SIGGSIT SIGSA INPTSP SIGSA IRLKNI CGANN	GTLDL YRADI SGDFK STIMS KRML	SKNVN FNGTT FNGTT FNGTT FNGT TFKQ TFKQ TFKQ TFKQ TFKQ TPKQ TPKQ TPKQ TPKQ TPKQ TPKQ TPKQ TP
102 FKAKDIFITGAVGSGNEIWKTGGGALLV FESSNELSANGAYFONINRAGTOTSWIS NLISNNSVNLTNTDFGNOTPNGGFNAS MGRKITYNGGIVNGGNI:GFDNVDSNCT ATTISGVTFNNNGALTYKGGNGIGGSIT FTNSNINHYKLNLNANSVTFNNSALGS MPNGNANTIGNAYILNASNITFNNLTFN GGWFVFNIPDAHVNFQGTTTINNPTSP FVNMTGKVTINPNAIFNIONYTPSIGSA YTLFSMKNGSITYNDVNNLWNIIRLKNT QATKDADKNHTSSNNNTHTYYYTYNL GGTLYNFRQIFSPDSIVLGSVYYGANN LYYTNSVNIHDNVFNLKN	104 AFLGAIKANGLVDFSKVI ONTTIGTLDL GPNATFKANHLIVNNAFNINSNYRADI SGNLNVVKGAALSTNENGLNVGGDFK SEGSLIFNLNNKTNOTIINVAGNSTIMS YNNOALIHFNTQLKQGAYTLINAKRML YGYDNOIIRGGSLSDYLKLYTLIDFNGK	RMQLNGDS 106 GGIRYDLKANNIIFNNSQI AVIDVSKNVN QSSLNGNVTFNNSRLSVI(PNAAINIGD SQTQTALENASSLSFYNNSVANFNGTT AFNGVSYLNLNPNAQVSI-NQVNFNNGT AFNGVSYLNLNPNAQVSI-NQVNFNNGT NVTFYGIPLFGKTPDFGNSARLINFKGN TNFNQATLNLRAKNIIHINF-QGVSTFKQ NSTMNLAESSQASFNALIV-GGETNFNL NNSSLLNFNGNSVFNAPVSFYANHSQI SFTKLATFNSDASFDLSN VSTLNFQSV LLNGALNLLGNGSNNLAINAKGNFSFG SKGILNLSYMNLFGGDKKDY SFDNGVHSWRFTNPLNTFTITETIHN NRLKVQISQNGVSNNKMFNLFTITETIHN NRLKVQISQNGVSNNKMFNLAPSLYDY OKNPYNFTENSVNYTSDLVGTVAN TENSVNYTSDLVGTVAN
FKAKDIFITGAVGSGNEN FESSNELSANGAYFONIN NLISNNSVNLTNTDFGNG MGRKITYNGGIVNGGNI ATTISGVTFNNNGALTYK FTNSNINHYKLNLNANS MPNGNANTIGNAYILNAS GGWFVFNIPDAHVNFQG FVNMTGKVTINPNAIFNIG YTLFSMKNGSITYNDVNN GGTLYNFRQIFSPDSIVL LYYTNSVNIHDNVFNLKN	CANGLVDF KANHLIVN VKGAALST NLNNKTN(IHFNTGLK(IDS KANNIIFNI KANNIIFNI KANNIIFNI KENTONNA PLEGKTPC TLNLRAKNI RESSOASF FINSDASF FILGNGSNI SYMNIFGG ILLGNGSNI SYMNIFGG IGNNGYEK SYMNIFGG SNI SYMNIFGG SNI SYMNIFGG SNI SYMNIF SNI SNI SNI SNI SNI SNI SNI SNI SNI SNI
PESSNE FESSNE NLISNN MGRKIN ATTISG FTNSNI MPNGNI GGWFV FVNMTC YTLFSM QATKDA GGTLYN GGGTLYN	A AFLGAIK GPNATF SGNLNV SEGSLIF YNNOAL	RMQLNGDS GGIRYDLKA GGSINGNIKA SQTOTALEN SQTOTALEN AFNGVSYLN NVTFYGIPLF TNFNQATLN NVSTRINEAES NNSSLLNFN SFTKLATFNK CNIDGLNLLSYN ONIDGLNGVHSN SFDNGVHSN SFDNGVHSN NRLKVQISQN
		01
101 ITTTAAGGCAAAAGACATTTTTATCACAGGGGCTGTTGGATCGGGCAATGAGTGGAAAACGGGGGGGG	103 CGCTITITTAGGTGCAATTAAGGCTAATGGATTAGTGGATTTTCAAAAGTTTTACAAAATACTACGATGGGGACTTTA GATTTAGGGCCAAACGCTACTTTAAAGCGAATCATTGATCGTGAATAACGCTTTTAACAATAACTCTAATTACAGG GCTGATATTAGCGGTAATCTCAATGTGGTTAAAGGAGCGGCTCTCAGCACGAATGAAATGGTTTGAATGTGGGG GCGATTTCAAGAGCGAAGGGTCATTAATCTTAAACATAAAAACCAATCAAACGATTATTAATGTGGCTGGC	AGGGGGCATTCGCTATGATTGAAAGCTAATAACATTATTTCAATAACTCTCAAATGGTTATTTGATGGGGGATTTAAT TTGGGGATAGCCAAACGGCTTTAACATTAACATTATTTCAATAGCCTTCAAGCCCAATGGGTATTTAAT AACGGCACAACCGAACGGGATGTTAATTAAAAAGGCTTTCTTT
GGTGGGG CCCTAATE TTGATAAT TTGATAAT TTGATAC GGGTTAC AGCGTTAC ACCTATA ACCTATACAGG	TACGATCE FAACTCTA/ STTTGAATI TTAATGTG SCGCTTAC	TGATGTĞT SAATGCGG SAGCGTGC CTTCAATC WATCTAAT SGCTCTTA CAACGCT TTACAATTAACAATTAACAATTAACAATTAACAATTAACAATTAACAATTAACAATTAACAATTAACAATGAGG
TTTTÄÄGGCAAAAGACATTTTTATCACAGGGGCTGTTGGÄTCGGGCAATGAGTGGAAAACCGGTGGGGGGGGGCGTTGTTTÄÄGGCCAAAAGACTTGTGAAAGCCGGTGGGGGGGGGG	CGCTITITIAGGTGCAATTAAGGCTAATGGATTAGTGGATTTTCAAAAGTTTTACAAAATACTACGATCGGGACTTTPGATTACAAGGGCCAAACGCTACTAATTACAGGGGCTTTPGATTACAGGGGCCAAACGCTACTATTACAGGGGCTAATTACAGGGGGGTAATTAGCGGTAATTACAATGGTTAGAATGGTTTGAATGTTACAGGGGGGGG	105 AGGGGGCATTCGCTATGATTTGAAGGTAATAACATTATTTTCAATAACTCTCAAATGGTTATTGATGTGTGTCTAAGAATGGTAATAATAGGGGGGGG
CAATGAGT TTCAAAAT ATTTGGC GCCGCGC CCCCCTCA CAATCTTA VACCCCT TTACTATT GAAAATC GAAAATC CCAATAGCT TATAAATT CCAATAGCT CCAATAGCT CCAATAGCT	MAGTITTA ATAACGCT GCACGAA ACCAATCA CCCAACTC GAGGGAG	ACTOTICA ACTOTICA GCTTTCAG GCTTTT STACCOTO ACCOCAG ACCOCAG ACCOCAG ACTOTICAG TOTICAG TOTICAG TOTICAG TOTICAG TOTICAG TOTICAG
GATCGGG GGCTTATT AACACA TIGTCAAT ACTAACG CTATAGCA TTTAGCAT TTTAGCAT	ATTAGTGGATTTTCAAAAG SAATCATTGATCGTGAATA AAAGGGGGCTCTCAGC TTAATCTTAACAATAAACC STTTAATCCATTTAATACCC CAATTAAACGGCGGTTCA	TTCAATA WATTCAATA TTCAACCC TTGAAATTTA GAAATTTA CGACTTTT CCTAAACC TTTGAATC GATAACCC GATAACCC
GCTGTG SCTGTG ATTTGACA SGCGGGA TTTCATATA TTTGTTTT TTTGTTTT ATAGGCAACA ACACGCAACA	TTAGTGG/ ATCATTTG AAGGAGC/ TTAATCTTA AATCAAAT	AACCETTA AATTGAAT ATTGAAT ATTAGAT ATTAGCT ATTAGCT ACCTTGTT AAATTAG AAGGGAT AAGGGAT AAAATAT
TCACAGGG ACTACAGG CACTACAGG SCATACAGGGA ATGCCAA AGCGCTTA TTACACAA ACCTACAAA	TAATGGA FAAAGCGA FGTGGTTA TTAATCTT ATCAAGCT STTATGAC	AGCTAAT SATGTTAG SGCTTTAG SGTGTCTT TTAATCAG ACGATGA TAACTCAC TCTTTCAC TCTTTCAC TCTTTAA TGGGTCTA
SATTITIAN CCAAACGA CCAATAGC AAGATCAC TCACTAGC TATGCCTA TTTAGGG CATCAGGG CATCAGGG	ATTAAGGC SCTACTTT ATCTCAAI VAGGGTCA TTATAACA	TGATTTGA TGAATGGG CCCAACG CCCAACTT TACGGATT TACGAATT AAAACTCI AAAACTCI AAAGCGT TTTAGTTT TTGACAATT
CAAAAGA TITGAATTT TITGAATGT GGGGGGGA CAACCAC TAGGGAG CAACCCC CAACCCC CAACCCC CAACCCC CAACCCC CAACCCCA CGCATTA	AGGTGCA SCCAAACC AGCGGTA VAGAGCGA ACCATGTC	TTCGCTAI STCATCAT AGCCAAA WCCGCTA GCTAATGI TTTTAAAC SAATTTC AATCATTI GAATTTTC AGGGAAT
TTTTAAGGG CTGGTTTTT TGGATCAA AATGCTAT CAATGGCG GGGGGAGC CAGTGCTT TTTTAATAA AAAATTACA AAAATTACA AAAATTACA ATAACTTAT	CGCTTTTTAGGTGCAATTAAGGCTAATGG GATTTAGGGCCAACGCTACTTTTAAAGCG GCTGATATTAGCGGTAATCTCAATGTGGTT GCGATTTCAAGAGCGAAGGGTCATTAATCT ATTCTACGATCATGTCTTATAACAATCAAGA TAATGCGAAACGCATGGTTTATGGTTATGA	AGGGGGCATTCGCTATGATTTGAAAGCTAA GTGAATCAGTCATTGAATGGGAATGTT ATTGGGGATAGCCAAACCCAAACGGCTTTA AACGGCACAACCGCTTTTAACGGGGTGTCT TTCAATAACGCTAATGTAACTTTTTATGCA TCAATTTCAAGGGAATACGAATTTTAATCA TCAATTTCAAGGGAATTCAATAACCA GGTTTCTACTTTTAAACAAACTTTAATCA TTTTTATGCTAATCATTCTCAATACTCA TTTTTATGCTAATCATTTTAAATTTCTTTTCA CAGCGCTAAAGGGAATTTTAGTTTTGGGGTCT AAAAACTTCCGTTTATGATGTTTTGGGGTCA TTTTTATGGCATACAGATTGAAGCCTGAT CAAAACTTCCGTTTATGATGTTTTGCAAGCC
0 2 2 2 2 2 2 2 3 3 4 4 4 4 4 4 4 4 4 4 4	103 0 0 0 5 1 5 0 0 0 5 1 5 0 0 0 0 0 0 0 0	6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
HP1542	HP1542	HP1542
<u> </u>	<u></u>	오

76

	_	2	
Ę	J	ς	
-		÷	ī

02/066501	1	1= \ I	PCT/EP01/
108 LDGISLALGYLCLFFVLSASLISEKALSP KQYLQTAKDKITSLKNLKVIAITGSFGKS STKNFLLQILQTTFNAHASPKSVNTLL(S) STKNFLLQILQTFNAHASPKSVNTLL(S) LANDINGNLDDRSEIYIAEAGARNKGDP KEITCLIEPHLVVVAEVGEGHLEYFKTL ENICETKAELLDSKRLEKAFCYSVEKIK PYAPKDSPLIDYSSLVKNIQSTLKGTSF EMLIGSVWERFETKVLGEFSAYNIASAI LIAKHLGLETERIKRLVLELNPIAHRLQL LEVNQKIIIDDSFNGNLKGMLEGIRLASL HKGRKVIVTPGLVESNTESNEALAGKI DGVFDVAITGGELNSKTIASQLKTPÓKIL LKDKAQLENILQATTIQGDLILFANDAP NYI	110 NLEVITLYLHTEGITNPMLFAMGAIFLIG AIGFRVSLVPFHTWMPDVYEGNNPVF ASYISIVPKIAGFVVATRLF	112 HKÖKHÄKTRNYÄDEELDSÜKVEĞVTEİ LHVNERGTLGFHKELKKGVEANNKIQV EHLNPHYKMNLNSKASVKITPLGGLGE IGGNIMWNETPKSASVKITPLGGLGE FGVDILIPDFSYLHQIKDKIAGIIITHAHE DHIGATPYLFKELÖFPLYGTPLSLGLIG SKFDEHGLKKYRSYFKIVEKRCPISVĞ	114 IFDNNNKSANAKTGPATIAGGTKIKGE LHLDYNLHVDGELEGVVHSKSYVVIGQ TGSVVGEIFTNKLVVSKFTGTVEAEV VEIMPLGHLDGKISSQELVVERKGILIG ÉTRPKNIQGGALLINEQEKKIENK
107 ITTGGATGGGATTTCGCTCGCGCTAGGCTATTTGTGTTTTATTTCGTTTTAAGGCGCTTCTTTAAAAGAAAAAAAA	109 AAATÓTTGAAGTCATTACCCTATACTTACACACTGAAGGCATCACAAACCCCATGCTCTTTGCGATGGCGCTATCTT TTTGATTGGAGCGATTGGCTTTAAGGTTTCTTTGGTGCCTTTTCATACCTGGATGCCTGATGTGTATGAGGGCAATAA CCCGGTCTTTGCGAGCTATATTTCCATTGTGCCTAAAATCGCCGGCTTTGTGGTAGCGACTCGCCTTTTTG	111 CCACAAACAAAACATGCCAAAACACGAAATTACGCCCAAGAATTGGATTGGATAGCAACAAAGTAGGGGGCGTTACGG AAATTTTGCATGTGAATGAGAGGGACTTTAGGCTTTCATAAGGAGTTGAAAAAGGGCGTTGAAGCGAATAACAG AAATTTTGCATGTGAATGAGGGGACTTTAGGCTTTCATAAGGAGTTAAAAAGGGCGTTGAAGCGGAATAACAGG ATCCAAGTGGGGGGAACATTATAAGATGAACTTTAAACTCTAAAGCGGACGTTGAAACTCACGCCTTTAGGG GGCTTGGGTGGGGATTGGGGGGACATGATGGTCATTGAAACCCCAAAAAAGGGCCGATCGTGATTGAT	113 AATCITTGATAACAATAATAAATCGGCTAATGCAAAAACAGGACCAGCGACTATCATCGCTCAAGGCACAAAATAAAAAAAA
42	2	42	25
HP1542	HP1542	HP.1542	HP1542

wo	02/06650

HP0452	115	115/TAGAAGTTTATTTGGATTTAAGAGACAAGCATGAACGATTGCAGCAAGAAATCACCGAATTGCAAAGCAAGAATGTGCI	116E	VYLDLRDKHERLOGEITELGSKNVRL
		GCTTGCAAAAGCGTTTGTTTGAGTTGAAGGAATTACGGCCTAGAGATTTAGATTTAAGGAAAATGGTAGTGTTAAAAAA GATGATAGGTTTGGTGGTGGTTTTAAGCGTTTTTTTATTGGCCACCCTTTTGAGCCTGAAATCCAATTCCAAGAA TTTGCAAGGGGGCTTTAATGGGATCTATGATAGTTATTTTAAAGAAATCCATGTGGATTTGCCCACGAGCGCTAGGAT CTTAAAACAAATCACGCTCACTTACCAAGATATTGATGGCTCTATCCATTCTAAAGTCGTGGGCATTGATAAAGGCAT TGATTGGCATTACCCTTTAAAACTCTCCCAACACCCTTGATCCAGCCGCTTTGAAAACGCTTTGAAAACGCTTTAAAACTCTCCAACAGATCTTGCGTTTGAAAACTCTCCAACAGATCTTTGCGTTTGAAAAATTTTAAAAACTCTTTAAAAACTCTCCCAACACACAACA	<u>ō</u>	OKRLFELKELRPRD
HP0452	711	117 AGGTGTTCAAAGACAGCAAAAAAGACGCTTGCGGGTTCATCTATGAGATCAGCGAGTTCATGAAAGCCTATACCGCA TTGCTAAAAAAACAAGACCGATACGTCTATTTATTGAGGTACTCCCCTCTAGGTATTGGGCCAGCATTTTAACGACT TTGCTAAAAAAACAAGACCGATATTTGACGCTTTGAAAAAGCTTTTGGTGTTTATTACCAAACTTGCATTGCAGC GCCCTTTATGCAATAGCATCAAGCAAACCGTTTGAAAAAGCGTTAAAAAGCAATAAGAGCGTTGAAACC ATCAAAGAGCTTATATTGAATAGCATCGACTCTTATAACACCTTTGATCAATAACACTCTATAAGCGCTTTT CTGTTTATCATAGCAAATGGGTGCGTCCTGTTATAGCCCTAGCTAATTATTTCATGGCAGTGAAGAGAAACCCCATT TTATCGCTATGGAAAAGAAAGAGGGAAATGGGTAAAAAAAGAGGGAATAGCCAAATTGACCAAAAGAGGCGTCAATGGAAAAGAGCCCATT TTATCGCTATGGAAAAAAGAAAAAAGAGAAAAAAAAAA	# 	118 VFKDSKKDACGFIYEISEI-MKAYTALLK KQDRYVYLLRYLPSRYWASILTTALYV KYPDFDALKKLLVSYYYCTWIAGGTITR IKQTSINIIKNVKSNKSVETIKELILNSIDS YNTFDQYLYNLWDSSSV YHSKWVRPV LALANYFWADEEKPHFIA MDAETQVEH ILPQTPKRGSQWNADFDKEKREEWVN NIANLTLKRK
HP0452	119	119 GAACAAATTGCAAGAAACAGATAATTTATTAAAAACATTGAATGTGAAATCGCTTTTAGAAGCCTTGCTTG		120 NKLQETDNLLKTLNVKSL.EALLVYTPK GYKDLNLLERFETGLSGVLEVGILEKR NYAKVLKIFAYSKRFYKNI.ELVFFNYSA FHHSQFKTGESLFIYGKLIEQSSFNQAYI INTPKIITKFGKISLIFKKVKNHKKIOENL QKLISLENLKKEGVKENIAHLLLEIFFPT PHFVKDFETNKNFPSQH.NALKYIEML FYMKNLERKKLQFGAKIACPNNNERLK AFIASLPFKLTRDQQNAI
HP0336	121	121 ATGGATGGGAGGTTTGAAGATCCTAATCTAACCCCTTTAGAAGTCTTTGATAGAATCCATCATAAAAAAATCGCTAGC GTGCATTTAGCGGATAAGGAAGCGATTTTAAAAGCCCTAGAAGTGGCTAAAAGCGATAAGAGCCGTTTCAGTCAAAA GTGCATTTACAGAAATCCATGCCTTAATGAGTCAAACCGCCCAGCTTTTTAGAGAAAGAGGCGATTTGATAGGGA TTTCCGCTTTACAAATCCATGCCTTACAGGTTTCGCTGAACGGACGCTGAAGTGAGCGATTGATAGGGAT TTCCGCTTTAGAAGTGGGTAAGACTTTCGCTGAACGGACGCTGAAGTGAGCGATTGACTTTTTAGAGTTT TACCCTTACAGCTTAAGGGTGTTGCAAGAGCAAAACACAAAAACGCAATTCACCCCTAAAGGCGTGGGCGTGGTCAT TGCCCCTTACAGGTTTCCCTGTGGGCATTCTGTAAGGCTTTGTGAAGTGCCTCCCCCTAGGGGCGTGGGCGTTT ACCAAGCCCTCCAAGGGCGTAACGGGCTATAAGCTTTTTGTGAGTTTTGGGGATTGCGTGCCTA	122 M CGE H H SV SV	122 MDGRFEDPNLTPLEVFDRIHHKKIASV HLADKEAILKALEVAKSDKSRFSQKSFT EHALMSOTAQLFRERRGDLIGISALEV GKTFAETDAEVSEAIDFLEFYPYSLRVL OEQNTKTQFTPKGVGVV,APWNFPVGI SVGTIAAPLATGNRVIYKFSSLSSVTGY KLCECFWDAGVP
HP0336	123	123 CAACAATGGGGGGCCATCAAAAACCACACCACCAAGATTTCCCTAAAGCCCCTGATGATTTCAAACCTTTTATCAA AAAAATCCATAGAGATTTTAACCAAAGAAATCTGGTGCCCGTAGAGCATAAAATCTATAATGGCGAGAAGCCTTTAGA AAAAATCCATAGAGATTTTAACCAAAGAAATGCGTTTGCATCTGGGCAAAGAAGCGGATTATGAGCCAAAAGGACTTGA AATGCCTAACACCCTTAAGGCCAATGAAATGCGTTTGCATCTGGGCAAAGAAGCGCATCGCAAAAGGACTTGA TGGTTGGGTTTGAAAATAGCGAATGCCATTGTTGGTGGTGAGTCAAAGATTTAAGCGCTCGCATCGCATGAAGC CTTTTCGCTCAAAATTTCAAGACTGCCAAAAGAGTTGCTTCTTCTACAAGGCCGTTGCAAGAGAGTTT GATGAGTTGAAAAAAACACCACATCACGCCCATGCAAGGCCCTTTTAGGAAAAAAAGCGCCTATGAATCCTAA TAGCGTGCTTGTGATAGACAACCAACGAAGCAAAATAAGGGGTGGAAAATTAAGATCGT TTTTAGAAAAAAGCCCCAAGACCAAAGAGTTGCAAAAATAGGGGTGGAAAATTAAGATCGT	22. 文主內田子中內四	124 NNGGHOKHHTKMSIPKAI>DDFKPFIKK IHRDFNGRNLVPVEHKIYNGEKPLEMP NTLKANEMRLHLGKEADYEQKDLMVG FENSESHLLVVSODLSARIALMKLFAQ NFKTANKELLFVNAEKRLARELDELKK HHITPMQGPLGSVLDTAMINPNSVLVID NLNEAKELHDKIGVEKLRSFLEKATDN

PCT/EP01/15428

1	•	۰,
-	٠.	_
-	-	•
	٠.	

WO 02/066501 분일	2 - E	M- WO Z Z Y > M	10 (2 < > PCT/EP01/15428
126 PYSEYLLRLEDVKRTCEMLGIELLEGO YELEKFLDKAKGKELLGEKSERCFEGO DLRLEASALKAFELGEEKFTTLLTSION BLRLEASALKAFELGEEKFTTLLTSION KDPNOLIAKGOSIAORHNLEFVVFRNON NFEHFKSELDLNLOALARENELYROUS CGCOFALKIQKESONRSPFELYSPLPU OILPASIERTQVFRTLDMAKKDANKPF	CILARSKSKAKV 128 ARPPÝSLAYSLRHNRILPRDYLGYRSL GEEISIFNPKDYDSWQERADTEILRQL QESKKYFVFIKGCGIFAYHRELSKLME VFDLIENSCKVLRLGDLMDYCYNDDPR LSV	130 YLKPEELRLYTLIYKRFLASGMGDALFE SGSVVVACEKGEFKASGRKLLFDGYY KILGNDDKDKLLPNLKENDPIKLEKLES NAHVTEPPARYSEASLIKVLESLGIGRP STYAPTISLLGNRDYIKVEKKOISALESA FKVIEILEKHFEEIVDSKFSASLEEELDN IAONKADYOQVLKDFYYPFMDKIEAGK KNIISGKVHEKTGÖSCPKCGGELVKKN SRYGEFIACNINYPKCKYVKÖTESANDE ADĞELCEKCGGEMVÜKFSRNGAFLA	132 QEGČYHĆHSQLIRPFÖAEVDŘYGAYS LSGEYAYDRPFLWGSKRIGPDLHRVG DYRTTDWHEKHMFDPKSVVPHSIMPA YKHLFTKKSDFOTAYAEALTOKKVFGV PYDTENGVKLGSVEEAKKAYLEEAKKY TADMKDKRVLGSVEEAKKAYLEEAKKY NSLĠNSRINANONAK
(D) = (D)			
125 CCCTTATAGCGAATACTTGTTGCGTTTAGAAGACGTGAAACGCACTTGTGAGATGCTAGGGAATTGAATTGCTTGAGG GCGATTATGAATTAGAAAATTTTTAGATAAAGCTAAGGGTAAGGGAATTGTTAGGGGGAAAAAAGGCCAACGCTGTTTTG AGTGCTTTGAATTTACGCTTAGAAGCGAGTGCATTGAATTGAGTTAGGGAAAAAAAA		129 CTACCTTAAGCCTGAAGAATTAAGGCTCTATACCTTAATTTACAAACGCTTTTTAGCAATCCAAATGCAAGAGGCTCTTTTGATGTTTTTGAAGGGGGGGG	131 CCAGGAGGTTGCTATTGCCATTCCCAGCTTATTCGCCCTTTCCAAGCTGAGGTGGATCGATATGCCCCGTATA GTTTGAGTGGGAATACGCGTATGACAGCCCATTTTGTGGGGTTCTAAAAGGATTGGCCCTGATTTGCACAGGGTA GTTTGAGTGGGGAATACGCGATTGACAGCACATTTGGCGCTTTTGCCCCACAGCACAGCATGTGCCCCACAGCATTTGCCCCACAGCATTTTGCCCCACACACA
HP0336	HP0336	HP0336	нР0336 НР0336
<u></u>	[1	I	主

PCT	ÆΒ	11	1	5/17Q	
$\mathbf{r} \mathbf{c} \mathbf{r}$		vi		3470	

134 SVIKHHLIGLEAINOAFVDERLRALDGO PNYANLGANAVLGVSMALARASAKAN NLPLYRYLGGANALTLPVPMLNIINGGO HANNSIDFOEYMIMFLGFESFKEALRS SAEVYHTLKKLLDGKNQLTSVGDEGG FAPNFSNNVEPLEVISÖAIEKAGYKLCL EIALALDVSSELVDESNFYHLKGENKI LDSHELVAYYKELVAKYPIVSIEDGLSE DDWEGWAFLSKELGROIQLVGDDLFV TNASLLQKGIEKNIANAV	136 NRLGGNSVSEAVVA GMIIGDYFASHCL EAQIEINTQKVEAFIKESQDYMHFLLHN EGKEDVYEIRERMKI:VMDEKVGVFRE GKRLEEAL	138 ERCLEAARILGIKNDERVLNLOGDEPF LEKEVILALLEATKNAPFMATCAKVIDE EQAKSPNLVKVVLDSGNNALYFSRSLI PFLRDFDAKRQTPLLGHIGIYGFHNKEI LEELCALKPCVLEEIEKLEQLRALYYOK KIAVKIVQSESVGIDT OEDLQNALKIFSP DLLER	140 DGYAIGGLAVGESAČIEMLETIAHTAPLL PKDKPRYLMGVGTP.ENILDAISLGVDM FDCVMPTRNARNATI.FTHSGKISIKNA PYKLDNTPIEENCAC YACKRYSKAYLH HLFRAKELTYARLASI.HNLHFYLELVKN ARNAILEKRFLSFKKE:FLEKYNSRSH
133 TAGCGTGATCAAACACCATTTAATAGGGCTTGAAGCGATCAATCA	135 AACCGCTTGGGGGGTAATTCTGTGAGTGAAGCGGTGGTCGCTGGCATGATCATTGGGGGATTATTTTGCCTCGCATT GTTTAGAAGCGCAAATTGAAATCAACACGCAAAAAGTTGAAGCTTTCATTAAAGAAAG	137 GAACGCTGTTTGGAAGCGGCGCAATTTAGGGTTAAAAAACGATGAAAGGGTTTTAAACTTGCAAGGCGATGAGGCCTTTTTAGAAAAAAGGCGATGAGGCCAAAAACGCCCCTTTTAGAAAAAAGGCCCTAAAGT TATTGATGAAGAAGAGCCAAAAGCCTTATTAGAAGCCACAAAACGCCCCTTTTAGAGAATAACGCCTTGTATTTTTC TATTGATGAAGAAGAATATTAGGAGATTTTGATGCGAAACGCCAAAACCCTTTTAGGCCATATCGGTTTTTGG GCGCTCCCTTATCCCCTTTTTAGGAGAATTGTGCGCTTTAAAACCCTTTTAGGGCATATCGGTATTTATGG CTTCCACAATAAAGAAATATTAGAAGAATTGTGCGCTTTAAAACCTTGCGTTTTAGGAAAATAGAAAAATTAGGGCAAGA TTAAGGGCTTTGTATTACCAAAAAAAGATTTGCGAGTGAAAATCGTTCAAAGTGAAAGGGGGGCATTGAAAAAATTTTTC AGATTTGCAAAAAGCTTTTTTTAGCAAAAAAAAAA	139 GATGGCTACGCTATAGGCGGTTTAGCGGTGGGGGAAAGCGCTGATGAAATGCTAGAAACCATCGCGCCACCCCCCCC
HP0336	HP0336	HP0336	нР0336

к	╮	
-	-	
÷	_	
	_	

NSPN ON NSPN O	DLNKI VSMN VLIFM VRQA IYDM KNPT	TOIA PLREE SLDF! GNLT SYEY OKSS
142 KIMELLHSINDFNEAKQVIAGGVINSPO AFKSVKGTPPFILKGKGAYLYDVDNINSPYDFYONNSPO YIDFVQSWGPLIFGHADEEIEENIINAISP KGTSFGAPTELETTLAKEIISCYEGLCSP VRLVSSGTEATMSAIRLARAYSQKDCSP VRLVSSGTEATMSAIRLARAYSQKDCSP KFEGCYHGHSDSLLVKAGSGCATFGS FSSLGVPNDFSKHTLVARYNDLNSTEE CFKKGNVGCVIIEPIAGNMGLVPAQKE FLLGLKALCEKYQAVLILDEVMSGFRA SLSGSQEFYGVVPDLVTFGKVIGAGLP L	144 NPNSTESVNERKIFGGNPTŚMFDLNKI KYQWADHLWKTMLANTWFAEEVSMN DDKRDYLKISAEEKIGYDRALAQLIFW DSLQANNLIDNINPFITSPEINLCLYRQA YEEALHSHAYAVMVESISANTEEIYDM WRNDMQLKSKNDYIAQVYMELAKNPT EENI	146 YAPHKLLGGIGGCGLGISKDLIDTÖJA PSFSAGGVIKYANRTRHEFIDELPLREE FGTPGLLGFYRSALAYGLRDECGLDFI HKKENNLLRVIMHGLKDLPAINIYGNLT AHRVGVVAFNIGGISPYDLARVLSYFY AIETRAGCSCAGPYGHDLLNLNAÖKSS DFN
MDFNEAK SPLIFGH SPLIFGH TELETTL TELETTL TELETTL SEATMSAIF HSDSLLV OFSKHTL CVIEPIAK CVIEPIAK CVIEPIAK	VERKIFGO WKTMLAI SAEEKIG DNINPFIT YAVMVE SKNDYIA	GGCGLL KYANRTR YRSALAY YLMHGLK WIGGISP
MELLHSIN MELLHSIN DFVQSWC STSFGAP STSFGAP SEGVPIG SEGVPIG SEGVPIG SEGSQEF)	NSTESVI OWADHL IKRDYLKI LOANNLII EALHSHA INDMOLK	PHKLLGG FSAGGVII TPGLLGF KENNLLR RVGVVAF TRAGCSC
<u>24</u> <u> </u>	KYC KYC DOK DSL YEE WRN	146 YAP PSF FGT HKK AHR AHR OFN
34 AC 37 CA 37 CA 37 CA 37 CA 36 CA 36 CA 36 CA 36 CA 36 CA 37 CA	AAE T E &	55 8 5 8 P F
TAAAATCATGGGGTTGTTGCACAGCATTAATGATTTCAATGAAGCTAAGCAGGTGATCGCTGGGGGGGTCAATTCAC CTGTTAGGGCGTTTAAGAGCATTAATGATTTTTTTAATTTTTTTAATGATGTG CTGTTAGGGCGTTTAAGAGCGTTAAAGGCACTCCCCCCTTTATTTTTTTT	AACCCCAATTCTACAGAAAGTGTGAATGAAAGAAAGATTTTGGGGGCAATCCTACAAGCATGTTTGATTTGAATAAGATCAAGTGTTTGATTTGAATAAGATCAAGAAGTGTGTTTGAATAAGATCAAGTGTCAAGAAGTGTGAAGAAGTGTGAAAAGATGAAGAAGTGTGAAGAA	145 ITATGCGCCTCATAAGCTITTAGGGGGCCATTGGAGGGTGCGGTCTTTTAGGCATTTCTAAAGATTTGATTGA
SGGGGG STATCTTT SAAGAG TTAGCTA AGGCG CGACTCC TTTAGCA GCGTCA GCGTCA	STTTGAT AGAAGTG FAGCGCA AATCAAT ATAAGTG SCAAGTG	VITTGATT VITTATTC TCAATTC VAAAGAC GATTTCC SGGCCTT
TCGCTG GGGGGCC TGCTGAT AACCACT SACCATG SACCATG SACCATG SACCATG SACCATG SACCATG SACCATG SACCATG SACCATG SACCATG SACCATG SACCATG SACCATG	AAGCAT(TGCTGA GAGCTT SCCCCGA GAAAGC	CTAAAGA GCATGA TAGCGTA TTGGCCTTA TTGGGGC
SAGGTGA TGGGCAAC ATTAGAC ATTAGAC ACCATGC SGGCATI GGGCATI TGAGCG	ATCCTAC CCTGGT TATGACA TCACCAG SATGGTA	GGCATITI SCACACG GCGCTC TAATGCA TTAATAT
TAAAATCATGGAGTTGTTGCACAGCATTAATGATTCAATGAAGCTAAGCAGGGG TAAAAACCACCATTAAAAGGCGTTAAAGGCACTCCCCCCTTTATTTA	GGGGCA SCTACA SATCGGT CCCTTCA TGCGGT GCAAGA	TCTTTTA CTAATC TACAGGA GAGGTGC GTGGCT GGCAGG
CAATGAA CCCTTTA GGGCCT GCGCTC TCAGTAG TTTGAAG CTTCTTC AATGCT AAAGAG	ATTTTTG ATGCTC GGAAAA(FATCAAT ATGCGTA	TGGAGGTGCGG CTGATTAAATACG ATTGTTGCAATTTTAA AAACAACCTTTTAA CGGGTGGGGGTA CTATTGAAACCCG
NTGATTT ACTCCC AGCTGG AGCTGG ICTTTG SATCAAG SATCAAG GCAGAAG GCCCAA	AGAAAG SAAAAC GGCAGA TGACAAT ACAGCC	TGGAGG SGTGTTC ATTGTTC AAACAAC CGGGTG CTATTGA
GCATTAA AAAGGC GTGCAA GGCACT AGGTGC ACTTTTG ACTTTTG AGTGCCG	SAATGAA TTTGGG ATTTAAT CCCTAC, TAACGAI	GGGGCAT GGGGGG GCCAGG GAAAGA GGCGCAT AATACG
TGCACA SAGCGTT AGATTTT WAAAAA TTAGATA WAAAGA SIGGTTTA SGGGTTA AGATGA	AAGTGT GGATCA ATTTGAA ATTTGAA SCGAATA SAGGAAG GTGGCG	TTTTAGG AGCGCAC TGCATAA TTTAACA AGCTATG
TAAAATCATGGAGTTGTGCACAGGATTAA CTGTTAGGGCGTTTAAGAGCGTTAAAGGC GATAACAACCATTATATAGATTTTGTGCAA AATATTATTAATGCATTAAAAAAAGGCACT TTTCTTGTTATGAAGGCTTAGAATAGGTGC GCTAGAGCTTATAGGCTTAGATAAGGTTTG GAAAGCGGTATAACGATTTAAACTCCA TAGTGGCTCGTTATAACGATTTAAACTCCA CCATTGCCGGGATATGGGGTTAGTGCCG CCATGCCGGGATTTGGTGATGGTGCCG	AACCCCAATTCTACAGAAAGTGTGAATGAA ATCAAGTATCAATGGCCGCATCATTTGTGC TGATGACAAAGGGATTATTTGAAATTAAG TATGGACAGCTTGCAAGCGAATAATTTAAT TATGGCGTCAAGCTTATGAAGAACCCTAC GGTGCGTCAAGCTTATGAAGAAGCGTACAGATATTAGA	TTATECECCTCATAAGCTTTTAGEGGGGCAT AGATCGCCCCGAGTTTAGCCCACGGGGG CCTTTGAGGGAGGTTTGCCACGCCAGG ATGCGGTTTGGACTTTATCCATAAGAAAGA ATGCGGTTTATGGGAATTTAACAGCGCAT ATTAGCGAGGGTTTAACCATAGGCGATACGG
ATCATGE TAGGGC ACAACC) TIATTAA TIGITAT GAGCITI GCCGGG TGCCGG CCGGGAT	CCAATTC AGTATCA BACAAAA BACAGCI CGTCAAA AGATTTA	SCCCCC SCCCCC SCCCCC SCTTTCC ATATTTA GCCAGG
141 TAAAATCATGGAGTTGTTGCACAGCATTAA CTGTTAGGGCGTTTAAGAGCGTTAAAGGC GATAACAACCATTATATAGATTTTGTGCAA GATAATTATTAATGCATTAAAAAAAGGCACT TTTCTTGTTATGAAGGCTTAGATAAGGTGC GCTAGAGCTTATAGCCAAAAAGATGATTTG GAAAGCGGGTAGCGGGTGTGCTTTTG TAGTGGCTCGTTATAACGATTTAAACTCCA CCATTGCCGGGAATATGGGGTTAGTGCCG CCATTGCCGGGATTTAGATGATGCCG CAGGCGGTGCTGTTTAGATGATGCCG	143 AACCCCAATTCTACAGAAAGTGTGAATGAA ATCAAGTATCAATGGGCGGATCATTTGTGG TGATGACAAAGGGATTATTTGAAATTAAG TATGGACAGCTTGCAAGCGAATAATTTAAT GGTGCGTCAAGCTTATGAAGAAGCCCTAC GAAGAGATTATGACATGTGGCGTAACGAT ATTAGCCAAAAACCCCACAGAAGAAAACAT	AGATC CCTTT ATGCC ATTTA ATTTA GATTTA
		7
нР0336	нР0336	нР0336 1
王	<u> </u>	I

_	_
r	7
_	-
•	_

148 ENKESAEEFLKTLÖTEAGEFESAYGP LKNLDATGFANALKHYENLSEKISRVIS AYAGLLFAKNTKEAKFYSQCEMACAIS AYAGLLFAKNTKEAKFYSQCEMACAIS GOHLLFFEIEFKNLDAKKGLAFIKKCKS HAFYLNNLIERKKHTI.NLDEEKIALAL:SPYGVGAFSRLFDEHFSSLKIPFEEGNL SEEEILALLHNPKRKIRKKSGKAFSKAL EKSRPLLTYILNMVRRCILIETRLKYD KKESFRHIDNQISQE;VDSMIEVNANF SLVHRYYHOKAGILGHKLKOYDRYAPL NDESITMTYSQALEEVLKTLKAFSPEFH KIASKAIKEGWVDSHYNDFKGGGAFSH GGVPSAHPYVLLNTGNRRDAFTIAHE	ASVFSEMLFFEHLKK3LKSDELLFMLA GKLEDIFSTLFRQVVMTNFERRIHEMD EELDTKDFDRIWFEENQRMFEKSVKLT KNYHLWWSYIPHFIHSPFYCYAYSYGQ LLTLALYGLYKKSDAKEFVKTYTEFLSL GGSKSPKELVSMFGFDIDSKEFWEIGM QEVRHLLEEFERLLACKEN 150 LREEQKARKETPRYDNRYRDFKGTPP KGIEPVVRIKVPQNEVIGFNDGVKGEV	KVNTNELDDFIIARSDGTPTYNFVVTID DALMGITDVIRGDDHLSNTPKQIVLYKA LNFKIPNFFHVPMILNEEGQKLSKRHG ATNVMDYQEMGYLKEALVNFLARLGW SYQDKEVFSMQELLEI.FDPKDLNSSPS CFSWHKLNWLN 152 EKOKINTQTEIGNMQIALGKNNEIIKLK MNQQNALLEALKNSFEPSYTLKTQME MI.SQALGSSSDNAQYIAYNTIGIKAFEE TI.KGFETWI KYAMOKATI IIDYNSI TGO	ALFQSAIYAPALSFFSSMGAPFGIIETFT LAPTKCPYLDGLKISACLMEQVIQNYR MIVALIQNKLSDADFQINIAYLNGINGEIK TLKGSVDLNALIEVAILNAENHLNYIENJA EKKADLWEEQLKLERETTARNIASSKA VK 30
147 GAAAATAAAGAAAGCGCAGAAGAATTITTAAAAACCTTACAAACAGAAGCACAAGAATTTGAGAAAAGTTTCTAGAAAATAAAAAATAAAAAAATAAAAAAATTAGAAAAATTTGAGAAAAAA	149 TTGAGAGAAGAGAAAAAGCCAGGAAAAGAAATGACCATCGCTATCGTGATTTTAAAGGCCACGCCTCC TAAAGGCATAGAGGCTGTGGTAAGGATTAAAGTCCCCCAAAAATGAGGTGATTTAATGACGGGGGTTAAAGGGCAAAAAAAA	TTACTATTGATGACGCTTTAATGGGGATTACTGATTAGAGGGGATGATTGAGATGATTGAGATGATTGAGAGAGAGAGAGAAAAAA	TTGGGATCATCATOR CANCEST IN CANALA ISCALCI IN IGAGACCTGCTTAGTTTTTTTCAAGCATGGGTGCACCA TTGGGATCATCATGAACATTCACTCTGCGCCCCACAAATGCTTGATGTGATGGGCTAAAATTCAGCATGCTT ATGGAACAGGATTTCAGATGAGATG
HP0336	HP0336	HP0336	

•	ς	г
4	-	١,
٦	•	•
•	•	-

154 IFSVWALOEGWDNPNIFTLIKLANST; CANTROPORTICAL TERHODVGRGLRIAINOEGKRYTHGIN KGNDNAFYKINYLDMLVSGEEVGFIES LOKEIEASFIGGBALDREDLAKLGISTERINKLFVELENSNALEFDETNNAYIS APICETMONNEERIKDFLSDEEYHAVL	156 DSWLFWIQKPAYATGRFGNFYPGOON TAGVTATLNIFDDIGLSLOKOSIMLGOL ANEKNLAYKKLEGEKDEQLYRKSLDIA RAKIESSKASLDAANLSFANIKRKYDAN LVDFTTYLRGLTTRFDAEVAYNLALNN YEVQKANYIFNSGHKIDDYVH	158 LIENSSALERELKÖKNEHLENALKEÖE YLKNAWLLEMEKOKEIFHNKKLELEKS YQQALNILKSEVASKOTSSMHKEIHKA SEILSKHK	160 KALEENRLKNSDGESLYŘĽVIĽYEDKP CESVESAYMKLLALSLGKAPLRSLNLE GIFNOLSNAAWSGNKPYELEWLŘMNE VALKMROHFPSIDFIDKFPKYLMQLIPE FDNIŘLLDSSKTŘFGAYLGTGGYTÖMP GASYVNFNAGAMĞVCMNEGRISSSVV VGAĞTDIGGĞ	162 SHDENLFWGEIDATKRLENVIDLLWDM NIPAFILEKHALLQDIARSGGLLLDNKP CQVFELEVLRALLNSPIKARLTFEYRCK H	164 NHÍÐN KNPMPLSI ÝTHLPFCŘSAČYFČÍ ACSVIYTSLEEKKÍRYISYLKRELALLKN AMDTNREVAÓFHYGGGTPTFFSPIQL DEITÓSIÓEVFPNFSKÓIEMSCEIÐPRHE FTKEHMÓTLFÓRGFNRLSFGVOÐFÓFE EVÓKÁI	15428
153] TATTITTAGCGTGTGGGCTTTGCAAGAGGGCTGGGATAATCCCAAACATTTTTTACCCTTATTAAACTGGCAAATTCTAC CAGCGAAACCAGCGGCCATCAGCAAGTGGGGCGGGTTAAGATTGCGATTAATCAAGAGGCGAGCGGTTAC CAGCGAAACCAGCCGCTTAGGAAGAGGCGTTTTTAAAATAAAT	155 TGACTCATGGCTTTTTTGGATCCAAAAACCCGCTTATGCCAGGGGCGTTTTGGGAATTTCTACCCCGGTCAGCAAAAAAAA	157 TTGATTGAAAATTCCAGCGCGCTAGAAGGGAATTGAAACAAAAGAATGAACATTTAGAGAACGCTTTAAAAGAGCAAAAAAAA	159 AAAGGCTTTAGAAGAAAATCGTTTGAAAATAGCGATGGGGGGGTCTCTTTATCGCTTGGTGGTCTTGTATGAAGATAA GCCTTGCGAGGGGGGGGGG	161 ATCGCATGATGATATCTTTTTTTTTTTTGCAAGAATTGATGCAACTAAACGGCTAGAAATGTGATCGATC	163 TAACCATGACAACCTCAAAAACCCCATGCCTTTATCGCTTTATACGCATTTGCCCTTTTGCAGGAGTGCGTTATTT TTGCGCTTGTTCAGTCATTTACACCAGCTTAGAAAAAAAA	
HP0336	HP0336	НР0336	НР0336	HP0336	HP0336	

1		٦
1	c	3
	_	

0.02/06/501: - 44: 47	TV =	
166 EEKGRILKGFKEKFÜLEFLNSOIKPEIO FOFNYLGIKTLYDRYLLKDANINNPIENS OHMWSIAMFLAQNEQEPNKIALEFS VLSKFEAMCATPTLÄNARTTKHOLSIS YIGSTPDNIEGIFDSYKEMALLSKYGKS IGWDFSLVRSIGSYIDGHKNASAGTIF LKIANDVAIAVDQLGTRKGAIAVYLEW HIDVMEFIDLRKNSGDERRRAHDLFPA LWVCDLFLKRVLEDAMWTLFDPYECK DLTELYGGDFEKRYLEYEKDPKIIKEYI NAKDLWKKILMNYFE:AGLPFLAFKDNA NRCNPNAHAGIIRSSNLCTEIFQNTAPN HYYMQIEYTDGTIEFFEEKELVTTDSNI	168 RLIKTSGSPEAAKNALMERFTLSEIGSK AILEMRLGRLTGLERDKIKEEYGNLLELJ DDLNGILKSEDRLNGVVKTELLEVKEG FSSPRRTEIGESYENIDIEDLIANEPMV VSMSYKGYVKVDLKAYEKGNRGGK GKLSGSTYEDDFIENFYANTHDILLFIT NKGQLYHLKYYKIPEASRIAMGKAIVNL ISLAPDEKIMATLSTKDFSDERSLAFFT KNGVVKRTNLSEFEENRSCGIRAIVLD EGDELVSAKVVDKNAKHLLIASHLGIFI KFPLEEVREIGRTTRGVIGIKLNENDFV VGAVVISDDGNKLLSVSENGLGKQTLA EAYRGQSRGGKGVIGMKLNENDFV GVISVDDENLDLMILTASAKMIRV	170 CDTCIQCQSALNNHHIDIIEMDGASNR GIDDVRNLIEQTRYKFSFGRYKIFIIDEV HMFTTEAFNALLKTLE:EPPSHVKFLLAT TDALKLPATILSRTQHFRFKKIPENSVIS HLKTILEKEQVSYETSALEKLAHSGQG SLRDTITLLEQAINYCJNAITESKVAEM LGAIDRSVLEDFFQSI.INQDEARLKERY AILENYE
		17
165 GAAGAAVAGGGCCGCATCCTTAAGGGCTTTAAGGAAAATTTGATCTAGAGTTTTAAAATAGCCAGATCAAGCCCTGAAAGAACCCTAAAAAGACCCCTAAACAACCCTAAAAACCTAACAACCAAC	167 GCGACTCATTAAAACAAGCCCAGAAGCGGCTAAAAACGCCCTTAATGGAGCGTTTCACTTTGAGGCGAGATTC AAAGCAAGGCATTTTAGAAATGCGTTTGCAACGCTTAACAGGCCTTGAAAGGAGATACCAA AAAGCAAGGCTTATTGATGATTTGCATTGGCATTTTAAAAGGCTTGAAAACAGAG AACTTGTTGGAGCTTATTGATGATTTCTCCCAAGGCCTTAAAAGGCTTATGAAAAAGATTTGAAAAAGATATTGAAACAGAG CTTTTAGAAGTCAAAGGCAATTTTCTTCTCCAAGGCCACTGAAATTCAAGAAAAGATTATGAAAAGCTTATGAAAGCTTATGAAAAGCCTATGGCGAAAGCTATGAAAGCTTATGAAAGGCTGAAAGTTTTGAAAGCTTATGAAAGCTGTATTTTTAGAAGCTGCTATAAAATTCCCTTTAGAAGGCGCAAAAGTTTTGAGGCGCAAAAGTTTTGAAAGCTTATGAAAGGTGCGCAAAAGTTTTGGCGAAGAGTTTTGAAAGCTGTATAAATTCCCTTTAGAAGGGTGCGCAAAAGTTTTGGCGAAGACTATGGGGGGTGCTTAAAATTCCCTTTAGAAGGGTGCGCAAAAGTTTTGGCGAAGACTTTTGAAAGCGTGCGT	189 TGCGATACTTGCATGCAATGCCAGAGCGCTTTAAACAACCACCACATAGATATTATAGAAATGGATGG
HP0336	нР0336	HP0336

	•	٦
ì	ä	=
٠,		,

T72 KORAVCKESOAKALDAMLNYMAYTI O EIKSMILEQLEEELEAQKSALIRRYEKN AKEEGKKKSYAILAEATARFAGNYAAB NLTTRIALPCSDYIGRYIGKDGKNIEAB KVSGVDIEFSEDSSELCLSSFNLYRRG VASETLKILIEDGRIQPNRIEEVYHRVAN NLEKELLSEGESVVLELELGAMEDELKI LIGKMRYRSSFGQNALQHSKEVALLAG LIGKMRYRSSFGQNALQHSKEVALLAG	174 WLDALGAKGMIELCAKFSVARMLERD DFTKRYKENRPISIVEFLYPLLGGYDSV AMDADIELGGNDÖKFNILVGRFLÖRA YGLNKEÖSVITMPLLEGLDGVÖKMSKS LGNYVGITEEPNAMFGKIMSVSDÖLM WRYYTLLSTKTLEEIEDLKHGILNÖTLH PKAVKEÖLASEIVARYYDNDQAIKAKE ÖFSKVFSANILPEILSESÖFÖEGVGILD VLKGIGFCPSTSÖARRDIÖGGGVKIN	176 EGMRWLQNFKYHDSDLKNDPKEFYEL AKNDLYREDINVFSPHGDTYTLPVGAIA LDFAYMVHSDLGDKATDAYINSKKALL NGELRSGDVYKIIKGDKIIPŘFIWMDOL KTSKAKNHLRIORŘNRLKEVDTKSMINI LATFFGRSVFEDMDLKDYKNFEERLTD CGVETTLTEAMKSFENLAKLTEEIENKV FSLKEDAILEYQEMSLWTRGLRYLGFK TNVLNFLAPNRCWQCKELEHFSVCSS NALEIKÖVLLNDCCYPKYGDEIIAIVTDL KDPKAIAHHKFCKKAMAEVDAKVPMV	178 TVEKKGKÍNVÝNGRILÉIEGÍPĎÍKMEQ AFELSDASAERSAAACVORLNKEPMIE YLKSNÍKLÍDÉMÍASGYEDKETLKKRRĎ AMÓAWVDNPVLLEPĎSNAQYAAVIEÍD VAEITEPILACPNDPDĎDVATLSEVLADŤ TGKRPHAÍDEVFIGSCMTNIGHFRAFCŢ EIVKNAPPSQARLWVVPPSKMDEGEÍŢ NEGYYAIFGAAGARTEVPGCSLCMGÍÐ QARVRĎNAVVFSTSTRNFÖNRMGRĞÐ AKVYLGSAELGAACALLGRIPTKEEYNĽ NLVSEKLESÖKÖKIYRÝNMFNLMENFÍÐ
171 AAACAGCGCGCTGTTTGTAAAGAATCTCAAGCCAAAGCGCTAGACGCGATGCTCAATTACATGGCTTATACTAAGA TGAAATTAAAAGGCTGTTTTAGAGCAATTAGAAGAAGTTAGAAGCCCCAAAAAAGCGCCTTAATCAGGCGTTATGA TGAAATTAAAAGAAGAGGGCAAGAAAAATCGTATGCCATTTTAGCGGAAGCGACAGCCCGTTTTGCGGGTAATT AAAAGCGAGAATTTAACAACTCGTATTGCTTTGCCTTTGCCTTATATAGCGAAGCGGCGTGATAGGCAAAGACGGG AAAAATTTGAAGCGTTTAAAAAAGGTCAGCGGGGGGGGGATTTGTCTAAAAATTTGAAGCGCCGTATCCAGCCTA CAGTTTCAATCTTTATCGGCGTGAAGTAGCGGGGGGGGGG	173 TGGTTGGATGCTTTAGGCGCAAAAGGCATGATAGAATTGTGCGCGAAGTTTTCAGTCGCTAGAATGCTAGAAAGGGA CGATTTCACTAAACGCTATAAAGACACTGCCCCATTAGCATCGTGGAATTTTATACCCTTTGTTGCAGGGCTTTTTTG TTCAGTGGCGATGGATGCGGACATTGAGCTTGGGGGCCAATGATCAAAAGTTTAATTGCTGGTGGTGGGGCGTTTTTTGC AACGAGCTTATGGCTTGAATAAAGACAGTCTGTCATCACCATGCCTTTATTAGAGGGGGCTTGATGGGGTGCAAAA ATGAGCTTATGGCTTGGGGAATTATGTGGGGATCACTGAAGAGCTAATGCGATGTTTGGGAAGATCATGAGCGTGA GCGATGATCTCATGTGGCCTATTACACCCTTTTGAAGAGCTTAGAAGAATTGAAAGACTTAAAAACATGGTA TTTTAAACCAAAGCTTGCACCCTAAAGGCGTTAAAAGAGGATTAGCGCCAAACCTTTGCCTGAAATTTATGAGAGAGCG ATTTTGATGAGGGGGGGGGG	175 GAGGGCATGAGATGGTTGCAAAATTTTAAATACCATGACAGCGATTTGAAAAGCGACCCTAAGGAATTTTACGGAGCTCGGAGGCATGAAAAAAGCTAAGAAAAAAAA	177 CACGGTGGAGAAAAGGGTAAAATCAATĞTÇİTİTAACGGGCĞTATİTİTAĞAAĞİTĞAĞĞÇİTĞÇÇTĞĞİTATAAAĞT GGAGCAGGCTTİTGAACTAAGCGATGCGAGTGCGGAAAGAAGTGCGGGCTTGCGTGCG
		-	÷
HP0336	нР0336	HP0336	HP0336

WQ_02/066501- A 关语专出	SAF SAF SAF SIVA SIGA SIONS	A K K K K K K K K K K K K K K K K K K K	PCT/EP01/15428
S H S B S H S S H S H S H S H S H S H S	15.23.25.	は スロマスマンシ	ほのうはないとうな

MACATION CONTRIBUTION OF THE CONTRIBUTION OF T	TOUSSE	170 MANCOCK CONTROL CO	W
181 TATGATATTACTGGGGCGTTTTAAAGGATGGATTGTTTATGAAAAGCGTTGGTTG		AACATGGCAGCGCGCGTTGATATTAAACTCCAGTGAAATTAAGGAGCCTTAAAGGAGCGGTTTACGATTGCGACTTCCGACTTCCGACTTCCGACTTCCCGACTTCCCGACTTCCCGACTTCCCGACTTCCCGACTTCCCGACTTCCCGACTTCCCGACTTCCCGACTTCCATTTCGCACTTCCATTTAAGGCGCCCAGGCCGCCCGGCGCCCCGGCGCCCATTTATTT	EIIKDAGLKGAVTIATNIN DEIKELGGLYIIGTERHE: RSGRCIGDPGTSGFYLS: DRIKGVMEKLGLKDGE ENACKVENLHFESRKI GRKSVYKFRDELLDVN: EYALNJIFSKLKAFDHQ INILKEI)FNAHVSLEDLK KLKSD YENKMKVLDSE ZILDNAWREHLYTMDNI
183 CCTAGGAAATACCACGCAGAGCATTTAGCCGGCAAAGAGAGCTTTTTTAAAGTGAAATTACACCAGATTCAAGCGCGGTTTAAA TGAAATGTTAGAAATCCACGCAGACTCGCTAAAATCGTGCTCATAATGAAGAGATTCAAGCCTTTAAA AGAAAGGGTTGAGGGGCAGTTTTTTAGAAAATCCTTGCCTAAAAGGGCTCTATAATGAAGAGTTGAAAAATTGATTG	HP0336	181 TATGATATTTACTCGCGCCTTTTAAAGGATCGCATTGTTTTATTGAGCGGTGAAATTAATGACGGTGGCGTCTTCT ATCGTGGCCCAACTCTTGTTTTTGGAAGCTGAAGAACAAAAGACATTGGATTGTATCAATTCTCCCGGTGG GGTGATAACAAGCGGTCTTAGTATTTATGACACCATGAATTTTATCCGCCCTGATGTTTTGCAATTTGCAATTGCAAGGTTA AGCGGCTTCTATGGGGGCGTTTTTACTGAGCTGTGGGGCTAAGGGGCAAGCGCTTTTCGCACCCCATTCAGGGATT ATGATCCACCACCACCCTTTAGGGGGGGCTCAAGGGGCAAGCGGATTTGAAATCATTCTAATGAGATTCTCAGGGCTAAAGGAGGGTTAAAGGGGGAAACCGCAAATCGCTAAAGAAGCTCAAAAGAGGGGAAATCAAATGGCTAAAGAAGCTCAAAAGAAGCTAAAAGAAGCTAAAAGAAGCTAAAAGAAGCTAAAAGAAGGAAAGGAAAGGAAATCAAAAAGAAGCTAAAAGAAGGAAAAGAAGAAGAAAGA	182 YDIYSRLLKDRIVLLSGEINDSVASSIVA QLLFLEAEDPEKDIGLYINSPGGVITSG LSIYDTMNFIRPDVSTICIGQAASMGAF LLSCGAKGKRFSLPHSRIMIHOPLGGA QGQASDIEIISNEILRLKGLMNSILAQNS GQSLEQIAKDTDRDFYMSAKEAKE
185 GCCGAGCGTGGAAGAACACCTTATTGAACAAAAAGGCTTTTTTTT	HP0336	183 CCTAGCAATACCACGCAGAGCATTTAGCCGGCAAAGAAGCTTTTTTAAAGTGAAATTACACCAGATTCAAGCGCG TGAAATGTTAGAAATGAACTCGCTAAAATCGCTGCTAGCTA	184 PSKYHAEHLAGKEAFFKVKLHQIQARE MLEINDELAKIVLANEENATLKLLKERV EGQLFLENKARLYNEELKEKLIENLDEK IVFDLPKTIIEQEMDLI.FRNALYSMQAE EVKSLQESQEKAKERFESFRNDATKS VKITFIIDALAKEEKIGVHDNEVFQTLYY EAMMTGQNPENLIECIYRKNNMLAAVK
	HP0336	185 GCCGAGCGTGGAAGAACACCTTATTGAACAAAAGGCTTTTTCATCCCGCCAAGCGCTTTATTTGTAATGCGCTAAAAATGCCGTAAAAAACGCGTGGAAGAAAAAACGCGTGGCTTGGCGTAGCAAAAATTTTTTTAACGAAAAAAATGCAAAAGCTTGGCAAAAAATTAGGGAAGAAAATGCAAAAATGCAAAAAAGCGTTGTTGCGGATTTTGGGGAATTAGGGAAGAAAATGCAAAAAATGCAAAAAAAA	186 AERGRKHLIEOKGFF. PPSALFCNALKN ACHNEDLNVTLONIFNEIEKSSLGTPSE ENVKGLFADLDVNSNKLGSSHONRVE KLTKILEAIGGMOLGDYLKSGIDVFGDA YEYLMAMYASNAGK;SGGFFTPQEVS ELLAKITLHGQESVNKVYDPCGSGSL LLOFSKVLGDKNVSKSYFGGEINLTTY NLCRINMFLHDINYSKFHIAHGDTLLDPY KHEDDEPFDAIVSNPIYSTKWVGDSNO

e	5	ė	•
2	•	3	7
		_	

188 LLESMSLKDACEFANAAAAVVVGKM O SALASLEEIALILNOTHPKILSLEKLLE'N DOOKIIFTNGCPDLLHKGHASYLOKA O HAGDILIVGLNSDASIKRLKGDKRPIVS KDRAFLLASLSCVDYVVFEEDTPIKIG GALKPDILVKGADYLINKEVIGSEFAKE'I HLMEFEEGYSTSAIIEKIKRTCND	190 PLASGLAEKIGEEIGÖLKİKSHLHİNDO ELKEKFVIKDHASGLLMIKENLTKMGIIK DFNQIDAGHRVYQGGOKFHAPVLVNE KVMQEIGNLSILAPLHNPANLAGIEFVQ KAHPHIPQIAVFDTAFHATMPSYAYMY ALPYELYEKYQIRHYGFHRTSHHYVAK EAAKFLNTAYEEFNAISLHLGNGSSAA AIQKGKSVDTSMGLTPLEGLIMGTRCG DIDPTVVEYTAQCANKSLEEVMKMLNH ESGLKGICGDNEKHRSQKRKR	192 LKELDÍKGPKNGMAKSVĎEAYSIANVIĞ FPIIVAPSYVLGGOHMÖILENIEELRHY LESVTHALEISPKNPLLI 194 ECLHTYSLIHDÖLPCMÖNAALRRNHPT LHAKYDETTAVLIGDALNTYSFELLSNA LLESHIIVELIKILSANGGIKGMILGOALD CYFENTPLNLEOLTFLHEHKTAKLISAS LIMGLVASGIKDEELFKWLQAFGLKMĞ LCFOVLDDIIDVTQDEEESGKTTHLDSA KNSFVNLLGLERANNYAOTLKTEVLNI LDALKPAYPLLÖENLNALLNTFKGKTL
187 TTATTAGAATCAATGAGCCTAAAAGATGCTTGCGAGGTTTGCCAATGCGGCGGGCG	189 CCCTTAGCGAGCGGTTTGGCTGAAAAATCGGCGAAGAAATAGGGCAGTTGAAAATTAAATGATTTGCACCATTTGCACCATAAAGGAGAAATTAAACGAAATTGAAAAAAGTTTGCACCATAAAGGAGAATTTAAACGAAATTGAAGGAGCACTTTTAATGATTCGTGAGAATTTAACGAAAAGTTTTAACCAAAAAGTTTGAAATTGATTTTTAAGCGCATTTCCATGAAAAAGTCGCAAAAAAATTGAAAAAATTGAAAAAAATTGAAAAAAAA	191 TAGAGAGATTA CARGAGAGCCCAAAAACGGCATGGCTAGGAGCTTATGCATCCAAGAGCTTATGCATCGCTAATGTAGCATCGTAATGTATGCATCGTAATGTATGT
HP0336	HP0336	нР б 336 НР 0 336

HP0336	195 GCTTTAGAAAATAGCGAAACAGCTTACAATGAAATGTTTTTAGAATGCGATAAGCAATTCATCTTAGAGGAGTTGGCTC	196 ALENSETAYNEMFI. ECDKOFILESWI
	AATGACTTTGACTAAAGATTATAACGAGACTATGCACTTAGTTTTTCTATCAAAGATAAGCCAGATGAAGAGA	DFDLTKDYNETMHI.VFSIKDKPDEET
	CAALGCAAGCCITITIACALICIACITIGGGAGAGCITAAAAATAAGATTGCCTGAAGTTTGCCCTTGTGCCAC	QGLLHSTWESLKIRLPEYKFALVPH/90
	AGGGGCATGAAGATTGTAAAGAATTTTTTAATGAAATTAAAGAGTGAAGTTGCTTATAAGATTGATGAATGA	OCKEEENEI DSEEA YBI NOUI SEE'S
	GCGAAGAATACTTGTATGTCAATGAGCCAAAACTTAAAGAGCTAGACAATACAAACAA	VVNEPKLKELDNIKGQLQDLEKEEK/T
	AAGAAGAAAAAGCCTTAGAACAAATCCCCACAAGATGGGGACTTAAACAAGCCTTTACAAAGCGAGTAT	EQIKSPQDEWDLNIKALQSEYLQELKYK
••		NKAKALDIQNNHSTPLKQKISEFKIALF
	ATAGATAAGAGAAAACCAGTAAGCGAACAACAAAAAAAAA	NHKDTSDDEKEQLIJIDRIDKRKPVSEH
	CAAAAGAATTAGATAAAAAAGAAAGAAAGCATTCAGGCTTTAAGAATTTGCTATTAGATTAAGAAGAAAGA	LENINKHELYELLGFYGKELDKKONHS
	AAAGAGAGACTAATGGCTATTCTGTTTTAAAGAAAAAGGAAATGCTTTTAAATAAGCTTGAACACCTAGACAACGCC	KEMLLNKLEHLDKFLLDKNSHLLAOL
	TTTTAGATAAAAACTCACACTTACTATTAGCCCAGCTAAGAAATGAAGTTAAAAACCAAGCAAACATCCAATACAACAC	RNEVKTKONIOYNTLTNPILLAKALELS
	ICIAACIA	KDKRPTLKTFKNAYFSARKYGFMLESF KTKQNDPTYKLNDNTYELVSKQLQDY
HP0336	197 TATGGAAAAAGATCACGCTTTAATTTTAGGGGCTAGCACGCAAGATCATAATTACAGCCTAAAGATTAACATTAACATTAACATTAACATTAACATTAACATTAACATTAACAATTAACAAC	198 MEKDHALILGASTODPNYSLSHAIRSR
	CAAAAACCAAATAGAGCCTAACTTATTAAACAACAACAACAACAACAACAACAACA	STITELIT LINGSCOADALI NI POLEA
	TTTTAGATTTGAGCGCTAAAATAGAAGATCCTATCACATTAAAAAAGGCTACAATCCTTAGAGCGCTAGAATGCTTAGAGATCCTAAAAATAGAATGAA	EPGANI TELINDAGDARAELNELDEDA KIEDDITI KTI OSI BISHSI NDGSVSODT
	TGGATCTTATAGCGATGATACGTTATACTTACCGTTAATCAAATCTTTAAGAGGGAGCGATGAAAACGC	HYNI TSAI IKSI RGSDENASIYYI ARI IA
	TTCCATCTATTATCTGGCGGGCTTGATTGCTGGCGGGGAAAACCCGGAATTTATCGCCAGAAGGCTGGTGATTTTTG	GGENPEFIARRLVIFASEDIGNANPNAL
	CGAGCGAAGATATTGGTAACGCTAACCCGAACGCCCTTAATTTAGCCGCTTCTTGTTTGCAGTCAAACAAA	NLAASCLFAVKQIGYPEARIILSQCVIYL
	GCI ACCCI GAAGCGCCCAI CAI I I AAGCCCAAI GCGI GATTI ATCT GGCTTGTT CGCCCAAGTCT AACACGGGCTTAT	ACSPKSNTAYRAINDALDCVQKGSLYP
	AGENCALIZACIONE DE LA PROPERTACIONE DEL PROPERTACIONE DE LA PROPERTACIONE DEL PR	IPKHLLPNAKDYLYPHDYNGYVKQDYL
	TCTCAAGGCATAGGATTTGAAAAAACCCTTTTAGAATGGCTTGATAAGAATAGAAATTGATAAGTTTAAATTAAATTAAAATTAAAATAAAATAAAA	EKPLDLVSSQGIGFI:KI LLEWLDKIKN
	ATGCGACAATGGTAATAAAAAATCAATATTTTGGATTGAATTAAAATAATAATGGTTTTATCTATGTTTCATCGCATT	
	ATTATTGTATAATAATAATATCTAGTTATAAAAATCATTTTACGGATAAGGAAGATATCAGCATGAAAAGATTAGAAACTTT	
HP0336	199 TCTCAAGCGCTGAATGTTGAAGCTTTTGAAAATTTTGCCGAGTATGTGAAAAAGGATTTTTGATGAAAAAGAGTCGTTG	200 SOA! NVFAFENFAF VVKKIFDEKESLS
	AGCGAGCGGTATTTGCAGCATAAGGTTAAGGACTTTTTGACTAGAGGGGGGTTTATGATCTGAGCTTTGAGCCTAT	ERYLOHKVKDFLTREGVYDLSFEPILAL
-	TTAGCCTTGAATGCGAACGCGAGCAAGCCCCATGCTTTGCCTAGTGCGAAGGATTTTTAAAAAGCGGAGCACAGCA	NANASKPHALPSAKDFLKAEHSILLDM
	TICLI I I GSA A I GGGGCTATIGCTCI GATAGGACTGGCACGGCTTTTTTGACCCTAAAGATT	GIKYERYCSDRTRT/AFFDPKDFVFKRE
	I I G I C I I I AAAAGAGAGGAGGAGGATAAAGAGGATAAAGAGATTTATGACATTGTGAAAGAAGGAGGGGAAGAAA	OSFKDKEROKIYDIVKEAGEKAISGIRA
<u> </u>	AGGC1AGGGGGATATTTCACTTCACGGGCACTTCACATTGGCTTAGACATCATCATCATAGATTATTTCATTATTTTCATTATTTTCATTATTTTCATTATT	GMTGKEADSLARGVISDYGYGQYFTH
	GCGCAGTGAAACCATTTTAGAAGAGGCCATGGTTTTCTGTAGAGCCTGGGATTTATATATCCTGGGTTTTTTGGGG	VESVEDGISLDIDELT 1130ASE TICEGOM
	TGCGCATTGAAGATTTAGTGGTGATCAAAAATTCTAGGTCTGAGCTTTTGTGATGCGAGAGATCCTTACTAGCCGCTT	ELL STATES OF THE STATES OF TH
		I 7/.

MO 05/000201 · C	パミッエマ	(≤ 0 = µµ0 = 1 = 1 > PCI/EP01/15428	
(一角のようについ)	医罗季萘	103025つよりと会ちに入りくず 16をそくごで ニー・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・	
¥ ₹ EZEZEE		SECTION OF THE PROPERTY OF THE	

HP0336	 	201 IATTITCGIGATGAAAAGGGCTTAGATGTTGATGTTTATTGACAACATCTTTAGATACGCTCAAAGCGGTGCGGAA	202 YFRDEKGLDVLMFIDNIFRYAGSGAE
		A MACAGE TATTER A THE MACAGE TATTER A TORONTO THE MACAGE T	SALLGRIPSAVGYOPTLAGEMGKLOF
		TRACCOCKTECTION TO THE CARL WAVE TO THE CARL WAVE TO THE CARL TO T	IASTKNGSITSVQAVYVPADDLTDPAF
		ATTACOCOCCES CONTROLL CONTROL CON	SVFAHLDATTVLNRKIAEKGIYPAVDF
		TECHT CONTROLL SEATING THE SEATING THE TRANSPORT OF THE SEATING SEATIN	DSTSRILSPOMIGEKHYEVATGIQQVI
		STOCKED A CCASCASSI I I ACADADA I ACADADA I I I ACADADA I I I ACADADA I I I ACADADA I I I ACADADA I I I ACADADA I I I ACADADA I I I I ACADADA I I I I ACADADA I I I I ACADADA I I I I ACADADA I I I I ACADADA I I I I ACADADA I I I I ACADADA I I I I ACADADA I I I I ACADADA I I I I ACADADA I I I I ACADADA I I I I ACADADA I I I I I ACADADA I I I I I ACADADA I I I I I ACADADA I I I I I I ACADADA I I I I I I I I I I I I I I I I I	AKYKDLADIIAILGLDELSEEDKKTVEI
		TO SACCESSAGE AND ANAMARACION OF THE SAC	ARKIEKFLSQPFFVAEVFTGSPGKYVT
:		II GAAGTTTTGGAGGGATTTTAGAGG GCAAATACGATCATATTCCCGAGAACGCGTTTTATATGGGG	QETLEGFGGILEGKYDHIPENAFYMV
HP0336	203	203 CATGCGGATGGAAGACAGCTTTTTGGATGATTAAAAGACAGATCGCTCAAAAAGAGGGCTTTCATTTGTTTTG	AND MEMOREOUS ENIMINERAL CONTROL OF THE CONTROL OF
		GGAAGAAGGTGCAACGATTTATCGCACCAGATTTTGAATAAAATCTTAGAGATTGATCATGTTTAGCGTGTC	MERCAN SHOULD NIGHT DEPOSITION OF THE PROPERTY
		GGAGAATTTGATAAGAAATTTACAAATCCATTGACACCTATTCTAAAGCGTATGAAAGCATTGAAATGAAGTG	I IRNI IYKSIOTYSKAYESIENISVAEKIKE
		CATGAAAAATCAAGCATTACAAACGCAAACTGCCCGTAGGGAGCGATGAATACGAGTTGGTGTTGAAAGGCTCTA	VKRKI PVGSDEVEI VEERI VEEEI RRK
		TGAAGAAGAATTAAGGCGCAAGGGTTTTTATAATGGTCTCTCTC	GFL
2000		AGITITIGGGGCTAGCGGCACGCAAGCGGGCGAGCTTGTTTTAACACTTGTATGAGCGGTTATCAAGAAGTCATTAG	
-IP0336	502	GAACGCICIAAIGAIGAGCGITITATCCCCCTTGCCAAAGCCTAGCATTGATACAGGCATGGGATTAGAAAGGGTGCA	206 ERSNDGVLSPLPKPSIDTGMGLERVQ/
		AGCCCTATIAGAACATAAGCTCAATAATTTGATTCTTCATTATTTGCGCCCCTAATGGAAGAAATCAGCGAGCTTAC	LLEHKLNNFDSSLFAPLMEEISELTSLD
		AAGCCIAGAIIAIGCGAGGTGCGAGGTTCCAGCCATTTAGGGTAGTGGCCGATCACGCAAGAGCGGTAGCATTCTTG	YASÉFQPSFRVVADHARAVAFLLAQĠ
		CTCGCTCAAGGGGTGCATTTCAATAAGGAAGGCCGTGGCTATGTTTAAGGCGCATTTTAAGGCGAGCCTTAAGGCA	VHFNKEGRGYVLRRILRRALRHGYLM
	·	1966BIAI II AAI GGGCTTGAAAGAAGCGTTTTTATACAAAGTCGTGGGCGTGGTGGTGCGAAGTTTGCTAACACGC	GLKEAFLYKWGVVCEGFANTHAYLKE
-	,.	A LECGIALLI GAAAGAGICI AAAGAAATGGTGGTAAAAGAATGTTTTGAAGAAGAAGAAG	SKEMVVKECFEEEEHFLETLESGMELF
		AN INTERESTANT OF THE PARTICULAR OF THE PARTICUL	NLSLKHLNENKIFDGKIAFKLYDTFGFP
	_	SCHILL SACALITIES FILECCITIES ACCARGAGGACATGTTAAGAAGTCATGGGGCGTGTGCGGATATGCA	LDLTNDMLRSHGACADMOGFELCMO
		PASSON I LEGAL I EL I LECAL ECCAGE ECCAGE GAACEC I CI AAAGCI I CATEGAAA GAAAAAAAA CAAACAACGATT	EQVKRSKASWKGKONNADFSAILNAY
		PASSOCIATI I AVACUE I I I I I I I I I I I I I I I I I I I	APNVFVGYETTECSAKVLGFFDSDFKE
		SELLI I I I SA I ACCALI I I AAAGAAATAACCGATGCAAATCCTAACCAAGAAGAGTCTGGGTGTTGTTAGAAAAACCC	ITDANPNOEVWVLLEKTPFYAEGGGAI
		CITITIA I GCAGAAGGIGGAGGGGCTATAGGCGCACTATTTAAAGACAATGGAGAAGTGGCTATCGT	GDRGALFKDNGEVAIVLDTKNFFGLNF
		GELGGE TACARARACH HILLIGGGCTTAATTITICACTCCTTGAAAAAAAGGCGCTAAAAAAAGGCGATCAAGTG	SLLEIKKALKKGDÖVIAQVSDERFEIAK
		A L C C C C C C C C C C C C C C C C C C	HHSATHLLQSALREVLGSHVSQAGSLV
			ESKALAFDFSHAKALNDEELEKVEDLV
			NAQIFKHLNSQVEHMPLNQAKDKGAL
MDA336	202	207 TOTAGGGGGAATOTAAAATTI TAAAATTI AATA	ALFSEKYAENVRVVSFKEASIE
0000		TITION TO A CONTRACT TARGET OF TAXABLATIC TRACKLOCK THE TAXABLA CONTRACTOR OF TAXABLA CO	208 LGEESKIFRVLNDFYMNPICGAGRFAF
		TGCGAATAGGTGGGGATATTACGAATGAAGAGGCGTTTTTAATAGAGCGTTTTAAGAAAAGAAAAGAAATGATTTAAAAAATT	OVSSSPKGSANLKEAUNALKEUEAVRI
		ACAATCAAGAGCGTATCGTTTCCAGCAATTCTTAAAAGTATTGGGCGGAAATTAAAGGCCCCAGCGTTGAAGAGATTA	YREODE KVI GEIKRPSVEEKTSHI VV
		AAACTICICATTTAGTCGTTACGATAGGATCTTCTATCAAAACAGAAAACCCTTTGGTGCGCTATGCCATCAATAACG	TIGSSIKTENPLVRYAINNALKLNKASLI
		CTITITION AND ANALYSIS TO THE CONTROL OF THE CONTRO	AMHPIKDNALANLCRSSFCITHEVGAEC
		CITTTTAAAAAGCTTAGAAGATTCCA CGGCCCTAAAAAGCTTAGAAGATTCCA	EILLGMLLKMLNIESAALKSLEDS

W	7

O 02/066501			PC	T/EP01/1542
210 SNPDYISTHSESALDL_KLLKKNOMNA O SAIEIAHLLINODDDLKAKEQALYDLGAN LYARIKDFKNAHLYNLOYLQDHAELDK O ASVVRARDEKALFSMEGNTOEKIAHYI99 KIIQNFPNSNEALKALELKAQLLFENKRO YAEVLSMQKNLPKDSPLIQKTLNVLAK TPLENHRCEEALKYLSQITTFEFSPKEE IQAFDCLYFASLKEKAQIIALNAFKTAKA PSSEKLIWLYRLGRNYYRLGDFKNSTLA	212 REKKLIHPNDDVNMS(3SSNDTFPTAM HIVSVLEITHRLLPSLE NLLKTFKEKSQ QFKEIVKIGRTHLQDATPLTLGQEFSGY ASMLEHSKQQILESLEHLRELAIGGTAV GTGLNAHKELSEKVAEELSQFSGVKFV SAPNKFHALTSHDAIAYAHGAFKALAA NLMKIANDIRWLASGPRCGLGELNIPE NEPGSSIMPGKVNPT(3CEAMTMVAVQ VMGNDTAIGIAASQGNFELNVFKPVIIY NFLQSLRLLSDSMESFNIHCASGIEPN REKIDYYLHHSLMLVTALNPHVGYENA AKIAKNAHKKGISLKES	214 EDLGSFFEDAFGFGAF.GSKRQKSSIAP DYLQTLELSFKEAVFGSKTTIKVQYQS VCESCDGTGAKDKALIFTCKQCNGQG QVFMRQGFWSFAQTCGACQGKGKIVK TPCQACKGKTYILKDEEIDAIIPEGIDDQ NRMVLKNKGNEYEKGKRGDLYLEAQV KEDEHFKREGCDLFIKAPVFFTTALGH TIKVPSLKGDELELKIPINARDKQTFAF RN	216 SNHEILRPLVEKFDIPYFYAPCDNÖVLH EKEVLEIIKNLELKHKV:3ADLLVLAKYM RILSHDFTKRYENQILNIHHSFLPAFIGA NPYQQAFERGVKVIGATAHFVNESLDA GPIIIQDTLPINHNYSVEKMRLAGKDIEK I VI ARAI KI V	218 ELEILKSYLKIPYTLLETNTLNSKACLKD LSOKISAFFPKLDTONKLLLTSLAGKIAL ENAITELQNAKNHLETI.ELFSYHILSAIE NLNLLTRPYETSOMLDSMFSEFCLGK
209 ATCCAACCCTGATTATATTTCTACGCATAGCGAATCAGCCCTAGACTTGCTCAAGTTATTGAAAAAAACCAGATGAA TGCAAGCGCGATTGAGATCGCTTGCTCCTCAATCAGATGATGATGATCTGAAAGCTAAAGGCAAGCGCTTTATG TGCAAGCGCGATTGATGCCAAGGATCAAGGACTTTAAAAAAGCCCTTTACAATCTGCAAAGGCGTTGTG AAAAATCGCCCACTATGACAAAATCATTCAAAATTTCCCTAAAGGCCTTTAGAATTTGCAAGGCCTTGAAAGCCTTGAAAGCCTTTGAAATTTGCAAAGCCTTTGATTGA	211 AGAGAAAAAACTCCACCCTAACGATGACGTGACCTCCAAGGTCCAACGACCTTTCCCTACCGCCAAT GCACATTGTGAAAAACTCCTCAACGATGACGTGAACATTTGAAGCACCTTTAAAAAAAA	213 GAAGATITAGGCTCGTTITTGAAGACGCTTTTGGCTTTGGCGTTAGGGGGAGTAAAAGGGCAAAAAAGGCTCTATCGC ACCGGATTATTGCAAACCCTTGAATTGAA	215 TCCAACCACGAGATTITACGCCCTTTAGTGGAAAAATTTGACATCCCTTATTTTTAGCGCCTTGCGACAATCAGTTTTAG TGCATGAAAAAGAAGTTTTAGAAATCATTAAAAAACCTGGAATTAAAGCACAAAGTGAGTG	217 GGAGCTTGAAATTTTAAAATCTTATCTTTAAAATCCTTTTACTTAGAGACCAACGCCTAAATTCCAAGGCTTGT TTGAAAGATTTGAGCCAAAAAATCGGCCCTTTTCCCCAAACTTGAGAGACCAAGAGCTTTACTCACTTCCCTA GCCCAAAAAATTGCCCTAGAAAACGCCATTACTGAATTGCAAAAGCCTTAAAAAACGTTTAGAGCTTTTTTTT
HP0336	HP0336	HP0336	HP0336	HP0336

	_
_	
_	
-	_

VO 02/066501	>00= -F	T . W	
220 TIAAIATPLGKGAISIIKISGHNALNILKÜL TOKODFTPRYAYVHDIFSNGVLLDKAL VIYFKAPYSFTGEDVCEIQCHGSPLLA ONILOACLNLGARLAKAGEFSKKAFLN HKMDLSEIEASVOLILCEDESVLNALAR QLKGELKIFIEEARGNLLKLASSEVLID YSEEDIPSDFLDGVSLNLEKQIASFKDL LDFSNAQKORNKGHALSIVGKPNAGK SSLLNAMLEERALVSDIKGTTRDTIEE	V 2222 IDALVSAYHLODEDLYYHYLKIARDTLY KDYKKSFYSYAYALKSYYAGEYFEALS PLMHPNSNAFLKPNTRLASKLFLMFKD ETNAYEOLOKSANAODELALGLOARL GHYKGALEHLOHYLHNYPKDLNALMA LELVSLKKGOTLKASEALKLASHTKEDT ILANSFYPIKPTI	224 ESGIHLPNANTIIIDNAQNFGLADLHQL RGRVGRGKKGFCYFLIEDQKSLNEQ ALKRLLALEKNSYLGSGESVAYHDLEIR GGGNLLGQDQSGHIKNIGYALYTRMLE DAIYELSGGKKRLEKSVEIQLGVSAFLN PELIASDSLRLDLYRRLSLCENTDEVG QIHEEIEDRFGKIDDLSAQFLQIITLKILA NQLGIIKLSNFNQNITITYSDEKKESLK	226 KYINSPQSKLFÖKSSLLYGYHLAKEHIY KQKQVIVTEGYLDVILLHQAGFKNAIAT LGTALTPSHLPLLKKGDPEILLSYDGDK AGRNAAYKASLMLAKEQRRGGVILFEN NLDPADMIANGQIETLKNWLSHPMAFI EFVLRRMADSYLLDDPLEKDKALKEML GFLKNFSLLLQSEYKPLIATLLQAPLHV LGIRERVSFQPFYPKTEKPNR
	Í	18	8
219 CACCATTGCCGCTATCGCTACCCCTTTAGGCAAGGGGGCGATTAGCATCATTAAAATCAGCGGCCATAACGCTCTAA ATATCCTCAAACAACAACAACAAGAGCTTCACCCCCAGATACGCTTATGTGCCACGATATTTTTCTAATGGTG ATATCCTCAAACAACACCCCAAAAAAATCATTCAAAGCCCCTTATAGTTTCACTGGCGAAGATGTGGTGAAATCCAAT GCCATGGAAAAAGCCTTTTAGCGCAAAATATCTTACAAGCTTGTTTGAATTTAGGGGCTTGCTAAAGCGGGG GAATTTAGTAAAAAAAGCCTTTTAAACCATTAGTGAATTGAAGCGGGGTTTAGAAGCGGGGGGGG	221 ATTGATGCGTTAGTGAGCGCTTATCATTTGCAAGATTGTATTATCATTATCTAAAAATTGCGAGGAGACCTTTGTATTATCTAAAAATTGCGAGGAGACCTTTTATACGCCGGGAGACCTTTTTACGCGCGTCAAATTGCGCCGGGGAGTATTTTGAGCCCTTTTTGAGCCTTAAAAGCCTTAAAAGCCTTAATACGCCGGGGAGTATTTTGAGCCTTTTTGATTGCTAAATTGTTTTTGATGCTTTAAAGATGAAACGAACG	223 GAATCAGGGATTCATTIGCCTAACGCTÁACACGATCATTATAGATAATGCGCCÁAAATTTCGGGGCTGGCTGGATTTGCACACACACACACACA	225 CCAAGTATATCAATTCCACCCAAAGTAAGCTTTTTGATAAATCCAGTTTGCTCTATGGCTATCATTTGGCTAAGAACA CATCTATAACAAAAAGCAAGTCATTGTAACAGAGGGGTATTTGCATCTTTGCACCAGGCGGGTTTTAAAAA CGCCATAGCCACGCCTTGGGACAGCGCTTTAACGCCATTTGCCTTAAAAAAGGCGGATCCCGAAATCCTTT TGAGCTATGATGGGGATAAGGCAGGGGGGGGCCTATAAAGGCGAGCTTGATGGCCAAAGGCGAAACCTTT TGAGCTATGATGGGGATAAGGCAGGGGGGGGGG
HP0336	HP0336	нР0336 	HP0697

		PCT	/EP01/15	5428
1728IL	ZSSF	>= \ \	الخيا	

227 CAGTEGAATIGGCTITTGAITTTATAGGCCCTTGTTGCAAGTCCAGCCACTCAGTGCCCATTTTAAGCCATTTTAAGCCATTGAAACAACAACAACAACAACAACAACAACAACAACAACAA	HP0697 Z27 CACTCAAATGGCTTTTGATTTAATACGCCCTTTTTAAACGAATGCCACCATTGAAAAACGCCCACTTTTAAACGCTTAATCAAAATGGCTTTAAAAAATTGGGGGGGAGTTGGAGAAAACGCTTAAAAAAAA	000		TGCGGAGTTAAAAAAGGAAGT VQSLLNLCLHGGVGRNUKVVFKSGN VAGCLACATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
4	227	CACTCAAATGGCTTTTGATTTAATACGCCCTTGTTGCAAGTCCAGCACCACCA AGACGCATTGTTACAAGATCCGCATTTAATTGCCACCTTTTTATAGGCATTGTCTGC ATAAGATTTATGGGGGGGGGTGTTTTGTGGGGGGATTTTGGAACGCATTGAAAA TAAGATTTAAGGGGGGGAACAAAGCGATCAAAGAGCCTTGGACGCCTGGTTTTAGAAATT CTTTTTAAAGCGCGTTCAAAGGCGTTTTAAAGAAGCGAATTAGAAATTTCCAA GCTTTTAAAGCGCGTTCCATAGGGCGTTTTTAAAGAAGCGAATTAGGAATTTTCCAA AGACAGAGAGGCGGGGTTTTTAGAAAATCTAGCCTTTAATCGAAGCGATTGGG TAAGAAATTTTTTTAACAGCCTAGTAGAAATCTAACCGCTTTAATCGTGCCTTT GTGGGGGCGTGTTTTGCAACCAATTATTATGCGAACAATTAGCCAAACGGTTGA ATCAAAAAAGGATTCCCCCCTAATGACAGCAGTACCGTGCGGGGGGGG	TATTGCGTGAGCCGGGATGCGATCAAGGAAATGCCTGACCCCGGAATGCGATCCAGGAATGCGATGCGATGCGAGGAATGCCTGACCCATTTGGTTTTGGTTTTGGAAGGAA	CATAATGITTGGGAATAAGCAGTTGCAACTTCAAATCAGTCAGAAAGATTCTGA CAATCTTTATCAAAGCCTTTTAATTTGTGCTTGCATGAGGGTTTTGTAGGTAT CAATCTTTATCAAAGCCTTTGAACAATTTGAGAGGACCAGGGTTTTTTAAGA AGGGGAATCTTGCAAAAAGCCAAAATATTGATGGCGTGCAGTATTTTT GGGGGAATACCATAAAAATGATTTGTTTAAGACTTTTTGCGCGGGCTGCAGTATTTTT GGGGGACGGTTAATAAAACGGGGCAGCGCTCTTTTAATGAAAGGT TTGGGGACGGTTAATAAAACGGGGCAAGACATTGAATGCATTCTTTGATGAAAGAT CTCTCCAACCAACGGAGCAAGACCCGAGGGGGGGGGG

HP0697	233	233 GGGATTTGAATGCGATTTTAGAAGATCTCAACAGCAAACAGCTATTGCCAGAATACGCTTACAAGGTTTATGGCGCA GTGGTGAGTCAAAATAAAGACGGCGTGTGGGTCGGCGATGAAGCCCAAAACGAAAGCCAGAAGAAAGA	234 X X X	234 DLNAILEDLNSKOLLPEYAYKVYGAVV SONKDGVWYGDEAKTKARRKEILENR KARSIPVKQWMEQERNAILEKEASKQY KHMYATSFDLSPK
HP0697	235	235 AGACGCAATCAAAAAAGCGCATCAAAGTTTATCAACTATCCCTCTAAGTTCTTCACTCTATGCCTATAATCTCTGTTTTAAACAAAAAAGCGCATCAAAAAAGGAAAAAAAA	236 D	236 DAIKKAHQSLSTIPLSSSLYAIISVLKHY GMLEDIQQNPSKPTNLKKETIQGTH
HP0697	237	237 AGACGATCGCTCGTTTTTTATCACTGATTCTCGCTACACCTCAAGAAGCTAAAGAAAG	238 DI	238 DDRSFFITDSRYTGEAKESVÖPKNGVL AEVVESSDLVQSAIDLIVKSSVKKLFFÖ
HP0697	239	239 GCTTGGCTACAACATGGCTTTAATGGCGATGGTCAATATTTTAGCCGAAATGAAGCGTTCCAGGAGCCCCAAAAAAAA	24 102 103 103 103 103 103 103 103 103 103 103	Z40 LGYNMALMAMVNILAEMKAFQEAŬKN NPNNPINNQK
HP0697	241	241 CTCTAAAGAGAGCTTGATGCATTAATTCAATTAGAGTGGGCATGCAT	242 SK T T T C V V V V V V V V V V V V V V V V	242 SKEŠLMHAINSIRVGMHFKELSČILESTI TERGFVPLKGFCGHGIGKKPHEEPEIP INYLEKGVKPNSGPKIKEGMVFCLEPM VCQKČGEPKILADKWSVVSVDGLNTS HHEHTIAIVGNKAVILTEŘ
HP0697	243	243 AACAGCTCAGCGGTGGGCAAAACAACGAGTGGCGATCGCTAGGAGTTTAGCGAATTGCCCTGATTTATTGCTTTGCGTTTGCGTTTGCGTTTGCGTTTGCGTTTGCGTTTGCGCAACAAAAAAAGGCGCAATTCAAAAAAAGGCGAATTGAGGGGGCATTCAAAAAAAGGCGTTTGAGGCGCATCGATTTGAGGCGCATGAGGTTTGAGGGGGATTGAGGGGGGAATTGAGGGGAATTGAGGGGAATTGAGGAATTGAGGAATTGAGGAATGTGCGTAAATGTGCGTGATCAGCAGCGGGGGGGG	244 OL AT FIT	244 OLSGGÖKÖRVAJARSLANCPÖLLLÖDE ATSALDSKTTHSILTLLSGIÖKKLÖLSIV FITHEIEVVKELCNÖMCVISSGE

v	
_	•
_	-

02/066501				PCT/EP01/15428
246 PHLFVVQDAQKKWVIKCSCGHAFCAP EENWKLHANIYVRDTAEKMEEVYPKLL ASDTHWQVYREYICFDCGILLDVEAPT PWYPVIHDFEPDIEVFYKDWLGIQPPE RR	248 QSLLLKLNAFASKLEKKLFDSGFSHSD FKLVTRVKRPYSIYLKMQRKGAVNIDEI LDLLAIRILLKNPIDCYKVLGIIHLNFKPIV SRFKDYIALPKENGYKTIHTTIFDESSV YEVQIR	250 DILSSIFGKGGFSÖRF:SONSOGFSGFN FSNFAPENLDITAALNVSVLDTLLGNKK OVSINNETFSLKIPIGVEEGEKIRVRNK GKTGRTTRGDLLLEIHIEEDEMYRREK DDITOIFDLPLKTALF/SGKIEIATWHKTL TLTIPPNTKAMOKFRIKEKGIKNRKTSH VGDLYLQARLILPKTE TLSNELKALLEK EL	252 VGGTASRSQDEREIVASKEGFVRFYNL RTYTNKEGKNIIANRF.NASILVVEPKIKA PFDGELRIETVYEEV/VSVKNGDQEAK FVLRRSDIVKPSELAG-VGGKIEGKVYLP YASGHKVHKGGSIAD.IIQEGWNVPNRI PYASELLVKDND	254 RVEENYHAFFTEASG FLNERIFKDYLR RLAYGIDASCYRYIPKIVAWVKNEEEV, OKLCYLAKKHGVSLTFRAAGSSLSGQ AICDGVLVMYTHFKDAOILDNAQSIQL SCGVIGSNANALLKPYHKKIGPDPSTIN TAMIGGIVANNASGMCGGVEDATIN LKSLRVILADGTLLDTANGESVESFKNAHKDLEGVLNURKEILEDKELHALIKKKYEIKTTGYSLNALIDFEDPIEIISHLFIGS EGTLGFISSVELECVKDYAYKTCALLFYENLERCAKAAQILAAI.KAKOPEMISSAELMDYACLKSVKGLEGMPSVVLEIKEPN ACLLIQSESDDPLILENSMQTILNALSAI PVVLDSQISSDPSIYCSWWKIRKGIFPI AASKRKSGSSVIIEDICFS
	247 GCAGTCTTTACTCTTAAAGCTCAACGCTTTTGCGAGCAAGTTAGAAAAAAACTTTTGATAGTGGGTTTAGCCATTC GGATTTTAAACTCGTTACAAGGGTGAAACGCCCTTATTCTATCTA	249 CGATATITIAAGCTCTATITITIGGGAAAGGAGGCTTITCGCAAAGATTTCTCAAAACTCGCAAGGCTTTTCTGGCTTTT AATTTTTCCAATTTCGCCCCTGAAAATTTAGACATAACCGCCGCTTTAAATGTCTCTGTTTTAGACACCCTTTTAGGCA ATAAAAAACAAGTGAGCATCAATAATGAGACTTTTAGCCTTTAAAATGTCTCTGTTTTTAGAGAGGCGAAAAGATTA ATAAAAAACAAGTGAGCATCAATAATGAGACTTTTAGCCTTAAAATGGCGTGGAAGAGGCGAAAAGATTA GGGTTCGCAACAAGGGGAAAACGGGGCGAACGATTGAGGGCGATTTGCTCTTAGAGATCCATATTGAAGAGGATGA AATGTATAGGCGCGAGAAAAACGTAAACCTTAACCCAAATCTTTGATTTACCCTTAAAAACGGCTCTTTTTGGAGGGAAAAT TGAAATCGCTACTTGGCATAAAAACCTTAACCCTAACCCTTAACAAAGGGCTCTTTTTGGAGGGAAAAT TGAAAAGGGGTCAAAAAACGTTAACCCTAACCCTTACCAAAGGGCTCTTTTTGCCTAAAACTTCGCAAAACTTGCAAAACTTGCAAAAACTTGCAAAAACGGCTTTTTTGCCTAAAAACGGCTTTTTGCCTAAAAACGGCTTTTTGCCTAAAAACGCTTTTTGCCTAAAAACGGCTTTTTGCCTAAAACCGTTTAAAAAACGCTTTCTAATGAAAAAGCGCTTTTTTGCAAAAAGCGGTTTTTTTT	251 GTGGCGGGACAGCAGCAGGAGTCAGGATGAGCGCGAAATCGTAGCGAGCAAGGAAGG	253 GGTGTGGAAGAAATTATCATGCTTTTTTACCGAAGCGGGGTTTTTAAACGAGCGGATCTTTAAGGATTATTTA CGCGTTTGGCTTATGGCATTGACGCGTCATGTTATCGTTATTATCCCTAAAATAGTCGCTTGGGTGAAAAATGAGAA CGCCGTTTGGCTTATGGCATTGACGCGTCATGGCGTTTCATTGACTTTTTAGAGCGCTGGTAGCTCCTTATCA GAAGTCCAAAAGCTTTGGGTGTGTTATGGTTATGGTTATGACTTTTTAGACGCGCTGGTAGCGCTCCAAAAGAGACGCTCA AAGCATTCAGCTCTACGATGGGGTGCTGGTTATGGTTACGCGAACGCTTATTGAAAAAAATTTAGACAAAAAAAA
HP1423	HP1423	HP1423	HP1423	HP1423

•	4	1

<u>Q 02/066501</u>		
256 TLNIRVPRLKPLSLEDFTFKASDPKSLK DLALKGHNILISGETSSGKTSLLNALLD CVNKDERVVSVEDSGELDLKAFSNCV GLLVGKOENTFNYEDALNMAMRLNP DRLVGEIDTRNAALFLGNTGHKGM LSTIHANSAQNTLEALSLNLSMRYMYS LDKDLMRAYFKSAIDVIVHVNRINNERQ IAEVLWTKEL	258 LKEILSQNKVGMHLAHSVDVRIEVAPKI QINAQSNINYKAIKTSVKDSYTFENFVV GSCNNTVYEIAKKVAQSDTPPYNPVLF YGGTGLGKTHILNAIGNHALEKHKKVV LVTSEDFLTDFALKHLDNKTMDSFKAKY RHCDFFLLDDAGFLQGKPKLEEFFHT FNELHANSKQIVLISDRSKNIAGLEDR LKSRFEWGITAKVMPPDLETKLSIVKÖ KCÖLNQITLPEEVMEYIAQHISDNIRĞM EGAIIKISVNANLMNASIDLNLAKTVLED LQKDHAEGSSLENILLAVAQSLNLKSS EIKVSSRQKNVALARKLVVYFARLYTP NPTLSLAQFLDLKDHSSISKMYSGVKK MLEEEKSPFVLSLREEIKNRLNELNDK KTAFNSSE	260 IKRAAKELKEGMYVNLGIGLPTLVANEV SGMNIVFOSENGLLGIGAYPLEGSVDA DLINAGKETITVYPGASFFNSADSFAMI RGGHIDLAILGGMEVSÖNGDLANWMIP KKLIKGMGGAMDLVHGAKKVIVIMEHC NKYGESKVKKEČSLPLTGKGVVHÖLIT DLAVFEFSNNAMKLVELÅEGVSLDQV KEKTEAFFEVRL
255 ACGCTCAATATCCGTGTGCCTAGGCTTAAGCTTTAGGGGATTTCACTTTCAAAGCCAAGGCGTCCAAAAGGTTTAGAAGCTTTCAAAGCGGTAAAAGGGCTATAAAGCTTTGAAAGGGGAGACTTCAAGGGGGAGACTTCAAGGGGGTAAAACAGGCCTATTAAACCTTTTAGATTGCGTCCAATAAAGGGCATTCAATAAGCGGGGGGGG	257 CTTAAAGAAATTITAAGCCAGAATAAAGICGGCATGCATTTAGCCCACAGCGIGGATGIGCGTATTGAAGTAGCGCC TAAAATCCAAATTAACGCCCAATTACAATTACAAAGCCATAAAAAAGGCGTCAAAGACTCTTACACTTTTTAAAAAATTTTGCAAAAAAAA	259 TCÁTTAAAAGÉCGÉCAAAGEAATTGAAAGAGÉGCATGTATGTGAATTTAGGGATAGGCTTGCCCACGCTTGTGGCTTAGAGGATAGAGAGGGATAGAGAGGGAAGCGAGAAGCGAGAAGCGAGAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGGCTTTAGGGGCTTTGCTTTTTAGAGGGCTTTTTTAGAGGGCTTTTTTTT
HP1423	HP1423	HP0691

	•	•
-	•	
-	-	-

O 02/066501	·	
10 4.	264 LFSSADKYDSGCGWPSFS'KPINKDVV KYEDDESLNRKRIEVLSRIGKAHLGHV FNDGPKELGGLRYCINSAALRFIPLKD MEKEGYGEFIPYIKKGELKKYINDKKSH	266 HYLESVTHALEISPKNPLLIIKFLEKAVE LDVDAICDKKEVYIAGILCHIEEAGIHSG DSACFIPSTLSPEILDEIERVSAKIALHL GVVGLLNIQFAVHQNSLYLIEVNPRAS RTVPFLSKALGVPLAKVATIXVMVLEDL KEALKFYDKKNIVGYSKGVYKPKMPHF VALKEAVFPFNKLYGSDLILGPEMKST GEVMGIARSLGLAFFKAQTACFNPIKN KGLIPVSIKDKDKEEACVLWKRLVQLGF ELCATEGTHKALEKAGVKSLKVLKISE GRPNIM
261 GGGGATTGAACAAGACGCTGATATTGTTTTTATATAGAGGCCTATATCTACAATGAGGGCTGAAGACAACAAAAAACAAAAAGAAGAAAGA	263 CGTTÁTTTCTTCAGCGGATAAATACGACTCCGGTTGCGGGTGGCCAAGCTTTTCTAAGCCTATCAATAAAGATGTGGTGGGTG	265 CCATTATTTGGAAAGCGTTACGCATGCTTTAGAGATTAGTCCTAAAAAACCCGCTTCTCATTGATAGTTTTTAGAAAAA CCGGTGGAATTAGATGTGGATGCTTTTTGCGATAAAAAAGAGGTTTATTGCCGGCATTTTACAGCCATTGAGAA GCCGGAATCCATTCAGGCGATTCGGCGTGCTTTATCCCTTCCACTCTAAGCCGTGAAATTTTAGATGAAATTGAGGG GGTGAGCGCAAAAATCGCTCTGCATTTGGGCGTAGTAGGGCTGTTTGAAATTGCAATTTGCTGTGCATCAAATTCGC TGTATTTGATTGAAACCCTCTGCAATCCAGCCGCAACCGTGCTTTTTTTAAGCAATTTGCTTTAGCTTTAGCTTTAGCAAAATTCGC AAGTGGCGACTAGGGTTATGGTGCTAGAAGACCGTTTTTTTAAGCAAGAGCGTTTTAATAAAAAATTTTATAAAAGAAATTTTATAAAAGATTTAATAA
HP0691	HP0224	HP0224

HP0224	267/ATGGGGAATTGCACAAATACGACAATTCTTTATTGGCGCTCAAAAGGACGACTGAAAAAAAA	O VASI DE LA LA LA LA LA LA LA LA LA LA LA LA LA
	TATGAAGAAGAGTTTTTACTCTCTTACATTCCAAGCCCTAAAGAGCTTAAAGAGCGGTTTTAAAATATGTAAAGAG	O TOPO THE PROPERTY OF THE PRO
	CAAGAGCAGCTAAAAAGGTTTTTCCGTAGCCGTGTATAACCATTACAAACGCTTATCTTTAAAGAAAACTCAAA	AKKYESVAVYNHYKRI SEKEKI KKODNO
		ODSNVELEHLEEVELSKSNILLIGPTGS
	ATCGGCCCTACAGGATCAGGCAAAACTTTAAATGGCGCAAACTCTGGCCAAGCATTTGGATATTCCTATCGCCATTAG	GKTLMAQTLAKHLDIPIAISDATSLTEA 😇
	CATGCGACTAGCTTGACTGAAGCGGGCTATGTGGGCGAAGACGTGGAAAATATTCTCACAAGATTGTTGCAAGCG	GYVGEDVENILTRLLQASDWNVÓKAQ I
	A GECACTEGA TET CCAAAAA GECCAAAAA GECATTETTATTEA TEA GATTEA TAAAA TCA GCCGTTT GTCA GAA	KGIVFIDEIDKISRLSENRSITRDVSGEG
	AACCECTION CAN CONTRACT TO TO GO COAGO CONTRACT CAN AAAA TOO TOO TOO TOO TOO TOO TOO TOO TO	VQQALLKIVEGSLVNIPPKGGRKHPEG
	GAATALCCCCCCCAAAGGCGGCAGAAAGCCCCGAGGGCAATTTCATTCA	NFIQIDTSDILFICAGAFDGLAEIIKKRTT
	I I I I I I I I I I I I I I I I I I I	QNVLGFTQEKMSKKEQEAILHLVQTHD
	GAAAAGA I BAGCAAAAAAGAGCAAGAGCGA I CI I GCATI I AGI CCAAACCCATGACCT GGTTACTTATGGGCTTAT	LVTYGLIPELIGRLPVLSTLDSISLEAMV
	CCC GAGECIIAII GGCCGIIII GCCGGCIII AAGCACGCIAGATAGCATCAGTITAGAAGCGATGGTGGTGATTTTAC	DILOKPKNALIKOYOQLFKMDEVDLIFE
	AAAGGGATTAAAGAAATGGC	EEAIKEIAQLALERKTGARGLRAIIEDFC
		LDIMFDLPKLKGSEVRITKDCVLKQAEP
		LIIAKI
HP0224	269 AGG 16 TI CAAAGACACAAAAAGACGCTT GCGGGTTCATCTATGAGATCAGCGAGTTCATGAAAAGCCTATACCGCA	270 VFKDSKKDACGFIYEISEFMKAYTALLK
	I I SU I ANA ANA CHARLACE I I ATTITATI GAGGIATO COCOTOTAGGIATT GGGCCAGCATTITA ACGACT	KQDRYVYLLRYLPSRYWASILTTALYV
	SCUCTITATION AND THE CONTROL OF THE CANADA AND THE CONTROL OF THE CANADA AND THE	KYPDFDALKKLLVSYYYQTWIAGGTITR
	GAGECACIGATICACIGATICACIGATICAACATTATCAAAACGTTAAAAGCAATAAGAGCGTTGAAACC	IKÓTSINIIKNVKSNKSVETIKELILNSIÓS
	A LAAAGAGU I A I I IGAA I AGCA I CAACACTOTA AACACCTOTT GATCAA TACCTOTATAACTTA TGGGATAGCTCTT	YNTFDQYLYNLWDSSSVYHSKWVRPV
	CIETTATICATEGECAGATEGECETECTETCTAGECECTAGETATTTECATEGECAGATEAAGAACCCCATT	LALANYFMADEEKPHFIAMDAETQVEH
	ITALCEC A I SEA I SCCEAAAACCCAA I SEA SEA SEA SEA SEA SEA SEA SEA SEA SEA	ILPQTPKRGSQWNAĎFDKEKREEWVN
	GGATTTAACCCTTTTAAACGTAAAAAGACCC	NIANLTLLKRKKNAHALNGDFDEKRKIY
	GCA1GCTTTAAACGGGGATTTTGATGAAAAAAGAAAAATTTATGGAGGCAAAGACACGACAAAGTGATTAGCTGTTA	GGKDTSKVISCYDITKELYSNYRKWNE
	JIGACAICACTAVAGAATTGTATAGCAATTATAGGAAGTGGAATGAGAAGTCCCTCCAAG	KSLO
MP0692	Z/1 GGAGCGGGTTATGCGGCCGCTATGTGGCTAAAATTTGGTAGCGAGTGGGGGTTTGCGATAAAGCGACGTGC	272 SAAYAARYVAKNLVASGVCDKATVQL
_	AGC BC BC BC BC BC BC BC	AYAIGVIEPVSIYVNTHNTSKYSSAELE
_	CCCATTATTCCCTCACTCACCCCACATTTCCCCCCACATTACCCCCACACACCCCACACACCCCACACACACACACACAC	RCVKSVFKL PKGIIESLDLLRPIYSLIS
		AY GHIGKELEET I WEK I NKAEEIKATI
	JAATTCACAAGGAGTTTAA	XX.
HP0692	273 GGGTGAGGTGATGTTTGAAAGGAATTTAGCCATTCGTTTGAATGAA	274 GEVMVFERNLAIRLNEILDSNAIVYYLA
	[TCTCGCTAAAAATTCATGAGATTGTTATTCTTGTTATTGAGTGCTGCTTTTATGTTACTGGCTGAAGAAAAATATCTTT	KNS
	AAACGATGACCCCCCCATTAAACTAGTGCATTGGCAAAATGCATTAAAAGAGTCCAACCTGATTCAAACGCTCCAG	
	CAACACCIA TAAAAA GOCAAAA GOCAAAACCACGO TAAAAA GOCO TAAAAAA GOCO TAAAAA TAAAAA GO GAAAA GO TAAAAA TAAAAA GO AAAG	

1	۰	٦	٠
1	۰	•	
•		-	-

VQ 02/066501	· ·		CT/EP0 <u>1/154</u> 28
276 PEGGYKDKPKDKPShITTONNANNNO ONSAQNNSNTQVINFPNSAQKTEIQPTNO QNSAQNNSNTQVINFPNSAQKTEIQPTNO OVIDGPFAGGKDTVNNIDRINTNADGTISK VGGYAGGYALAGSSANFEFKAGTDTKNGTA TFINNDISLGRFVNLKVDAHTANFKGIDT GNGGFNTLDFSGYTHFSEDIGGSARINTVRLETGTRSIFSGGVKFKSGEKLVIDEFYYSPWNYFDARNIKN VEITRKFASSTPENPWGTSKLMFNNLT LGQNAVMDYSQFSNITIQGDFINNGGTINYLVRGGQVATLNVGNAAMFFSNIN VDSATGFYQPLMKINSAQDLKNKEHV LLKAKIIGYGNVSLGTISISNVNLIEQFK ERLALYN	B MAQIFVRENYVLGAIGFVVLLYEIISFIYY KRSLVYLLGVAIGALC:LLFVFYYTPYIL NAOKAGEAALQSAEFARSHAQSEWLF KELFVLVCALFFWRLLGKNVL	280 LIGTPLDESRIAFRDAFDSRGYKLKNLV EEVNOKSPNARNELDKOVLKVDERNL VYTLFSAQFLRIFPSDKTTAWLSPIEAIS SPNKEISSVATEFLKNIFSGFDDALKTN OWDKVEKTLKDLSIYCIKEHAKNLYLSS SKVDSEIFLNHTNFFNIR.TLPYILLGLL FIVVISSLVKNTIPNIWLTKILYFAILLCAL AHSMGLVLRWYVSGF SPWSNAYESM LYTAWASVIAGFILRSKI ALSASSFLAGI ALFVAHLGFMDPQIGFLVPVLKSYWLN IHVSVITASYSFLGLCFVLGILSLVJFILR KQGRFNLDKTILSISAINEMSMILGLFMI TAGNFLGGVWANESWIGRYWGWDPK ETWALISICVYALILHRFLGSHNWPFIL	ZIKILLVGHLITPVFFMSI-IFÖMWÖAYFLK ÖGVKEÖYL-VFYIAFÖNSILIHFLKASS YSÖKIALSSLVVLLGVSPLLLSNIPYCFI GVYALMVAFFTYMSYCLNYÖFSKFVS KNNISSLSSCVRVVSVLILSLSSLE LRYFSPLTIITMHFALTI.IILFFFLYKAKP FDE
	278	28	282
275 CTCCAGÀAGGCGGTTATAAGGATAAACCTAGGATAAACCTAGTAACACCGCGCAAATTGCTAACAACAACCAAC	277 TCATGGCGCAAATCTTTGTGCGTTTCAATTATGTTTTAGGCGCGATCGGTTTTGTAGTGTTAGTGAATCATTTC GTTTATTTATTACAAAAGATCGTTAGTGTATTTGATCCTTGGCGTGGCGTTGTGTTTGTT	279 AGCTTATIGGCACGCCTTTAGACGAAAGCCGTATCGCTTTTAGAGATGCGTTTGATAGCCGTGGGTATAAATTAAAAAAAA	281 ACTTAAAATTCTGTTAGTGGGGCATTTGATTACGCCCGTCTTTTTATGAGCCATTTTCAAATGTGGCCAAGCGTATTTTTTTT
НР0692	HP0071	HP0071	HP0071

02/066501 I 9 4 9 2 4 9 9 2 3 2 4 4 2 3 2 1	³ Ω → '' ≥	1000-40-
284 NAPNAQHFSTTQTTPQENLLSTISFEH AREIDSLGRIKQVYLKDKYLTPKQKG FLEHVGHLFSSKENAQPPLKELPLLAA DKLKPLEVRFLDPTLNINKAFNTPYSAS KTTLGPNEQLVLTQDLGTLSIIKTLTFYD DLHYDLKIAFKSPNNLIPSYVITNGYRP VADLDSYTFSGVLLENSDKKIEKIEDKD AKEIRRFSNTLEJSSVDRYFTTLLFTKD PQGFEALIDSEIGTKNPLGFISLKNEAN LHGYIGPKDYRSLKAISPMLTDVIEYGLI TFFAKGVFVLLDYLYQFVGNWGWAIIL LTIIVRIILYPLSYKGMVSMQKLKELAPK MKELQEKYKGEPQKLQAHMMQLYKK HGANPLGGCLPLLQIPVFFAIYRVLYN AVELKSSEWILWIHDLSIMDPYFILPLM GASMYWHGSVTPNTMTDPMQAKIFKL LPLLFIIFLITFPAGLVLYWTTNNILSVL	286 SVKECAKKLGIŠNYHÁHLTPEDKAČTIŠ SYKGVCAMYGDGNNDALALKQASVSL GFEKSALSKSACDILLLEEĎLSLIKKAF DNAČKYYČVVLČNIVLSLIYNAILIPVAM	288 FCCTGCARVYALLLDLNLESFYDKIND STLAPVTPQDSMSALELEQALEENIKG STLAPVTPQDSMSALELEQALEENIKG DFILNLLLEKTHCNACLWLNGKVLERLS GVKKVSVNFTTHHLQIVFEKSLNPKEII ÓKIESLGYGAKIYNAGNYTLKACKEOR SYLLTLSVGFFATMNLMFIAIAKYASYG GASYGGANYGAGMDKLMCRNLDLVS LFLSLLVLVVVGRFFIKGAFYGLKNGVL GMDLSVSFGALSAFVYSVYAMLVSGE
283 CTAACGCGCCCAACATTTTAGCACCACTCAAACAACCCCCCCAAGAGGAATTTGCTAAGCCGCTTTTTGGGGCGCATCAACCCCTGAACGGGTTTATTTTAGCTCCAAGGAAAACGGGTTTATCTCAAGGAAAAGGATTCAACCCCTAACCCCTTTTTAGGGCCGCATCCAAGAAAACGGCGCAACCCCCTAAAAGAGTTCAAACCCCTTTTTAGGCCCTTTTTAGGCCCTACGGTTTTTAGAAAACGCGCAATAAAAAGGCGTTCAAGGACTGGTTTTTAGACCCAAGAAACGCGTTCAAGCCCTTTTTAGCCCCTTTTTAGCCCCTTTTTAGCCCCTTTTTAGCCCTTTTTAGCCCTTTTTAGCCCTTTTTAGCCCTTTTTAGCCCTTTTTAGCCCTTTTTAGCCCTTTTTAGCCCTTTTTAGCCCTTTTTTAGCCCTTTTTAGCCCTTTTTTAGCCCTTTTTTAGCCCTTTTTTAGCCCTTTTTTAGCCCTTTTTTAGCCCTTTTTTAGCCCTTTTTTTT	285 CTCGGTTAAGGAGTGCGCGAAAAATTAGGGATTTCTAATTATCATGCCCCTGAAGGATAAGGCTCAAA CCATCAGCTCTTATAAGGGCGTTTGCGCGATGGTAGGCGATGGCAATAATGATGCGTTAGCCTTAAAACAGCGAG CGTTTCTTTAGGGTTTGAAAAAAGCGCTTTGAGTAAAAGCGCATGCGATATTTGCTTTTAGAGGATTTGAGTT GCTAAAAAAAGCGTTTGATAACGCTCAAAAAGTCTATCAAGTGGTGTTGCAAAAAAGATTTGAGATTTAAAACGCTTGATTTAAAAAAGCGTTGATTTATAAACGCTTGATTAAAACGCTTGATTAAAACGCTTGATTAAAACGCTTGATTTAAAACGCTTGATTTAAAACGCTTGATTAAAACGCTTGATTAAAACGCTTGATTAAAACGCTTGATTAAAACGCTTGATTAAAACGCTTGATTAAAACGCTTGATTAAAACGCTTGATTAAAACGCTTGATTAAAAAAAA	287 ITITIGCTGCGCGGCTGCGCTAGGGTGTATGCGTTATTGTTGATTTTGATTTTGGAGGCCTTTTTGGAGAAAAACA CGATTCCACTTTAGCCCCCCGTAACGCCCCAAGATTCAATGAACAAGGCTTTTGGAAAAAACA ATAAGGGCGATTTTATCCTTAATCTTTTGTTAGAAAAAAAGGCTTTGGAATTAGAACAGCCCTTGAAAAAACA ATAAGGGCGATTTAAGGCCCCCAAAAAAGGTTTT AGAACGTTTAAGTGGGGTTAAAAAAATGAGCGTTTGGAATTTCACCACCACTTGCAAATCGTGTTTGAAAAGGTTTT TAAAAGCCTAAAAAATTATCAAAAAATTGAGAGTTTTGGGGGCTAAAATTTTTTGCCACTATGAAATTTGATGTTTA TCGCCATTGCCAAATACGCACTTGCTCACTTGCTCACTTTTGAGGGGGTTTTTTTGCCACTATGAATTTGATGTTA TCGCCATTGCCAAATAGGCGTTTTTGGGCGTTTTTTAAGGCTTGTTAAGGGTTTTTTGAGGTTTTTAAGGCTTTTTAAGGCTTTTTTTT
HP0071	HP0071	HP0071

HP0714	289 AGGGCGTAGCCACCCACAAGGGGGTTATGGGGGGTGATCACTTACATGAGACCGTAGCTTGATTACCCCTAAAGATATGCGTAAAGA GGCTTTAGAAGAAGAAGAATAAGATTTTAAAAGACTATGGCAAAGACTATTTACCCCCTAAAGCCAAAGGCTATTC CAGCAAGAATAAAAAGCCCAGAAGCCCTGAAGCCTTATTTACCCCCTAAAGCCAAAGGCTTTAA AAGACTACCTTAAGCCTGAAGAATTAAGGCTCTATACCTTAATTTACAAAGCCCTTTTTAGGCTAATGCCTTTTTG AAGACTACCTTAAGCCTGGTTGTGGCTTGCGAAAAAGGCGAGTTTTAGGAGAAATGCCTCTTTTTG ATGCTATTATGAAATTTTAGGCAATGACGATAAGGAAAATGCTCCCCAATTTGAAAGAAA	290 GVATPOGVMGVITYMRTD SLNIAKEAL EEARNKILKDYGKDYLPPKAKVYSSKN KNAQEAHEAIRPTSIILEPNALKDYLKP EELRLYTLIYKRFLASQMQIJALFESGS VVVACEKGEFKASGRKLLFDGYYKILG NDDKDKLLPNLKENDPIKLEKLESNAH VTEPPARYSEASLIKVLESI.GIGRPSTY APTISLLQNRDYIKVEKKOISALESAFKV IEILEKHFEEIVDSKFSASLETELDNIAQ NKADYQQVLKDFYYPFMDKIEGKKNII SQRYHEKNI
	ACCGGTCAATCATGCCCTAAATGCGGGTGGGGAATTAGTCAAAAAAAA	GEFTACNNYPKCKYVKU IESANDEAD QELCEKCGGEMVQKFSRNGAFLACNN YPECKNTKSLKNTPNAKETIEGVKCPE CGGDIALKRSKKGSFYGCINNYPKCNF LSNHKPINKRCEKCHYLMSERIYRKKK AHECIKCKERVFLEEDNG
HP0714	291 GCGCAATCAATTTAAACGGCACTTTAGAAGTGGGTAATCGTGTGGGATCGGGAGCTGGCACGCCACCGGCACAGC CACTTTAAACTTGAACCTTATAGGTCAATTCCAATATCCAATATCCAATATCCAATGTGGATAAAACTTCGCAAGTGAATATAGGC CACTTTAAACTTGAACGCTTATTACCATTTGGTTCGTTTTGCTTTGCTTAGATTTAGGCTTAGATTAGGC GGGCTAATTGCTCCACTTTTGGTTCGTTTTTTTAACGGCATCTTTACATTGGTAATTGCTAATGGCCTTTTTAGTTAG	292 AINLNGTLEVGNRVGSGAGTHTGTATL NLNANKYNINSNINAYKTSCIVNIGNANS VITIGSVSLSGDVCSSLASVGIGANCST SGPSYSFKGTTNATNTAFSNASGSFF EENATFSGAKWNGGTYF WEFSATN NTAFSSGSFNGTSFSNAS YTFDNGATFQNSSFNGGTYFTWEFSATN NTAFSSGSFNATGTIFTNNGTN PTNNAQHPQIQNSSFNGGTIFTNNGTN FQQAFNNSNHQLTIQNASFNNATFNNT GKITIEKDASFNNTTFNTSVDTNNMSVT GGVTLSGKNDLKNGSTLDFGSSKITLA GGTTFNLTSLGSEKSVTILNSSGGITYS NLLNHAINGLTSALKTNESLSNPQSFA QGLWDIITYNGVTGQLLNEMAATSKPT DSSPSKSSTNSTQVYQVGVKIGDTIYK LQETFSHNSIIIQALESGTYTPPPVINGS KFDLSASNYINADMPWYDFKYYIPKSQ NFTESGTYYLPSVQIWGS
HP0714	293 AACCGAAGCTGAGAAAAAGAATGCGAAAAATTGCTCACGCCTGAAGCGAAAAAACTTTTAGAGCAACAAGGCGTAG ATTGTTTGAAAAACGCTAAAACCGAAGCTGATAAAAAAGGTGTGTCAAAGGTCTCCCTAAAGGCTTGCAGAAAAGG TTTTAGCCAAAGAGGCCTGAAAGCTTATAAAGACTGCGTATCAAAAGGTAGGAATGAAAAAGGGAAAAAAAA	294 TEAEKKECEKLLIPEAKKLLEGGALDC LKNAKTEADKKRCVKDLPKDLGKKVLA KESLKAYKDCVSKARNEKEKKECEKLL TPEAKKL

HP0714 HP0714 HP0714	292 293 293 301 293 293 293 293 293 293 293 293 293 293	289 CCAMGANTITITAMAACAAAAAAAAAAAAAAAAAAAAAGAAAAAAGAATAAAAAAAA	305 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	296 GEFLKTKKLIVDAPDPKELEEÖKKALEK EKEAKEGAGKAGKALEK EKEAKEGAGKAGKOKREKERKEERAKN RANIENLTNAMSNPONGENAGOANA LKOIEELNKKOAEETIKORAKOKINIKTD KPOKSPEDNSIELSPSDSAWRTNLVVR TNKALYGFILRIAOKDNFASAYLTVKLE YPORHEVSSVIEEELKKREEAKROKELI KOGENLNTTAYINRVMMASNEGIINKEKI REEKOKIILDOAKALETOYVHNALKRN PVPRNYNYYQAPEKRSKHIMPSEI REEKOKIILDOAKALETOYVHNALRN PVPRNYNYYQAPEKRSKHIMPSEI ELTKLHOOYYLGEVSOIIERLOLPP KIKAKIEAVMTÖKNAKELYFÖRLLEEKN Q ENVLVLLNEKKIEPCMGLSALLELOLPP KIKAKIEAVMTÖKNAKELYFÖRLLEEKN Q SOO EENRFKÖSGYLKEKIKKÄKÖLIDALNI G RKATIYKIGLMLLEYÖYÖFFKGKELRP KILDLANEFNHSVSTISRAISNKYLAČE RGVFPIKHFFSIALDNSETSNAVIKÖYLL ELIKNEÖKKEPLSDAKILELIEEKFHLKM VRRTITKYRÖLLNIASSSERKRLYLMRA VRRTITKYRÖLLNIASSSERKRLYLMRA OVSKNEÖTLODTNTKIASIÖKKMSEIKS FREI ÉSI NIEFDIAKERSNÖANDEIEKI
	<u> </u>	ACAGAGAATTGAAAACTTGCAAAATGAAATCAAGCACAAAAGCGAAAAAGAGGATTTGAAAAAAGAATGCTAGAGCTTGAAAAAAGAATGCTAGAGCTTGAAAAAAGAATGCTAGAGCTTGAAAAAAATGATGAAAAAATGAATCAATGAAAAAAAA	ONE TEP CGC	CGGCFIRLDAYCHANGANACHANGANACHANGANACHANGANACHANGANACHANGANGANACHANGANGANACHANGANGANACHANGANGANACHANGANACHANGANGANACHANACH

2/066501				PCT/EP01/15428
304 EDLNPLELARSYKELLESYGMTGEELS KIVKKSRAHVANIMRLL TLSSKVGNALL EEKITSGHAKVLVGLDGEKGELILNSIIG QKLSVRQTEDLARDFKINANFDNKKHG FKQTQTLIAGDELERLNGSLWDHYKLK AALKGNKIVLRCYENSI.LEAFMKKMMS	306 YKTLSAVG	308 DSKDVLDKKÖVTIAISNKGSFYFDDKEI SFENLKHKVSTLAKDTI/NLGGDKKSN LDNFIKVVDLLQTNNLKQLYILVEDKKN QKN	310 RPNIPNIPNIANIPAIIDGISFIKSMHLKHE NLKRNQTALEEVLRLLIOGKHQLLNEW HALDKSAKLSDEIYQTCIAKRLELQGAQ NILKTTIGIFQKDSDEAI;SIVKSQVKNQL FKLVYVFLAALLSVVFAWILKIISSKYIEN NERVYTVNKAINFVNV;SVIIL	312 EHLDKVIYLDQAPIGKTPRSNPATYTGV MDEIRILFAEQKEAKILGYSASRFSFNV KGGRCEKCQGDGDIKIEMHFLPDVLV QCDSCKGAKYNPQTLEIKVKGKSIADV LNMSVEEAYEFFAKFPKIAVKLKTLMD VGLGYTLGQNATTLSGGEAQRIKLAK ELSKKDTGKTLYILDEPTTGLHFEDVNH LLQVLHSLVALGNSMLVIEHNLDIIKNA DYIIDMGPDGGDKGGKVIASGTPLEVA QNCEKTQSYTGKFLALELK
303 AGAÁGATTTAAACCCCTTGGAATTGGCTAGATCTTATAAAGAATTGCTTGAAAGCTATCAAATGACCCAAGAAGAGCTTCAAAATGGTTCAAAAAATGGTTCAAAAAAATGGTTCAAAAAATGGTTCAAAAAAAA		4 AGARATCTAAAGACGTATTGGACAAAAACCAGGTTACGATCGCCATTTCTAATAAGGGTTCTTTTTTTT		311
HP0714	HP0714	HP0714	HP0428	HP0428

•	ζ	1	l
		ï	
•			١
	-	•	

02/066501		PCT/EP01/15428
314 ISISEIMTKAIEGLLSNLDAHSAYLNEKK FKEFQAQTEGEFGCLGITVGMRDGVL TVIAPLEGTPAYKAGVKSGDNILKINNE STLSMSIDDAINLMRGKPKTPIQITVVR KNEPKPLVFNIIRDIIKLPSVYVKKIKETP YLYVRVSGFDKNVTKSVLEGLKANPKA KGIVLDLRGNPGGLLNQAVGLSNLFIKE GVLVSQKGKNKEENLEYKANGRAPYT NLPIAVLVNGGSASASEIVAGALQDHK RAVIIGEKTFGKGSVQMILPVNKDEAIK ITTARYYLPSGRTIQAKGITPDIVIYPGK VPENENKFSLKEADLKHHLEGELKKID DKTPNSKEADKOKKNEEKETPKMIN DDIQLKTAIDSLKTWSIVDEKMDEKAPK KK	316 STSKKŘADKĞLKKVFKDŠKKDACĞFIY EISEFMKAYTALLKKODRYVYLLRYLPS RYWASILTTALYVKYPDFDALKKLLVSY YYQTWIAGGTITRIKQTSINIIKNVKSNK SVETIKELILNSIDSYNTFDQYLYNLWD SSSVYHSKWVRPVLALANYFMADEEK PHFIAMDAETQVEHILPQTPKRGSÓWN ADFÓKEKREEWVNNIANLTLLKRKKNA HALNĞDFÖEKRKIYĞĞKDTSKVISCYDI TKELYSNYRKWNEKSLÜGRYKSLYNTI TPVLHIEGQEDDFEDDFDLE	318 TYMRTDSLNIAKEALEEARNKILKDYGK DYLPPKAKVYSKNKNAOEAHEAIRPT SIILEPNALKDYLKPEELRLYTLIYKRFL ASÖMODALFESOSVVACEKGEFKAS GRKLLFDGYYKLGNDDKDKLLPNLKE NDPIKLEKLESNAHVTEPPARYSEASII KVLESLGIGRPSTYAPTISLLQNRDYIK VEKKÖISALESAFKVIEILEKHFEEIVDS KFSASLEEELDNIAGNIKADYÖQVLKDF YYPFMDKIEAGKKNIISÖKVHEKTGÖS CPKCGGELVKKNSRYGEFIACNNYPK CKYVKÖTESANDEADDELCEKCGGEM VÖKFSRNGAFLACNNYPECKNITKSLK NTPNAKETIEGVKCPECGGDIALKÄSK KGSFYGCNNYPKCNFLSNHKPINKRC EKCHYLMSERIYRKKKAHECIKCKERV FLEDNIG
313 AATCAGCATTTCTGAGATCATGACGGATTGAAGGCGTTGCTCTTAATTTGGACGCGCGTTCAGCGTATTTGAA TGAAAAGAAGTTTAACGGATTTCAAGCCCAAACCGAGGGGCTTTGGGGGGTTCAGGCGTATTTGAA TGAAAAGAAGTTTAACCGTTATTGCCCCTTTAGAAGGCGCTCAGGGGGTTAAGTCAGGCGATAACAT TTAAAAATCAATAACGAAAAGCTGAGCATGAGCATTGATGATGCGATCAACCTCATGCGGGGTTAAACTAAACAAAA TTTAAAAATCAATAACGAAAGCATGAAAAAAACGGCAAAAACCTTTAGTGTTTAACATTTGAGAAGATCATTAAAACT CCCCTTTTCAGATCACCGTTGAAAAAAGAAAAACAAAAC	315 CTAGCACTÍCTAAAAAGAGAGCCGATAAGGGATTAAAAAAGGTGTTCAAAGACGCAAAAAGACGCTTGCGGGTTC ATCTATGAGATCAGCGAGTTCATGAAAGCCTATACCGCATTGCTAAAAAAACAAGACCGATACGTCTTTTATTGAGG TATCTCCCCTCTAGGTATTGGGCCAGCATTTTAACCGACTTGCTCAAAAAACCAAGACCGATTTTTATTGAGA AAGCTTTGGTGTCTTATTATTACCAAACTTGGATTGCAGCGCTTCAAAAACCGTTCAAAAACCGTTTCAAAAACGTTAAAAGCAACTTGGATTGCAGCACTCAAGCAAACCGTTTAAAACGTTAAAAAAAGCAATTATTAACCAAACGTTAAAAGCGATTGAAAAAAAGCGTTGATTAACCATTATAACCTTATAACCTTTAAAAAAAA	SACCGATAGCTTGAATATCGCTAAAGAGGCTTTAGAAGAAGCGGGGAATAAGATTTTAAAAGAGCTTTAAGAGAGAG
HP0428	HP0428	HP1518

v	٦
Ä	i
	7

066501			
320 NGVEIVGLEHLDKVIYLDQAPIGK I PKS NPATYTGVMDERILFAEQKEAKILGYS ASRFSFNVKGGRCEKCGGDGDIKIEM HFLPDVLVQCDSCKGAKYNATREM KGKSIADVLNMSVEEAYEFFRAFFKIAV KLKTLMDVGLGYITLGONATTLSGGEA ORIKLAKELSKKDTGKTLYILDEPTTGL HFEDVNHLLQVLHSLVALGNSMLVIEH NLDIIKNADYIIDMGPDGGDKGGKVIAS GTPLEVAQNCEKTQS	SVIFLSHKIETDTFFLFNAFKPLYCIFKDI KQAILAQQHATNYLLDSKII.FFMDLNDT ELWEICAKSQIDGVISKDS:.LLK	GHYKHFQNALKMQKGUTELTELTEL GHYKHFQNALKMQKVGQURAKTELGA QHYKHFQNALKMQKGKOKLEVSQL LSSKDDLVPSSKLEIRTEK XILPDLSFFV SSTLNSYPVLKTLENQIQISKENTKLQIA KFLPQVSFFGSYIMKQNNISVFEDMIPS WFVGVAGRMPILSPTGRIQKYQASKLA ELQVSSEQIQAKKNMELLVNKTYKETL SYLKEYKSLLSSVELAKENLKLQEQAFL QGLSTNAQVIDARNTLSSIVVEQKSVA YKYIVSLANLMALSDHIDLFYEFVY	326 ELALIALFMALVLGISVGVLAMINIT SVF DYSSMTFALAGISMPVFWLGLMLIYIFS DYCKLEDVYT.DGPTGLYLI DSLIARDYGAFMDTIKHLII.PSIVLATVS TAVIRAMTRAMEVSKEDYVRTAKAK GCSSFRVIPVIFILRNALIPVTTIAGLMLA GLLGGSMITETVFSWPGIGKWIVNALN QRDFPIIQSMSLIIAMMYIGANLLVDILY AFIDPRIRLS
319 GAATGGGGTGGAGATTGTAGGGTTGGAGCATTTGGATAAAGTGATTTATTT	321 CCAATAACGATATAGTGTGTTTTGAAGCGCACCCAAAAATTTGGAATTTGTAGTGTTTGTCAAACCTGTGTGTG	323 CACTITICAAGAGCITGTGAGCGTGTATTACGGCATGGTGTTTAAACGCAGAAGTGGCTGAAACTTTAGAAGGGTGGAGGGGGGGG	325 TGGGATTTGCTTTGTTTATGGCTCTTGTTTTGGGTATTAGCGTTGGCGTGTTAGCTGTTTAGCGTGCGATCAAACGCT 325 TGGCATTTGGTTTGATTCATCCACCATGACTTTTGCTTTAGCCGGGATTTCTATGCCGTGTTTTGGCTAGGCTCATGC TAAGCGTGTTTATTTTGATAGCGTGCATTGGGGTGTTTTTGGGCGTGTTTTTGAGCGATGTATTTGATTGCCC TGATTTATAGCTGTTAATTGATAGCCACGGTTTCTACCGCTGTTATTGGGCGGTGTTTTTGGATCAGCCACTTGATT CCACAGGTCTTTATTTGATAGCCACGGTTTCTACCGCTGTTATTGCGGCGTTTTTTGGATACGAGCACTTGCTATTTGCCAAGGCATTTTTGCCAAGGCATTTTTGCCAAGAGTTTTTGCCAAGAGTTTTTGCCATTGCAAGAGAGTTTTTGCCATTGTTAAAGAAGATTATTGCCATTGTAAAGCGCTTAAATCCCTGTAACTGAAAGGCGTTTTAATGCGCTAATTGCAAGTGATAATTGGGGCTTTTAATTCCCAGTAATTGCAAGTGATAATTGGGGCTTTTAATTTTATTGCAAGAGTTATTTGAGGGCGTTTTAATTCCAGTTAATTGCAAGTGAAAAGGCGTTAATTCCAGGTTTTAATTTAATTCCAAGAGTTTTAATTGCAACAAAAAAAA
HP1518	HP1518	HP1518	HP0547

7

02/066501			PCT/EP01/15428
328 TNIINAMINAHVOSALTONALKTSLERLS SGLRIINKAADDASGMTVADSLRSOAS SLGDAINTNDGMGIIQVADKAMDEQL KILDTVKVKATOAGDGOTTESRKAIQ SDIVRLIGGLDNIGNTTTYNGGALLSGD FTNKEFQVGAYSNQSIKASIGSTTSDKI GQVRIATGALITASGDISLTFKQVDGVN DVTLESVKVSSAGTGIGVLAEVINKNS NRTGVKAYASVITTSDVAVQSGSLSN TLNGIHLGNIADIKKNDSDGRLVAAINA VTSETGVEAYTDQKGRLNLRSIDGRGI EIKTDSVSNGPSALTMVNGGQDLTKG STNYGRLSLTRLDAKSINVVSASDSQH LGFTAIGFGESQVAETTVNLRDVTGNF NANVKSASGANYNAVIASGNQSLGSG VTTLRGAMKVVIDIAESAMKMLDKVRSD LGSVQNQMISTQVNNIKAAES QIRDVDFAGESSNFRNIILAQSGSYA	330 LMHKRYGIFIELGFMFIIFSLSFLIGGGV OKALETGFKFLSDGKEKVANEDLASL VGDGIIGGVGATVSFLPLIVVLYFGISLL ETTGYMSRVAFLLDGILHKFGLHGKSFI PLITGFGCSVPAYMATRTLQNYNERLIT LFVIGFMSCSARLPIYVLFVGSF	332 PKKIAALEKYAEVTRESLIVČANEHNÕG YLEVKKLKMGHLL	334 PNSSYTTLEKALGÝSFKDKRLLEGALT HKSCKLALNNERLEFLGDAVLGLVIGEL LYHKFYQYDEGKLSKLRASIVSAHGFT KLAKAIALQĎYLRVSSSEEISNGREKPS ILSSAFEAIMAGVYLEAGLAKVÖKIMÓ NILNRAYKRLÜLEHLFMDYKTALQELT ÓAÓFCVIPTYÖLLKEKGPDHHKEFEMA LYIQDKMYATAKGKSKKEAEÓQCAYÓ ALQKL
327 ATACAAATATCAATGCGATGAATGCGCATTCACTCAAAACGCGCTTAAAACTTCATTGGAGCGATTGGAGCGATTGGAGCGATTGGAGCGATTGGAGCGATTGGAGCGATTGGAGCGATTGAGGCTTTAAGGATTAATAAAAGCGGCTGAGGCGATTACCGGTGGCGATTACGGTTTAAAAATCTTTGCCAAAGCGATTAAGGCGATTAAGGCGATTAAGGCGATTAAGGCGATTAAGGCGATTAAGGCGATTAAGGCGATTAAGGCGATTAAGGCGATTCAAGGCGATTAAGGCGATTAAGGCGATTAAGGCGATTAAGGCGATTCAAGCGGATTCAAGCGGATTCAAGCGGATTCAAGCGGATTCAAGCGGATTCAAGCGGATTCAAGCGGATTCAAGCGGATTCAAGCGGATTCAAGCGGATTCAAGCGGATTCAAGCGTTTAAAGAGCGATTAAAGAGCGATTCAAGCGGTTCAAGTTGAAGCGATTAAAGAAGCGTTAATAAGAAGCGTTTAAAGAAGTGATTAAAGAAGTGAATATCAAGCGGATTCAGCAGCGATTAAAGAAGTGAATAAGAAGTGAATATTAAGAAGCGTTAAGAGCGTTATAAAGAAGTGATTAAAGAAGTGATTAAGAAGCGTTAATAAGAAGTGATAAGAGCGTTAAGAGCGTTAAGAGCGTTAAGAAGTGATTAAGAAAGTGTTAAGAAGCGTTAAGAGCGTTAAGAGCGTTAAGAAGTGAATACAGAAGTGATTAAGAAAAGCGTTAAGAGCGTTAAGAGCGTTAAGAAGCGTTAAGAAGCGTTAAGAAGCGTTAAGAAGCGAAAGCGGAATACGGAACAGTGAAGTGAAAAAGCGTTAAGAAAAGCGAAGAGCTTAAGAAAGCGAAGAGCGAAGAGCTTAAGGAAGAGTTTAAGGAAAAGCGTTAAGAAAGCGAAGAGCTTAAGAAAGCGAAGAGCGTAAGTGCAAAGCGAAGAGCTTAAGGAAGATTAAGAAAAGCGAAGAGCTTAAGGAAGAGGAATAAGAGCTTAAGGAAAAGCGAAGAGCTTAAAGAAAG	329 TTTAATGCACAAGCGTTATGGATTTTCATTTTTTAGGGTTTATCATTTTTTTGGGGTTTTTTATCATTTTTAATAGGGGGGGG	331 CCTAAAAAATCGCCGCTTTAGAAAATACGCTGAAGTAACAAGGGAGAGCTTTGATCGTGTGCGCTAATGAGCACAAATTATGAAAATTATGAAAATTATGAAAATTATGAAAATTATGAAAATTATGAAAATTATAAAATTATT	333 CGCCTAATAGCTCTTATACAACGCTAGAAAAAGCTTTGGGGTATTCTTTTAAAGACAAGCGTTTATTGGAGCAAGCCTTATTGGAGCAAGCCTTATAGGCGAAGCCTTAATTGTGGTTTTGTGTGTTTGTGTTTTGTGTTTTGTGTTTTGTG
HP0547	MP0547	HP0547	HP0662

HP0862 THATAGESCIGGENTITIECCARTCHTTETCARGENINGS THE COGENING CONTINUED	02/066501			
335 THATAGGCTGGGATTTTTGCCGTGGGGGGGTATTTTGTTTGT	SYKAGIFATLCVAGWGYFLYGGTIDPK GGIYTLWPLFGVSNOMLAGWALLLVTV VLFKMGRFKGAMISALPAVLILSITFYS GILKVVPKSDNSVLINNVSHVAQMGIIKE KMATTTDEKALKTLQKSFFNIHAIDAILC VFFMLVALLVLIVSVRICSNAYFKNKIYP PLAETPYIKAS	BJAFLIDADNVRYESEKALCVII-TPNYGAL EISQTSKNSDTTNYNTMLSIJTSFAIIT YELLNMVHPFDGNKADDSVENFIELPW IEDRKDDSNRSCGLLPFFLTRDLKNLLA	IO OLYRKSLDIARAKIESSKASLDAANLSF ANIKRKYDANLVDFTTYLRGLTTRFDA EVAYNLALNNYEVQKANYIFNSGHKID DYVH	KTGYLGTFTADRVYTGNIAMTGNGAO TGGGATLNFVGATEINIAGATFKNLKTT SQNSYMTFMALGDSSGSAKINVSQSD SQNSYMTFMALGDSSGSAKINVSQSD FYDWTGGGYDFTGNGVFDSVNFNKA FYDWTGGGYDFTGNGVFDSVNFNKF GKTTTEKSVLSDASYTFDGTNNTFTED GKTTTEKSVLSDASYTFDGTNNTFTED KENNGSFNFSGASSTFNGGVFNFNI PKVSFTDDTFNVNNQFKINGTOTTFTF NKGVVFNNAGGLLSSLSVGTTYQLLNA KSVDYKDNNALYQMLRWISGENPSGT LVNKDQSAPNSAKIYNVH;TDNGLTYY KENPNNGTLTRLCTLGYTHCVNIDND FNLKNVNNNASNTVFYLNGMTTWKIA
33 33 33 33 33 33 33 33 33 33 33 33 33	336	33	8. %	
HP0661 HP0661 HP0661	335 TTATAAGGCTGGGATTITTGCCACTCTTTGTGCGTGGCGGGGTGTGGGGGTATTTCTTGTATCAAGGCACGATTGATC TAAAGGGGGGATTTATACGCTATGGCGTTTTTGTGCGTGGCGATCATCAGATGTTAGCGGGCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	GCATCARAGEGECCC GCATCARAGEGECCCTAATGTGCGTTATGAGAGAGAGAGACCCTGTGTGTTATTTTTACGCCTAACTATG 337 CAGCGTTTTAATTGATGCGGATAATGTGCGTTATGAGCGAATTACAACACCATGCTTAGCGATACCTTTTCTT GGGCTTTAGAGATTAGCCAAACCTCTAAAAATAGCGATTACAACCATATACAACAGATAAGGCAGATGATGGTGTAGCAATTTTCTT TTGCTATCATAACTTATGAACTTTTAAATATGCGTTTGAAGAAGGCAAAAGATCGTTTGGGCTTTTTTTT	GCGAAGTTTTTATTT GCGAAGTTTTTATTT GCGAAGTTTTATTTGCCAGAGCCAAGATTGAATCTTCAAAGGCTAGTTTGCATGCGCCAAT 339 AACAGCTTTACAGAAAATCGCTTGATATTGCCAGAGGCTAATTTAGTGCATTTCACCACCG CTTTCTTTTGCCAATATTAAGAGGAAATACGACGCTAATTTAGTGAATTTCACCACCTATTTTAGCGCCTTAACCACG CTTTCTTTTGCCAATATTAAGAGGAATTAGCGCTCAATAATTATGAAGTGCAAAAAGCCAATTTCAACAGC CGCTTTGATGCGGAAGTGCCTTACAATTTAGGGGATGAAAA GGGCATAAAAATAGACGACTATGTGCATTAAGGGAATGAAAA	341 CCCCTTGGGCTAATGGCAGCATCCCTAAATGTAACAGCACGGTGCGTTTTGGGGGGTATGAGGGGGGGG
HP06661 HP06661 HP0666				
	НР0662	HP0661	HP066	HP066

)2	2/066501			PCT/EP
	344 I QAKRIFTYNNEFKVTSKELDGRÔSNE VKDLFRTNPDVNVGGGSVMGGKIYVR GVEDRLLRVTVDGAAGNGNIYHHÔGN TVIDPGMLKSVEVTKGAANASAGPGAI AGVIKMETKGAADFIPRGKNYAASGAV SFYTNFGDRETFRSAYQNAHFDIIAYYT HQNIFYYRSGATAMKNLFNPTQADKEP GTPSEQNNALIKMNGYLSDRDTLFS WNMTRDNATRPLRSNAIGLAYPCEAP FSPDSSQGCPNVLÖSFTRYMYHSINSA NNLSLQY	346 RFKKODGTLGEEVCFIDARLFGRTAEI ANQYLSKGSSVLIEGRLTYESWMDGT GKKNSRHTITADSLQFMDKKSDNPCA NAMODSIMHENSNINAYPANHNAPSQD PFNGAYAQNAYAKENLQAQPSKYQNS VPEINIDEEEIPF	348 PLSCLLVLRVLILPILERLSLNKDFKLKP FKAQINAPLKLKGERAHLILGNYSNHQF IPYNNNRYDSGAIQALARVDSIALIDEG VRLVQGEIEILRFEN	350 PKDSVFVAKEVPPSASVMLKLKPDMKL SPTQILGIKNLIAAAVPKLTIENVKIVNEN GESIGEGDILENSKELALEQLHYKQNF ENILENKIVNILAPIVGGKNKVVARVNAE FDF
110000000000000000000000000000000000000	343 CCACCCAAGCTAAAAGGATTTTCACTTACAACAATGAGTTTAAAGTAAACTTCTAAAGAACTAGATCAACGCCAAAGCA ATGAAGTCAAGCCTAAAAGGATTTTCACTTACAACGATGAGTGAG	345 GCGTTTTAAAAAACAAGACGGCAAGGGCGAAGAGGTGTGCTTTATAGATGCGCGTTTGTTT	347 TCCTTTAAGTT GCTTATTGGTTTTACGGGTTTTTAAAGCTTATTGGAGGGCGCTTATCCTTGAATAAAGATTTAAAC TAAAACCCTTTAAAGTTTTAAAGCTCAAATCCAATGAAAGATTTAAATTTTTAAATTTTTAAATTTTAAAAGTTTTAAAAGATTTTAAAAATTTTAAAAATTTTAAAAAA	349 TCCCTAAAGACAGCGTGTTTGTGGCTAAAGAAGTCCCTCCTAGCGCTTCGGTGATGCTCAAACTCAAGCCTGAAGATG AAGCTTTCACCCACTCAAATTTAGGGATTAAAAATTTAATCGCTGCAGCTGTGGCTAAACTCACGATAGAAAATGTG AAAATCGTGAATGAAAATGGCGAATCAATAGGCGAAGGTATACTAGAAAAACTCCAAAGAATTAGCCCTAGAGCA AAAATCGTTACAAACAAATTTTGAAAACATTCTAGAAAATAAGATTGTCAATATTTTGTGGGGGGGTAAAAAAAA
	HP0661	HP0661	HP1492	HP1492

HP1492	351 AGGCACGCCCTATTAGAA	351 AGGCACGCCCTATTAGAAGACAACGCGCAAGATAAAGCCACTAAAAACACTTTTGGCAACTACTTGCACACCTATT	352	352 GTPLLEDNAODKATKNTFGNYI HTYSY	ĮΣ
	CTTATACAGAATCCATTAAA TACAAGAAATCTATGGCCTT	CTTATACAGAATCCATTAAAGACAGACACACCCTAAAACTCCAGTTAGAAAGCATTGAAAGGCTATAAAAAATT TACAAGAAATCTATCGCCTTTTACAAGAAAGCATCACTATTGAAGAAGGAACGAAGTAAAAAAAA	<u> </u>	TESIKDRHTLKLOLESIETSYKEKLOEIY	``
	TGAAAATACATTAACGCCATGCTCTAT	TI DOMOGRAFICATION I GAAGACACACACACACA I LAGUAGACACACACACACACACACACACACACACACACACA		RLLOESITIEDTEVKKETIFNIJEKYINAM LYYIIROLLDFRRUNDNFRI KAMVVCFS	∑ υ.
	TTAAAGGCTATGGTGGTTTGTTTTCTAC GTCTTACAAGAAAACCCCAACCTAAGGA			SKOARLADCLFNEVOEKVLOENPNLRI	
	AAAGAAAGGTTCATTCTTT	AAAGAAAAGGTTCATTCTTCAAACATGAAGATACCGATATAGTCTTTGTGTTTAACATGCTTTTAACGGCTTTGATT		LNKLKSSLILHDEQEVREKVASFKHED TDIVFVFNMLLTGFDLPSLKI31 YIHBF1	$\overline{}$
	TACCCAGTCTCAAACGCCT	TACCCAGTCTCAAACGCCTTTATATCCACAGAGAATTAAAAGATCACAATTTGCTCCAAGCCCTAGCCAGAGTGAATC		KDHNLLQALARVNRSYKNWSFGYLIDF	, LL
	GCTCCTATAAAAACATGTCT	GCTCCTATAAAAACATTAAACGATTCAATCAAAGGGGTTTTGTAGGCATTCAAGAAATTTTGACAAAAAGGACGATGATTTTTTTT		VGIGENFDKTTDDYLKELNFIFNQSGAN	Z,
	TAAGACTTTAGAAGAAGAC	TAAGACTTTAGAAGAAGACATTAAAAAACGCCTATGATCTTTTTTAGATTACCCCATTGACGATATAGAGGGCATGAC	<i>.,</i> <u> </u>	SUSHIKUMFAUKK I LEEDIKNAYDDLF DYPIDDIEGMTSAI	_
	TAGCGCCATTG		-	•	
HP1492	353/AGGAGI I AAAAAGI GCAAAGCCTGTCAT	GCCTGTCATTAGCGACATTACCATAGGAGGGTTAAAAGGCCGCCCCAAAAAATAAGC	354	354 ELKSAKPVISDITIERVKRAA ÜKISOLSK	\mathbf{Y}
	AAGAAGAATAACGCTTTTAACCGATC	GITTGGATTTAGGGCCCTTTGAGGCTAAAGCCTAAATTTAGCCCTAAAATTGCCCAA	<u> </u>	DSGLDLGFKVYTLQDKVQIINDKEEITL	
	AAACGCTCAATCAAGCGCT	AAACGCTCAATCAAGCGCTAGAGATTATCATCAAGACAAACTCTACAAATGCGAAGACGCTTACTTTGTATCGTGT	<u></u>	FINNSUL I PLUNALINLALUCCIN I LNUAL FIIIKDKI YKGEDAYECINCOFIFAOFYI A	Je
	GCGATGAAGAAGCGCAAGA	GCGATGAAGAAGCGCAAGAGTATTTAGCCAAAAGCAAAACGAAATGATATTTTAGACGGCTATGAAGAGATTGATT	<u>, </u>	KSKNEMIFLDGYEEIDLEAFLNLNASFK	. J
1	TAGAGCCTTICTCAATCTC	TAGAAGCCTTTCTCAATCTCAACGCTAGCTTTAAAGAGCGTTTAAGCGTGGTGTATTGATTTGAAATAAAAGGGG	<u></u>	ERLSVVY	
HP1492	355 TGCAGCTCCCCCCAACGCA	TGCAGCTCCCCCCAACGCATTATGAAATCAAACTTAAAGGCATTGTGATTGGTGAGGGCATGGTGATGCCAGACAAG	356	356 OLPPTHYEIKLKGIVIGEGMVMPDKFLA	4
	11111AGCCAIGAAIACCGG	IIIIIAGCCAIGAAIACCGGIIIIGIGAAIAAGAAATTGAAGGCATTCCTACTAAAGAGGCCGGCTTTTGGAATGGAC	2	MNTGFVNKEIEGIPTKEPAF(3MDALW)	
	A LIVE ACCOUNT OF A LICENSACION OF A LIVE A COCON OF A LIVE A COCON OF A LIVE A	CCITICAL BEALT CANACITATION TO THE STREET OF	<u>m</u>	ETKNKEEAIIQGYTIIDPSTVIATHTSELV	$\overline{}$
	GCTTGGCCAAAGATTATCC	GCTTGGCCAAAGATTATCCTACGATTGTAGAAGAGAGAGA	Χ.	KKYAEDFITKDEVKSLLERLAKDYPTIV	
	TOCATOTACATOAAAAAA	GCCTTGCTGCTGCTGCTCTTTTAAAATCCCTCATTAAAAAATCCCTCACTAATTTTAAAAAA	<u>u 1</u>	EESKRIP I GAIKSVLQALLHEKIPIKUML	٠,
	AAAACGATGTGAATATCTTA	GOOGNET PANGAGAN DO LAGAGAGAT TAGAGAGATATA TAGAGATTTTAAAT ACCGAACAACAGGGGGGGGGGTTTCTAGGGTGATCACTAACGCTTTTAAAT	<u>- a</u>	LILETTTOPPLYGNDVNILTEQVRARLS RVITNAEK	
HP1492	357 CCAAAGGGAGCTTTAAAATC	CCAAAGGGAGCTTTAAAATGACCAAATACGAAGATGGTAAAATCTATGGGGATTTGACTCTTCGTGGCGTAACCAAG	358 K	358 KGSFKMTKYEDGKIYGDLTL RGVTKPV	7
	CCTGTCGTATTGGAAGCCA	CCTGTCGTATTGGAAGCCAAAATCCAAGCCCCCTTACAAAACCCCATGAATAAAAAGAATTCATGGTGTTACAAGCT	>	VLEAKIQAPLONPMNKKEFNVLQAEGK	V
	GAAGGCAAAATCAACCGCA	GAAGGCAAAA ICAACCGCAAGGATT TTGGTATGGTAAAACCTTTAGCGATGCTGTCGTTGGAGATGAGGTAAAGAT	=	INRKDFGIGKTFSDAVVGDEVKIELKLE	
	CACAAAACTTTATTCAAC	IGAGA I CARACTITTATT CAACTITGATACCCATATCCATATCCAAAAATTCGTATTCGCTTGTGTGATAAAAA CACAAAAACTTTATTCAACTTTGATACGCCATATCCCAAAACAGATATTCGTATTCGCTTGTGATAAAAA	∢	AYAQ	
HP1492	359 TCCACAGGGTGGGGAATAT	359 TCCACAGGGTGGGGAATATTTTTAGGCATTCTTCCACTTTAGAGCATCTTTATTACAATTTTGAAATCAAGGGTTTGAG	360 H	360 HRVGNIFRHSSTLEHLYYNFIEIKGLSR	\top
	CAGGGGGGGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGA	CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	<u> </u>	GALQELSRHRIASLSVKSSR'/TLRELK	
	GATAATGAAAAGTGAATGC	GATAATGAAAAAGTGAATGCAATGAGCGTTTTAGCTTTGGAAAATCTAAGGATCTTATTGAGCGAGC	<u>u ></u>	EVESTLPLNE I NLEKAKEFLYFVDNEK VNAMSVI AI ENI RII I SEHNIKNDI AKV	
	AACGATTTAGCCAAATACGC	AACGATTTAGCCAAATACGCCATGCCTGAAAGCTATAAAACGCATTTGGCCTATAGTATTAACGCTAGGAGCTTGCAA	<u> </u>	AMPESYKTHLAYSINARSLQIVFLTLRS	
	AATTICTTEACTTTTEAGAGCAGTAATAA CTGGCGAGCATCAGTATTTGTTTGAAGAT	AATTICTTGACTTTATTTGAAGCGGTTAAAAGAATTGCAAGATTTAGCCAAAGGCCTTATTTGACGCTTTAC	u	SNKALKEMQDLAKALFDALPGEHQYLF EDGI KH	u
-	TGTTTTAAAAACGCCTTGTT	TGTTTTAAAAACGCCTTGTTTTTGATTAGATGAGATTTTTAAGGGGGTTTGTTGT	<u> </u>		
1	250000000000000000000000000000000000000	COLINICACIONACANINA CANTOCANIN			

	∍
r	•
-	_

AAAAACTAATCGCTCTGCCCATAGATAAGCGCGCTTGGGGGTTTTGAACATGGAAGATGAAAGCGGGGTTGGATG AAAAACTAATCGCTCTGCCCATAGATAAGATCGATCCCACGCATTCCTATGTCAAAGATATTGATGATTTATCCAAAG
ACACTTTAGATAAAATCAAGCATTTTTTTGAAACTTACAAGGATTTAGAGCCTAATAAATGGGGGAAAGGGGTTTTGAGGGGTTTTGAGGGGTTTTGAAAGGGTTTTGAAAAAGCCTATCAAGGGTAAAAGGTTTTAGAGGTTTTGAAAAAGCCTATCAAGGGTAAAAGGTTTTAGGGGTTTTGAAAAAAAA
GENERAL MARIE DE LA MARIE DEL MARIE DE LA MARIE DEL MARIE DE LA MARIE DEL LA MARIE DEL LA MARIE DEL LA MARIE DE LA MARIE DE LA MARIE DE LA MARIE DE LA MARIE DE LA MARIE DE LA MARIE DE LA MARIE DE LA MARIE DE LA MARIE DE LA MARIE DE LA MARIE DE LA MARIE DE LA MARIE DE LA MARIE DE LA MARIE DEL LA MAR
GATTATTTAGCCATTAGGATTAAGGSCATGGCTAGAGGGCATGACATAGAAATTATAGAAAATAAGAAACGCTCGCCAGA GAGCTTTATAGAGATGTGAAATTAAACGCTGCCATACCAGAAGAATTGTTTGAAGCCGTGGCGATAGTCTTCGCTCA AGTGGCTAAATTAGAGCAAGAACGCCAAAAACAAAGATCATTAAACCCTCTTTAAGATTTTTTAAGCCGCTTTTAAGC CCTAAAAAAAACACTCAATCAAAAGGCTTTAGCTATTCCTATTTGAGCTTTAAATTTGATGTTCCAAACGCCTTAAGTG
GAATGAACATCTTTGCAATGCCACCACCACCGCTAAGAAATAAAACCCAATCGCATGCCATAGTATTTTTGTTTTTTTT
365 AGTTATGACGGATAACAAACCAATGAAAACCATGAAAACGCGGGGGGGG
AAAAGCGCTGTCCCATTAGCGTGGGCGAATTTATCATTGAATGGATCC 367 AGGTGCTCAAACTTTAGCGGATAAATTGCAAGCAAAATTGAATTGCATTGCATTGCATTGAATTGCAATTACAGCGTCAAGGTTGCTTTTAAAGACGATTTTAGATTGCTAAAGACGAATTTAGATTATAGAAAAAAATTGCAAGAATTATAGATGAAAAAAAA
GTIGAAATAAAAACACCGTTATAGAGCGGCTCAAAAAGACTTGCAATTGAGCGCGCAAGAAATGGGCGGCAAGAATTGAGGCGTGGGGGGGG

wo	02/066501

	1 C1/E1 01/1
4 MIGSFTRLNVADNSGAKEIMCIKVLGG SHKRYASVGSVIVASVKKAIPNGKVKR GQVVKAVVVRTKKEIQFIKNGSLVRFD DNAAVILDAKKDPVGTRIFGPVSREVR YANFMKIISLAPEVV	376 VFKDSKKDACGFIYEISE:FMKAYTALLK KQDRYVYLLRYLPSRYWASILTTALYV KYPDFDALKKLLVSYYYQTWIAGGTITR KYPDFDALKKLLVSYYYQTWIAGGTITR IKQTSINIIKNVKSNKSVETIKELILNSIDS YNTFDQYLYNLWDSSSVYHSKWVRPV LALANYFMADEEKPHFIAMDAETQVEH ILPQTPKRGSQWNADFIYKERREEWVN NIANLTLLKRKKNAHALNGDFDEKRKIY GGKDTSKVISCYDITKEI.YSNYRKWNE KSLQERYKSLYNTITPVI.HIEGGEDDFE DDFDL
37	37
373 CATGATACAGAGTITIACAAGATTGAATGTCGCTGACAATAGCGGCGCTAAAGAAATCATGTGCATIAAGGGTTAGG GAGCCACCACAACCGTATGCGAGCGTGGGTAGCGTGACCAAAAAAGAAAAAAAA	375 AGGTGTTCAAAGACAGCAAAAAGACGCTTGCGGGTTCATGTGTATGAGATCAGCGAGTTCATGAAAAGCCTATACCGCA TTGCTAAAAAAAACAAGACCGATACGTCTATTTATTGAGGTATCTCCCCTCTAGGTATTTATT
HP1073	HP1073
	373 CATGATACAGAGTTTACAAGATTGAATGTGGCTGACAATAGCGGCGCTAAAGAAATCATGTGCATTAAGGTGTTAG GAGGCAGCCACAACGCTATGCGAGCGTGGGTAGCGTGATCGTGGCTTCCGTGAAAAAAGCTATCCCTAATGGTAA GAGGCAGCACCAAACGCTATGCGAGCGTGGTGGTGGTGGAAAAAAGAAATCCAAAGAAATCCCTAATGGTTCTTTG GAGCCGAGAAGTGCAATTGCAGCAGTGATCTTGGACGCTAAAAAAAGATCCGGTTGGCACAAGGATTTTTGGGCCAGT GAGAAAAAAAAATGACATAAAAGTCAATTTCATGAAAATTATTTTCTCTAGCACCGGAGGTTGTATAATGAAAAGCGAAATC AAAAAAAAAA

c	١
~	
_	-

2/066501	PCT/EP01/1542
178 LVSSSEYAKKLNAIDKIKKTEEKOKVLD EELEDGYDFLKEKDFLEWSRSDSPVR MYLREMGDIKLLSKDEEIELSKGIRLGE DIILDAICSVPYLIDFIYAYKDALINRERR VKELFRSFDDDDENSVSDSKKDEDNE EDEENEERKVVSEKDKRVEKVQES FKALDKAKKEWLKALEAPIDEREDELV RSLTLAYKRQTLKDRLYDLEPTSKLINE LVKTMETTLKSGDGFEKELKRLEYKLP LFNDTLIANHKKILANITNMTKEDIIAQV PEATMVSVYMDLKKLFLTKEASEEGFD LAPNKLKEILEQIKRGKLISDRAKNKMA KSNLRLVVSIAKRFTSRGLPFLDLIQEG NIGLMKAVDKFEHEKGFKFSTYATWWI KQAISRAIADQARTIRIPIHMIDTINRINK VMRKHIQENGKEPDLEVVAEEVGLSLD KVKNVIKVTKEPISLETPVGNDDGGKF GÖVVEDKNIVSRIPHMEDLKAQIESV LDQLNEREKAVIRMFGLLDDESDRTL EEIGKELNVTRERVRQIESSAIKKLRSP OVGRII RNVLR	380 KLVLÁKNTRKSDAKSVELEDLYHEFSE DKRSIFYFAPTNAHKDMLKAVDFFKEK GHTAYLDEVRVSTDEKDFLYELHII 382 EĞVLRVLLNKKĞKLIKEYKTLEPLKSLEI RLSEAPIDKRNDFLYHKTTYAPFYĞKE RALIKKGVMFDEIFYNÖDLELTEGARS NLVLEIHNRLLTPYFSAGALNĞTĞVVĞ LLKKĞLVĞHAPLKLQDLQKASKIYCINA LYĞLVEVKIK
	ric ric
317 AATTAGTCAGCTCTTCAGAATACGCTAAAAAACTCCAATGCGATTGACAAGATTTTTAGATGAAGAAAGCCAAAAAGCTTTTTAGATGAACGCAAGAAGCCAAAAGCTTTTTAGATGAACTTTTTTAGATGAAGAAGCGATAGCCCAGTAGCCCAGTAGCCCATTTGATTTGAATTGAATTGAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCCAAAGCCAAAGCTGAATTGAATTGAATTGAATGCAATGCAAAGCCAAAGCCAAAGCCAAAGCAAGC	379 IGAAACTAGTTTTAGCCAAGAATACAAGAAAATCAGAGGCGTGAAGTTAGAGGATTTGTATTCAGTTTTAGATTGAAAAGGGTTTTTTAGATTGCCCCACAAAGGCGTGGAATTTTTTAATTGAAAAGGGTGAAGGGGTGAAGGGGTTTTTT
HP1198	HP1198

02/066501		PCT/EP0
384 ADETNALROKNRELNKKIDWOKDYDR EKLERDNRDLEGCKEDLLAANENLRN RIOEWENEKNKLDPRCERIKELEEEKR ELEGILAQKENAEOKYIJLSVKNKOLE AELOMLNEKFEKLKNMYAGVEDFEKR QKNIKEQIVKTNPKVLGAPSNEVEELAF LERIEKGMQEFNVFYPKRLLYMFHTAL KSTSLSPLSVLSGVSGTGKSELPKLYV HFGGLNFLSIAVQPTWDSPESLMG	386 NGVEIVGLEHLDKVIYL DQAPIGKTPRS NPATYTGVMDEIRILFAEGKEAKILGYS ASRFSFNVKGGRCEKCGGDGDIKIEM HFLPDVLVQCDSCKGAKYNPOTLEIKV KGKSIADVLNMSVEEAYEFFAKFPKIAV KLKTLMDVGLGYITLGCINATTLSGGEA QRIKLAKELSKKDTGKTLYILDEPTTGL HFEDVNHLLQVLHSLVALGNSMLVIEH NLDIIKNADYIIDMGPDGGDKGGKVIAS GTPLEVAQNCEKTQSYTGKFLALELK	388 GFLRILDVIKKVTTPKGGIEILRTLIDFTP KIENALNLAAKSHKGQYRKSGEPYIVH PICVASLVAFCGGDEANVCAALLHOVV EDTPCKIETIEQEFGQDVANLVDALTKI TEIRKEELGVSSQDPRNVVSALTFRKIL ISAIQDPRALVVKISDRL HNMLTLDALP HDKQVRISKETLAVYAPIASRLGMSSIK NELEDKSFYYIYPEEYKUIKEYLHKNKG SLLLKLNAFOSFYLKMQRKGAVNIDEILD LLAIRILLKNPIDCYKVLGIIHLNFKPIVSR FKDYIALPKENGYKTIHTTIFDESSVYEV QIRTFDMHMGAEYGNSAHWKYKAGG VDHEDHHEGMRWLQNFKYHDSDLKN DPKEFYELAKNDLYREDIVVFSPHGDT YTLPVGAIALDFAYMVHSDLGDKATDA YINSKKALLNGELRSGDVVKIIK
383 TGGCAGATGAACGAACGCTCTGAGACAAAAAACAGAGAACTGAACAAAAAATAGATTGGCAAAAAGAGATTATGAC AGGGAAAAATTAGAACGAGATTATGAACAATGCCAAAGGGGATTTAGCCGCTAACGAGAATCTAAG AGGGAAAAATTAGAATGGGAAATTAGGAATTAGAACAAGGGGATTATTATAGCCGCTAACGAGAATCTAAG AAATAGAATCCAAGAATGGAAAAATGAAAAAGAGCTTGATCCCAAGGAATGAAAAGAGTTAGAAGAAGA AAAAAGGGAATTAGAGAAATTGAAAAAGAGAACCAGAACAAAAATATAAACACTCTTTCAGTCAAAATAA GCAATTAGAAGCTGAGTTAGATATGCTTAACGAAAAATTTGAAAAACTGAAAAATATGAAAAATTTGAAAAACGCCCAAAAATAGCGCGCACCTTCAAACGAAGTTTGAAAAACCGCCAAAAATTGTAAAAAACCCCAAAGGGGGTATAGAAAATTGTAAAAAAGGGCATTGTAAAAAAGGGCATTAGAAGAGGCATTGTAAAAAGGGGCTTTATTGTA TATGTTCCACCCCCAAGCTTTAGAAAAGGGCGTTTTGTAAAAATTTTTTATGTA TATGTTCCACACCGCTTTAAAAAGGGCGTTTTGGGGGGTTAATTGTAAAAATTTTTTTGTA CTGAACTGCCCAAGCTCTTAGAGACGTTTTTTGGGGGGTGGGGAAAAT CCGGAATTGCTGCCCAAGCTTTTTTGGGGGGGTTAATTTTTTTAAAAAGGGCGTTTATTGTA CCGGAATTGCTGCCCAAGCTTTTTTGGGGGGGTTAATTGTAAAAATTTTTTTT	385 GAÁTGGGGTGGAGATTGTAGGGTTGGAGCATTTGGATTATTTAGATCAAGGCCCCCATAGGCAAAACCC CACGAAGCAACCCTGCCACTTACACGGGAGTGATGAAATCAGGATTTTATTTGCCGAGCAAAAAGAAGCTAAA ATTTTAGGCTATAGTGCGAGCCGTTTTAGCTTTAATGTTAAAGGAGGGCGGTGCGAGAAATGCCAAGAGCTAAA ACATTAAAATAGAAATGCACTTTTTGCCTGATGTTTTAGTCCAATGCCGATAGCTGTAAGGGCGCTAAATACAAACCCCC AAACTTTAGAAATCCCTAAAATCGCCGTGAAATCCCATTGCCGATGTGTTGAACATGCGGTGGAAGGCTTATGAATTTTAGAAATCGCCGTGAAAGGCTCAAAGGCTTATGCATTTTTAGAATCGCCGTGAAGGCTCAAAGGGCCAAA ACGCTACGACTTTAAATTTTAGATGGGGGGGGGG	387 CGGÁTTCTTACGGÁTTCTTGATGATTAAAAAGTTACGÁCCCCÁAAGGGTGGCATTGAAATCTTAAGGACTTTAAT TGATTTTACGCCCAAAATTGAAAATCATTTAGCGGCCCAAAGGCGCCATAAGGGGCCATACAGAAAAAGCGGCG AGCCTTATATTGTCCATCCTATTTGCGTGGCCATGGTGGCGTTTTGTGGGGGCCGATGAGGGCGATGTGTGTG
НР1198	HP1198	HP1198

SHICOSON AND AND AND AND AND AND AND AND AND AN	SS S S S S S S S S S S S S S S S S S S		<u>01/15428</u> 点台 日本 日本 日本 日本 日本 日本 日本 日本 日本 日本 日本 日本 日本
PKERVLSDEEINNRAERIAKSELEKDTK LVSSHDOYERMKKSGSLNTENLDSHIC ANSLOELNOKLLGPVGADRKYMPYTK AVGISLNNPNLKDLEVIDTPGVNDPIAS SREERTKALLKDCDVVFIISSSNÖFLTES DMSLFDRVSNKESLQEIYFVASQADSA VLSMSEVEKSRHHLPTALENAKKSLSS SLNKTMEALIQTNPNORGIFEKAIKNGV CYNAWRNLTNAYPLTLLTALINLKKAYY	SEKNIEKVLNAYDKOOHHHÖDDLAIÖY SEKNIEKVLNAYDKOOHHHÖDDLAIÖY TEELIKLARRYESALNDSFWGYAKTRV NGAMLDYLRSLOVISRSSRKLIKSIDIEI TKHLNEHGKEPSDAYLAOTLGENIEKIK EAKTASDIYALVPIDEOFNAIEQDEITKK IEAELLEHVOKALNOMSEREOILIOLY YFEELNLSEIKEILGITESRISQIIKEVIKK VRKSLGVDHG	EYNRLKÓRTEHÖLEMISATGVCKGIEN YARHFTGKAPNETPFCLFÖYLGIFERE FLVIVDESHVSLPGFGGMYAGDMSRK SVLVEYGFRLPSALDNRPLKFDEFIHK NCGFLFVSATPNKLELELSKKKVAEGII RPTGLLDPKFEVRDSDKÖVQDLFDEIK LVVARGERVLITTTKKMAEELCKYYAE WGLKARYMHSEIDAIERNHIIRSLRLKE FDILIGINLLREGLDLPEVSLVAIMDADK EGFLRSETSLIQTMGRAARNANGKVLL YAKKITGSMÖKAFEITSYRRAKQEEFN KIHNITPKTVTRALEEELKRDDEIRIAK KHNITPKTVTRALEEELKRDDEIRIAK KHNITPKTVTRALEEELKRDDEIRIAK	ESLRALKASÓEVÓANTLKÖÖSÖTLEDL RMEIHANQÓAIQÓLDKÖNKEMSELLTK LSÓDLVSÓIALIÓKALKEĞEEKAEKPLK SNAPANKTPSLKAESPKNOEGKTÖEK AKIEFÖKÖLSKÖKEIFĞEALSFFKNKSY AEAKERLIWLEANSYRLYYVRYVLĞEV AY
VERIAN GSLN VGADF VFIISS DEIYF OPTALE IORGIE	OCHIH PSSIC VDSFW VLAQT COFNAI ESRIS	AISATC CCLFD SGMYA NRPLK NRAEI ECSK KMAEI EVSLV SYRRA SYRRA SYRRA SYRRA	TLKOC CONKE CECEE KNOE SEALS:
SINNR/	AYDYC RLKERI RESALI SLDVIS SLDVIS PSDA VPIDE NKALING EILĞIT	HÖLEN NETP NETP PSALD SEIDAI SEIDAI OTMGI CAFEIT SALEEI	CKALP CKALP CKALP CKAESI CANSY
LSDEE DOYER DOYER DOYER JELNO DRVSI DRVSI DRVSI DRVSI MEALI MEALI MEALI MEALI MEALI MEALI MEALI MEALI	EKVLN AMAFF LARRY DYLRS SDIYAL SDIYAL SLEHVC SVDHC	CORTE FIGNAP FISHVS FIS	KASOE NOOAI SOIALI IKTPSI (DLSK LLWLE
390 PKERVLSDEEINNRAERIAKSELEKDTKO LVSSHDOYERMKKSGSLNTENLDSHICGO ANGLOELNOKLLGPVGADRKYMPYTK OF AVOISLNNPNLKDLEVIOTPGVNDPIAS I REERTKALLKDCDVVFIISSSNGFLTES DMSLFDRVSNKESLGEIYFVASQADSA VLSMSEVEKSRHHLPTALENAĞKSLSS SLNKTMEALIQTNPNQRGIFEKAIKNĞV ILTSGACFSMYKDFKNGASWESKKEE	SEKNIEKYLNA SEKNIEKYLNA TEELIKLARRY NGAMLDYLRS NGAKTASDIYAL EAETASDIYAL SEELNUSEIKI VRKSLGVDHG	EYNRLKÓRTEHÓLEMISATG YARHFTGKAPNETPECLFDY FLVIVDESHVSI-POFGGMYA SVLVEYGFRI-PSALDNRPLKI NCÓFLFVSATPNKLELELSKK NCÓFLFVSATPNKLELELSKK PPTGLL DPKFEVRDSDKQVQ LVVARGERVLITTLTKKMAEE WGLKARYMHSEIDAIERNHIIF FDILIGINILREGLDLPEVSLV EGFLRSETSLIOTMGRAARIV YAKKITQSMÓKAFEITSYRRA KIHNITPKTYTRALEEELKLRD ALKKÖKMPKSEREKIIKELDKI KNI ĎFEFAMÍRI ÞÓFAKNI ÞTI	SLRAL SCOLV NAPAN KIEFDY
390	392	96 	396 RAN SAN AFE AFE
ACCCAAAGAGAGGGTTTTAAGCGATGAAGAAATCAACAAGGGCTGAAAGGGATCGCTAAAAGCGAGTTAGAGGAAGGA	TTCA CCTC CCTC CCTC CCAA CCAA CCAA TTCA GTAA GTA	ATTG TTTG TTTG ATTGA GAA TGC CAT CTG CAT GACA GACA	AGG SCT SCT SCT GGG GTC TAT
389 ACCCAAAGAGAGGGTTTTAAGCGATGAAGAAATCAACAACAGGGCTGAAAGGGATCGCTAAAAGCCGAGTTAGAGGAAG GATACGAAGCTCGTTTCATCACACACACACACACAGGGATCGCTCAACACACGGAAAACTTAGA GATACGAAGCTCGTTTCATCAAGAGCGGATCAAAAATTGCTCCAATTCGTGGCGCGCGGATAGGAGTTAG TTCGCACATTCAAGCCGAGAAGTTTCTTTGAATAACCCAATTTGGAAGTTTGGACACCCCAGGAG TGCCTACACTACA	AGGGAAAAAATATAGAAAAGGTTTTGAACGCCTATGATAAGCAACACCCCCTCATCAAGAGCGACCTTTCACGACCTTCACGACCTTCACGAAAAAATATCACAGGACCGATCCTTTCACAGGACCCTTTCACAGGACCGATCCTTTTCACCAGGATTCATTGACCATTTCACAGGATTCATTGATTAACGATTCTTTTTGACGATTTTTGACAGTATTTTTTCCCTTTTTTTT	TGAATACAACCGCCTCAAACGCGCGGGGGTGATTTTGATTTGCCTGGGGGGTGTGTGT	AGAATCCTTACGAGCCTTAAAAGCTTCGCAAGAAGTGCAGGCTAACACGCTTAAGCAGCAATCGCAAACTTTAGAGGATGAGGAATTATATTGAGGAATGAGGATGAGTGAGTTATATAGAGAGGAAAAAA
CGAGA CGAGA CGACA CCTTC CCTTC CCACA AACAA AACAA AACAA	SATCT SATCT TITTE TAGE SECAN TETCE TAAN ATCGI CTTCT	TGTAN TTAGA TTAGA TTAGA ATAGA ACTGA AGAGA ATCAC	SAGAC SAGGA SAGGA SAGGA SAGAC CAGAC
ACCCAAAGAGAGGGTTTTAAGCGATGAAGAAATCAACAACAGGGCTGAAAGGGATCGCTAAAAGCGAGGGATAGCCAGGGGATAGCCAGGGATAGCCAGGGATAGCCAGGGATAGCCAGGATAGCCAGGATAGCCAGGATAGCCAGGATAGCCAGGATAGCCAGGATAGCCAGGATAGCCCAACATTCCAGGGCGCGCATAGCCAATTCCAAGCGCTTAAAGATTGGAAGTTGACGATGATTGACAGAGTTGATTGA	AGACA AGACA ATTCT ACTCT ACTCT ACTTT ACTCT ACTCT ACTCT ACTCT	STGTG VATTA VACCTT SGCCCTC/ CCTC/ AGTGA CATCA CA	ATCGC VAGAG ACAAC SCAAA TTTCA
CGCTA CGCTA CGCTA CGAAG CCAAG CAAAG CAAAG CATTGA	AACGO AACGO	ACCGC STITTG SGGG, ACCGC SAGGC AAAAA ATCC, GCTA	AAAGA WAAGA WAAGA WATCC WATCC
GGATI GGATI ATTCC ATTTG GATTG SAAAAA SAAGG GGGGG ATGGC	CCACC CCACC CCACC CCTTA TTCA TTCA AGTCC TTTCA	CGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TAAGC AGCAA TCTC SCCGA AAAGA
TGAAAGCTCCAAAGGCTCCAAAGCCTCCAAAGCCTCCAAAGCCTTCAAAGCCCTTCAAAGCCTTCAAAGCCCTTCAAAGCCTTCAAAGCCTTCAAAGCCTTAAAAGCCTTCAAAGCCTTAAAAGCCTTCAAAAGCCTTAAAAGCCTTTAAAAGCTTTAAAAGCCTTTAAAAGCCTTTAAAAGCCTTTAAAAGCCTTTAAAAAGCCTTTAAAAAGCCTTTAAAAAGCCTTTAAAAAGCCTTTAAAAAGCCTTTAAAAAGCCTTTAAAAAGCCTTTAAAAAGCTTTAAAAAGCCTTTAAAAAGCCTTTAAAAAGCCTTTAAAAAAGCCTTTAAAAAAGCCTTTAAAAAAAA	SAACA SAACA SAACA AGATG GAAAT AGTTTC AGTGA AGTGA AATCT GCCGA	ATTAGE ACAGI ACAGI ATAGA ATAGA ATTAGA ATTAGA	AGCAA GAAAC GAAAC GTTAC
GGGC SAAAA ATCTI ATCTI ATCTI AACAG AAAC AAAC	GCAAC AGCGCAAC AGCGCCTT CTTT CTTTA AAGA AAG	AATGO CGCCC TGCCC TGCCC AAGAT TTTTA AAGA	TAACA AGTTA CCAA TCTTA TTGTG
GCATO GCATO CAAAA CCCCA AAGCC GTTTC GTTTC AAATA	SATAA AAAG GGGCTT AACG AACG AACG STAAC STAGC ATGGC	TTAGA SAGTT SAGTT TGCC TGCC TGACG TGACG ACAGGAL	ACTTG ACTTG
GAGE GAGE GAGAT ATAAC ACCA AGTTT TCTTT TCTTT SGGCG AGAAC	CTATC SCCAGG SCCAAAAAAAAAAAAAAAAAAAAAAATC CAAAATC	TTGAT TTGAT TTGGAT TTGGAT TTGGA TTGG TTGG TTGG TTGGA	AGTGC CTATO CGCC AAAAG AAAAG
AATAGAATTTGAATTTGAATTTGAATTTGAATTTGAATTGCCCCATCTTGAAAACAAAAAAAA	WACGO TTAGO TTAGO TAGAT AGAGA AGAGA AGCG STGA	SAGCC VGCCC VGCCC SGTT TGGC TGGC TGGC TAAAC CGCG SAAAT	AAGA CAAAT CAAAT TTGAT CAAAT
ATGAA GATGAA ACAA(ATTTC AAATC AAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAAATCAAAAATCAAAAATCAAAATCAAAAATCAAAAATCAAAAATCAAAATCAAAATCAAAAATCAAAAAA	TTTGA TTAGA TTAGA TTAGA TCCAA TCCAA TTAGA TATCC	CACCC GTAAA ATATG ATATG CTTTT CTTTT CGGCT (CGCT SAAACC	CCAG CCCAG CCCAG CCCAG CCAG CAG CAG CCCAG CCCCAG CCCAG CCCAG CCCAG CCCAG CCCAG CCCAG CCCAG CCCAG CCCAG CCCAG
AGCG/ CACAV GCAAV GGAG/ GGAG/ GGAG/ AATCC AAGCGATFGAT	VAGGT GCCA1 GCCA1 GGCGAAAAAAAAAAAAAAAAAAAAAAA	AACG ACCG STGGA STGGA AGTTA AGTTA AGTTA AGTTA AGTTA AGTTA	AAGCTAA GCTAA TTGG CGCTC AAATT GCAG
CAACA CAACA CAACA CAACA CAACA AAGCA CAAAA	AGAAA AAGAA AATGG ATGG ATTGA ATTGA ATTGA ACTGA CAGC	CAAAC ATTTC TICATT TICCA ATCA ATCA ACCC CACT TAGAA	TCACA TCACA TCACA TCACA GCCGA
AGGG NAAGC NAAGC CATC CATCC C	AATATATATATATATATATATATATATATATATATATA	GCCTI CCCCC CCCCC AAATCA AAGTCA AGTCA AGTCI CCTT AGTCI CCTT	GAGCC GAGAT GAGCCX CAAA TAAAT TCTTG
AGAG CATTC ACCC ACCC ACCC GAAA GGAAA	AAAAA ACCAG CTCGC CTCGC AATGC AAAAT CAAAA CCAAA ACTGC	CATACC CGCG GAAA GAAA CATA CATA CATA CAT	TTAC GAAT GETTA CGCC CAAG VAAAA
CCCAA ATACCA SCCCT SAATG TITTG CCTTA ACCAA	AGCGAAAAAATATAGAAAAGGTTTTGA GTATTTACCAGCCGTGCGCGCCATGGCC TTTCTATTGGCACTGAAGAATTGATTAAA CGAAGACTCGTGTCAATGGGGCGATGTT ATTAAAAGCATTGAAAAAATTAAA ACTTTAGGCGAAAATATTGAAAAAAATTAAA CAATTCAATGCGATTGAGCAAGAGGAGCGAAG GAGTTTTAGGCCATTACTGAATCGCGCAT GTGGATCCAAAAAAAGGATATTATCCCGC GGAGCAACTGCGCTCTTTTAGGAGTATCC GGAGCAACTGCGCTCTTTTAGGAGTATCCGG GGAGCAACTGCGCTCTTTTAGGAGTATCC	AATTAC AATTA ACGGGG ACGCGG ATTC AAACC AAACC AAACC	AGAATCCTTACGAGCCTTAAAAGCTTCGCAAAAATTTGAGGAATGAGTTCACCGCAGCAGCCAGC
88 80 80 80 80 80 80 80 80 80 80 80 80 8	8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	393 TGAATACAACCGCCTCAAACAACGACCGGGCATTGATTTAGAAATGATTTAGCGGGACCGGTGTGTGT	395 AG AA GTT GTT GTT
198	198	86	86
HP1198	HP1198	HP1198	HP1198

wo	02/0665	01			
****			z	7	\$ 4

HP1198	397	397 GCACACTCTAAAAGAAATGCTCACCATTAAATCCGATGATATTAGAGGCAGAGAGAG	398	398 HTLKEMLTIKSDDIRGRENAYRAIAKGES QVGESEIPETFYVLT
HP1198	66C	399 CTTTAGCCCAAATGCGTTTAGCCATTGAAGCGGCTGAAGGCTCTGATTTGAGCAAGGCTAACATGGTTTTTAAAAGAA GCTTTTAGTCCCAAATGCGTTTAGCCATTGAAGAGGGGTGAAGTTGGGCTGAAGCAGGGTAACAAGAAGAGAGAG	4004 8	LADMRLAIEAAEGSDLSNANMLFKEAF, SNAKDKESASEIALNWAEAEINYQNFN NAKYLIDKVVQSNPDYISTHSESALDLL KLLKKNQMNASAIEIAHLLLNQDDDLKA KEQALYDLGALYARIKDFKNAHLYNLQ YLQDHAELDKASVVRARIJEKALFSME GNTQEKIAHYDKIIQNFPNISNEALKALE LKAQLLFENKRYAEVLSMQKNLPKDSP LIQKTLNVLAKTPLENHRC:EEALKYLSQ ITTFEFSPKEEIQAFDCLY*ASLKEKAQI IALNAFKTAKAPSEKLIWLYRLGRNYYR LGDFKN
HP1198	401	401 GCGCGAACAAAAAAAAAAAAAAAAAAAAAAAAAAAACAAAACCGGCGATCTTTTGGTATCAAGGGATTTTGAGAAAATC CTTTTTGCTAATTTAGAAACAGCGGACAATTACTATTCTTCTTTTACAAAGCGAACACACATCAATTCCCCCCTTGTCCAG AAGCGATGCTAGCGTAGGGCAAGCGCACATGAAAAAGAAAAGAAGCGAACACATTTTTACTTTTACTTTGATGAATACA TCAAGCGCTTTGGGACTAAGGACAATGTGGATTATTTGACTTTTTTAAAATTGCAATCGCATTATTACTGTAAAAAA CCATTCTAAAGAACAGGAATTTATCTCTAATTCTATTGTGAGTTTAGGCGAATTTATAGAAAAATACCCTAACAGACCGT TACCGCCCCTATGTAGAATACATGCAAATCATTTTAGGGCAAAATGAGCTCAAAAAAAA	402	402 ANKKKKDEYNKPAIFWYQGILREILFA NLETADNYYSSLQSEHINISPLVPEAML ALGQAHMKKKEYVLASFYFDEYIKRFG TKDNVDYLTFLKLQSHYYAFKNHSKDQ EFISNSIVSLGEFIEKYPNS.RYRPYVEY MQIKFILGQNELNRAIANVYKKRHKPE GVKRYLERIDETLEKETKFYPSHMPWY VLIFDW
HP1198	403	CCTTTAAACCCTTTAAAGACGCTTTTTACAGAGATTTCAATCATAATGAGCAAAAGTTACTGATAGGGGCAGCTAAAA GCGGTTGCATTCAATCTAGCGCTGATAAACTGGCTCAGTTAAAAACGCGCTTACTCTACTGGCAAGACAATCTGTTA AAGTGGATTGGGATAAACCCATTTTAATCAAGGACTTCTTTAAAGGCAATAATTACCTTTATAGGAGGTTTTTTTT		404 FKPFKDAFYRDFNHNEGKLLIGAAKSG CIGSSADKLAGLKTRLLYVJDKSVKVD WDKPILKDFFKGNNYLYFRFCFLLGK HFMDRFLKNNAKASVKDFMSSKEFVA KYRYTPKÖNTERAKKLGSYLENKRDFI GFVQALNSLKDNPQDPFLPNEETSFLV FAN
HP1198	405		00 10 5 7 7	LALNELNPGEWVVHUDYGYGYFSQLV OHSVLGSKRDFLEIAYLGEDKLLPVE NLHLIARYVAQSDSVPAKIRLGKGSFL KLKAKVRTKLLEIASKIIEL/AERNLILGK KMDVHLAELEVFKSHAGFEYTS
HP1076	407	GTTTGAGCGGCGACAAAAAGCCCTTTTAAGGAATTTGGAAAAATCGCTTAAAAATTAAGATTTTTGCCGAAGGAGGCTTCCGGCCTTTGAGACTTTTGCGGGCTTTCGCGGCTTTCTGCAAAAATTGCGGGGGCTTTTGCGGGCTTTTTGCTTGC	804	408 LSSUKRALLKNIEKSIKNNITRUAEANS LVSNAIKIQHCGLSAKNKFVGSFLYVGP SGVGKTELAKELALNILHFERFDMSE YKEAHSVAKLIGSPSGYVJSFGGGLLV NAIKKHPHCLLLLDEIEKAHSNYDLLL QVMDNATLSDNLGNQAS:*KHVILIMTS NVGSKDKDTLGFFSAKNTKYDKAVKEL LTPELRSRIDAIVPFNALSLED

PCT/EP01/15428

ď	0
	'n

WQ_02/06650	1 ISANYIN	Ja 🗸	1	РСТ	/EP01/15428
410 OTNKVVYAKEAAISAASLGDIKTAMHIO MLYOKITNNRNDVSINKILVDGYAOMIO QIDKAIELLHKIRKEEKTIATDNVLGTLÖLTAKRLDKAFYNOVHDEDSISKLITYFLONRKKEGLDLLQSHIDRYGIS	SECILCOK 412 DLPOKLHLDKKLSOTIOPCMOLNASKH YTSTGVREPDKCTKSFKKSALMSYDLA LGYLVSKNKQYGLKAIEILNAWAKELQ SVDTYQSEDNINFYMPYMNMAYWFVK KAFPSPEYEDFIKRMRQYSQSALNTNH GAWGILFDVSSALALDDNALLHNSANR	414 OKMCEYAKTLASEFHRFYNAGKILDTP KAKELLKICLIVSLSLSNAFKLLGIEIKTKI SARD	416 NLNAPKPLFECFVGVNLAKAKYYSKKE EREKEKMILNFCKIFEIILFEAIGKGPKP DFKNKDELLGDYPNLKNLDSLREVRED FLKRAFKNDEASLGAYVLVLLSCKYFE SVFEKVQEWLDFIARLALRGHVHKIT	418 QAKRCIĒNEDIĒKKIYYĪNRVTDIFTĒLL NILDYEKGGEVAVYLTGLYTHQIKVLTQ ANVENDASKIDLVLNVARGLLEAWREI HSDELA	420 LKRLKĎSNHIILĎTKNAĽLAČĎTKGĎGJ MAEPLEILFKAAĎTLLKDAYFENREVIVO MGASIEKIĎSVATISNLSSGIÓASALĎI LALYFKGAKÝTLIASNFPTPLPKEITSV VSĎTASYENALNSAANNLOKHALKPLIS FNLAAISĎÝVPKTSFNYKLKKSEIGETL N
409 AGCAAACCAATAAGGTGGTGTATGCTAAAGGAGCGGCCATTTCAGCGGCGAGCTTAGGGGGATATTAAAAACCGCTAT GCATTTAGCCATGCTCTATCAAAAATCACCAATAATCGTAATGATGTTCTATCAATAAGATTTTAGTGGATGGTTAT GCGCAAATGGGCCAGATTGATAGGCGATTGAATTGA			415 CAAACTTAAACGCACCCCAAACCCTTATTTGAATGTTTTGTAGGAGTTAATCTGGCCAAAGGCCAAATATTTTTTTT	417 CGCAAGCCAAACGCTGTATTGAAAATGAAGACATTGAAAAAAGGATTTATTATATATA	419 ATT TAAAACGCTT GAAAGATT CCAACCACATTATTTT AGACACCCCTTTT AGCATGCGACACTAAAGGGCG ATGGGGCGATGGCTGAGCCTTTT AGACATCCTTTTT AAACCGCCCTTTTAGCATGCGACACTAAAGGGCG ATGGGGCGATGGCCTGAGCCTTTTT AGACAAGGTTGACGCTCCTAAAAGACGCTCTAAAGTTCTTCTAGAAACA GAGAAGTCATGGCGTTTTGGCGTATATTTTAAGGGAGCCAAAGTTGATTGA
HP1076	HP1076	HP1076	HP1076	HP1076	97014

<=0.4		_ 1	PCT/EP01/15	428
422 SGIDFIAPLNTPVYASAUGIVDFVKINSS NVGYGNLVRIEHAFGFSSIYTHLDHVN & VQPKSFIQKGQLIGYSGKSGNSGGEKL HYEVRFLGKILDAQKFLAWDLDHFQSA LEENKFIEWKNLFWVLEIDIVQLQEHVD KDALISQ	424 PDFKAPAVLGNNEVDEHFELSKNLGK NGAILFFWPKOFTFVCPTEIIAFDKRVK DFQEKGFNVIGVSIDSEQVHFAWKNTP VEKGGIGQVTFPMVADITKSISRDYDVL FEEAIALRGAFLIDKNM′KVRHAVINDLP LGRNADEMLRMVDALLHFEEHGEVCP AGWRKGDKGMKATHGIGVAEYLKENSI KL	426 KKDACGFIYEISEFMKAYTALLKKQDRY VYLLRYLPSRYWASILTTALYVKYPOFD ALKKLLVSYYYQTWIAGGTITRIKQTSIN IIKNVKSNKSVETIKELII.NSIDSYNTFDQ YLYNLWDSSSYYHSKYVRPYLALANY FMADEEKPHFIAMDAETQVEHILPQTP KRGSQWNADFDKEKREEWVNNIANLT LLKRKKNAHALNGDFDEKRKIYGGKDT SKVISCYDITKELYSNYIRKWNEKSLQE RYKSLYNTITPVLHIEGJEDDFEDDFDL E	. 1-	HWFLNYILSULNFALLGEPLLSSYDFN ASSFYPKNDANLSLAT EMTYONPMFW HVGKIENEGLKTILLSK PSFLWLFEELK EDCLLLKEHDSLLDYKI.LQLFKLFENAL FSVLYNKVTL
421 ATCCGGGATTGATTTTATCGCGCCATTAAACACGCCTGTTTATGCGAGCGCTGATGGGATTGTGGATTTTGTGAAGA CCAATTCTAATGTGGGGTATGGGAACTTGGTGCGCATTGAACATGCGTTTGGTTTTAGCTCCATTTACACGCACTTAG CCAATTCTAATGTGGGGGTATGGGAACTTGGTGCGCAAAAGGTTGATTGGCTATAGCGGGAAGAGGGGTAATAGC ATCATGTCAATGTGCAGCCCAAAAGCTTCATCCAAAAAGGGGCAAAAATTTTAGGCAAAAATTTTAGGCAAAAATTTTTGGGTAAAAATTTTTGGGAAAAATTTTTGGGAAAAATTTTTGGGAAGAA	423 CCCCAGACTITAAAGCACCTECCGITTTAGGAACCAATGAGGITGATGAGCATTIGAGCCTTTCTAAAAATTTTGGTAAAAAGGGTGCGAAAAAAAA	425 GCAAAAAAGACGCTTGCGGGTTCATCTATGAGATCAGCGAGTTCATGAAAGCCTATACCGCATTGCTAAAAAACAAAAAAAA	427 TGAGTTTGGAGAGCATGAACAAGGAGCGATCAACCGCCTTTTTAAAGATTTGCAATACCAGI IAGAAAAAGGGI IAGAAAAAGGGI IAGAAAAAGGGI IAGAAAAAGGGI IAGAAAAAGGGGI IAGAAAAAGGGGGI IAGAAGGGGGAAGTGATTTAGTGGATTTAGTGGATTGAAGGGGCGAGAGTTTCAACAGGGCCATCGCCATCGCCATCGCATCATCATTATTAGGGCGAGAGTTTTAAAGGGCGAGAGTTTTAAAGGCGAAAAAAGGCTTATTAAAGGCGAGAGAAAAAGGCTAATAATTAAAAGGCGAGAGCAAGAAAATGAAATGAACTGCCCCTAAAAGAGAATGGAAGAAGAATGGAAGGAA	429 ATCAAGCTATGCCAAACTCATCGCGCAAACCATGTGCTTAATGGCGAAGCATGCGTGTTGTTGCGGT CTTCTAGGCACTGGTTTTTAAACTACTTCTTCTAACCTAAACCCCAAAGATTTAAAGGGCGCCCCTTATTGTCCGT CATTGATTTTAACGCTTCTTCTTCTACCCCAAAAACGATCTCTCTC
HP1076	HP1076	HP1196	HP1196	HP1529

v	•	•

2/066 <u>2</u> 01 	で の の の の の の の の の の の の の	PCT/EP01/154
432 GGIACANILHKNSGITIDIGGGSTECALINGERGKIKDLISLDVGTIRIKEMFLDKDLEV99 EKGKIKDLISLDVGTIRIKEMFLDKDLEV99 KLAKAFIQKEVSKLPFKHKNAFGVGGTIGGALSKVLMKRFCYPIDSLHGYREDAHK TONLAFIEKIVMLKEDQLRLLGVNEERLDSIRSGALILSVVLEHLKTSLMITSGVGVR EGVFLSDLRHHYHKFPPNINPSLISLK DRFLPHEKHSOKVKKECVKLFEALSPLHKIDEKYLFHLKIAGELASMGKILSVYLAHKSAYFILNALSYGFSHQDRAIICLLA QFSHKKI	434 FENAKAECSLVFIINKÖFSHAWVKNIKEI LETFKYEGEGVFLDQENKILYAGVKED DVHLLRESACLAVRTLKKLAFKSVKVG VYTCGAHSKDNALLENLKALFIGLKLG LYEYDTFKSNIKKESVLIKEAIVALELHKP CEKTCANSLEKSAKEALKYAEIMTESL NIVKDLVNTPPMIGTPVYMAEVAOKVA KENHLEIHVHDEKFLEEKKMNAFLAVN KASLSVNPPRLIHLVYKPKKAKKRALV GGGSAVIGLLNALAKLGVEAEVHGIIGA TENMIGPAAYKPODILISKEGKSIEVRN TÓAEGRLVLADCLSYAÓDLNPDVIVÖF ATLTGACVVGLGEFTSAIMGHNIEELKN LFETSGLESGÉLLAKLPFNRHLKKLIES KIADVCNISSSRYGGAITAGLFIRÐ EFKDKWLHIDIAGPAVVEKEWDVNSFG	ASGAGYMACIJAFYEELLKKA 436 DVIKKYTTPKGGIEILRTLIDFTPKIENAL NLAAKSHKGQYRKSGEPYIVHPICVAS LVAFCGGDEAMVCAALLHDVVEDTPC KIETIEGEFGQDVANLVDALTKITEIRKE ELGVSSQDPRMVVSALTFRKILISAIQD PRALVYKISDRLHNMITLDAPHDKQV RISKETLAVYAPJASRLGMSSIKNELED KSFYYIYPEFKKLFDSGFSHSDFKLVTR VKRPYSIYLKMQRKGAVNIDEILDLLAIR ILLKNPIDCYKVLGIIHLNFKPIVSRFKDY IALPKENGYK
431 M GOCGETTGATGGGGGGTAAAAATTCAGGGATCAGGATAGGAT	433 ITTTGAAAACGCAAAAGCTGAATGCAGTTTTATTTATCAATAAGGATTTTAGCCACGCTTGGGTCAAAAATAAA GAGTTGCTAGAAACCTTTAAATACGAAGGCGTATTTTTAGACCAAGAAATAAAATCCTGTATGCGGGCGT TAAAGAAGATTGCTGCATTTTATGAGAGGCGTGTTTTAGAAAATAAAAACCTGTATGCGGGCGT TAAAGAAGTGGCGCTTTATATTGAGAGGCGCGTTTTAAAGAATAAAAAAGGCTTTTAAAAG GGTTAAAGTGGGCGTTTATACTTGTGGCACATTCTAAAGATACCGCGCTTTTAGAAAACTTGAAAGGCGTTTTTT GGGCTTAGAATTGCACAAACCTTGCGCACATTCTTAGAAAAAGGCGTTTTAAAAGAGCGTTTAAAATA GGCTTAGAATTGCACAAACCTTGCGCAATTCTTAGAAAAAGAGCGTTTTAAAATA CGCTTAGAATTGCACAAACCTTGCGCCAAATTCTTAGAAAAAGGCGTTTAAAATA CGCTTAGAAATTGCACAAAAGAAAAACTTGCGCAAATTCATTAGAAATCCCTCCC	435 TGATGITATAAAAAAGTTACGACCCCAAAGGGTGGCATTGAAATCTTAAGGACTTTAATTGATTTAAAAAAGTTACGCCCAAAATT 6AAAACGCCCCTGAATTTAGCGGCCCAAAGGGGTGGCATTGAAGGGGCGGAGGCTTTTGTTGTCGTC GAAAACGCCCCTGAATTTGCGTGCCTTTTGCGTGGCCTTTTGCCTTTTGTTGTCGTTC GAAAACGCCCCTTGTAAGATTGAAACGATTGAGGGCCAAAAGGCGGCGGAGCTTTGCCTTTTGCGTTTTGCGTTTTGCGTTTTGCGTTTTGCGTTTTGCGTTTTGCGTTTTGCGTTTTGCGTTTTGCGTTTTGCGTTTTGCGTTTTGCGTTTTGCGTTTTGCGTTTTTGCGTTTTTGCGTTTTTGCGTTTTGGGTGTTTTGGGGTGTTTTGGGGGTGTTTGGGGGTGT
	HP0071	HP0071

c	3	١.
ĕ	÷	ì

нР6071	437 ITTIT 437 ITTIT TGCG ACAAA ACACAC ACACAC ACACAC ACACACAC	437 ITTTGCTAGCGATTGTGTTGTACTTTTCTACTTTTATTGCACAAGGTAAGATTAAGGTCAGTCTCCCTAACGCTAAAAAAAGAAAAGAAAAGAAAAGAAAAGAAAG	438 LLA SOF LEA TFIS	438 LLAIVLSISTFIAGGKIKVSLPNAKNAEK S SQPNDOKVVVISVDEHONIFVDDKPMNS LEALSAVVKQTDPKTLIDLKSDKSSRFES TFISIMDILKEHNHENFSISTQAQ	AQ AQ AQ
HP0071	AGCTTATA 439 AAGACAGG AAACAAGA GTCAAATAG ATCACGCG CTTATATTG FAGCAAATG AAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AGCITATAACCCAGGGGTGAGCAACGAATTITTAATGA 439 AAGACAAGCAAAAAAGACGCTTGCGGGTTCATGTAGGGGGTTCATGAAAAGCCTATACCGCATTGCTAAAA AAACAAGACAGCAAAAAAGACGCTTTGCGGGTTCTATTGGGGCCAGCATTTTAACGACTGCCCTTTAT GTCAAATACCCTGATTTTGACGCTTTGAAAAAGCTTTTGGTGTATTACCAAACTTGGATTGCAGGAGCCCTTTAT GTCAAATACCCTGATTTTGACGCTTTGAAAAAGCTTTTGTTATTACCAAACTTGGATTGCAGGAGCCTCAAAGGCGTTGAAACCATCAAGGGCGTTGAAACCATCAAGGGCGTTGAAACCATCAAGGGCGTTCAATTTTTTTT	440 DSKK RYVYY FDALL SINIIK FDQY ANYF QTPK NLTL KDTSI	440 DSKKDACGFIYEISEFMKAYTALLKKOD RYVYLLRYLPSRYWASIILTTALYVKYPD FDALKKLLVSYYOTWIAGGTITRIKOT SINIIKWKSNKSVETIKELILNSIDSYNT FDQYLYNLWDSSSVYHSKWVRPVLAL ANYFMADEEKPHFIAMDAETQVEHILP QTPKRGSQWNADFDKEKREEWVNNIA NLTLLKRKKNAHALNG DFDEKRKIYGG KDTSKVISCYDITKELYSNYRKWNEKS LÕERYKSLYNTITPVLHIEGGEDDFEDD FDLE	ALLKK LYVKY TITRIKC SIDSYN RPVL ARPVL SWCHIL CRKIYG CRKIYG
HP0316	441 ACCCCCATC GCTATC GCTATC GCTATC GCTATC TACCC TACCC TACCC AAAAAAAAAA	CCCCTAGAAGAAGCCTGGATTTAAAAGGTTTATCGCTCTTTTTAAAACCTTTTTTGCCCAAAGGAAGG	442 PLEE NDLII OONAN IALF KKE KHG GYF GYF GYF TGVI MKIN STEE	PLEESLDLKEFIALFKTIFFAKERDTIALE NDLINKLTKLGTLHEDEIFEIVRRLHYIVVL ONAFKTFTHLLDEIFEIVRRLHYIVVL ONAFKTFTHLKFHERINANVLPPFNDL IALFDDEGKIKOGANATLDALNESLNRL KKESVKIIHHYARSKEL APYLVDTGSHL KKESVKIIHHYARSKEL APYLVDTGSHL KKESVKIIHHYARSKEL APYLVDTGSHL KKESVKIIHHYARSKEL APYLVDTGSHL KKESVKIIHHYARSKEL APYLVDTGSHL KKESVKIIHHYARSKEL APYLVDTGSH KKESVKIIHHYARSKEL APYLVDTGSH KKIGTLSHSLAGKHLFLKFLKFFFFF DSLOARLNFAKAYNLEI-VMPSFTQKK MILENFSHPILKEPKPLIALFFKFKSMLAV TGVNAGGKTMLLKSLLSAFLSKKHLIP MKINAHHSIIPYFKEIHAIINDPQNSANNI STFAGRMKQFSALLSKENMLGVDEIE	KSVKE KSVKE LHYIVV PPFFNI WESLNI WESLNI WESLNI KEDGC KEPDE KSMLA KSMLA SXHLII CODE
HP0316	443 AAAAT TCTTT CTCTT	443 AAAAÍACAGCAAAAAACAGCTITITTAATTTAATCCATCAATTAGAGCGAAAAATCAAAAGATGCAAAATGATAGAATT TCTTTAAAGAAAAAATGGCTAAAGAATTGGAAAAAAGGGATCAAAACTTTAAGGATAAAATAGACGGTTAAATGAA CTCTTGCAAAAAATCAGTCAAGCTTTTGATGATAAAAG	444 KYSI KEKI KISO	KYSKKOLFNLIHOLERKIKKMONDRISF KEKMAKELEKRDONFKDKIDALNELLO KISOAFDDK	NLNELL
HP0316	445 TAAGG ACCG1	445 TAAGGAATTÍCAAGCCCAAACCGAGGGGGGGATTTGGGGGGCTTGGGATCACGGTGGGCATGCGCGATGGCGTTTTA ACCGTTATTGCCCCTTTAGAAGGCACTCCAGCTTACAAGGCTGGGGTTAAGTCAGGCGATAACATTTTAAAAATCAAT	446 KEFOAQ VIAPLEG	446 KEFQAQTEGEFGGLGITVGMRDGVLT VIAPLEGTPAYKAGVKSGDNILKINNES	ZDGVL KINNE

	_	
۲	_	2
	_	
ľ	v	

2/066501 —— 	ш (о∠ш>о>	1.40× -
448 RALGALVINTPTSEGISGAIKKSKELAE 18 SIPDSYLPLOFENDNPAAYYHTLAPEI 90 VOELGTNLTSFVAGIGSGGTFAGTARY 90 LKERIPAIRLIGVEPEGSILNGGEPGPH 10 EIEGIGVEFIPPFFENLDIDGFETISDEE	450 VEQVLADLKNFSKEÓLAQQAĞKNEDF NTGKNSELYQSVKNSVNKTLVGNGLS GIEATALAKNFSDIKKELNEKFKNFNNN NNGLKNSTEPIYAKVNKKKTGÓVASPE EPIYTQVAKKVNAKIDRLNGIASGLGG GQAAGFPLKRHDKVDDLSKVGLSASP GQAAGFPLKRHDKVDDLSKVGLSASP EPIYATIDDLGGPFPLKRHDKVDDLSKV GRSRNGELAQKIDNLNQAVSEAKAGF FGNLEQTIDNLKDSTKKNVMNLYVESA KKVPASLSAKLDNYAINSHTRINSNIGN GAINEKATGMLTQKNPEWLKLVNDKIV AHNVGSVSLSFYDKIGFNQKNMKDYS DSFKFSTKLNNAVKDIKSGFTHFLANAF STGYYCLARENAEHGIKNVNTKGGFQ	452 LLNHAKKTÖSLNĞVEIVGLEHLDKVİYL DÖAPIGKTPRSNPATYTGVMDEIRLFA EĞKEAKILĞYSASRFSFNVKGGRCEKC ÖĞĞĞIKIEMHFLPDVLVĞCDSCKĞAK YNPQTLEIKVKĞKSIADVLNMSVEEAY EFFAKFPKIAVKLKTLMDVĞLGYTTLĞĞ NATTLSGĞEAQRIKLAKELSKKDTĞKT LYILDEPTTĞLHFEDVNHLLQVLASLVA LĞNSMLVIEHNLDIIKNADYIIDMĞPDĞ ĞDKĞĞKVIASĞTPLEVAQNCEKTĞSY TĞKFLALELK
447/AGGGCTTTGGGGGCTTTAGTAATCAACACGCCTACTAGCGAGGGGATTTCTGGCGCCATTAAAAAAGTAAAGAGTTAAGAGTTAAGAGTAAAGAGTTAAGAGTTAAGAGTAAAGAGTTAAGAGTAAGAGTTAAGAGTAAGAGTTAAGAGTAAGAGTAAGAGTAAGAGAAGTTACAGAGAAGTAAGAGAATTACAGAAATTAGCCCTTACGAAAACCTTACGAGATTGTAGCCGGGATTAGCCGGGATGGTGGCACTTTTGAGCCGGGGGTTATTGAAGAGAATTTGAAAGAAGAATTGAGCGAATTGAGCGAATTGAGCGAAGGGTTCTATTTTTTAAAGAAGAAGAATTGAGGGGATTGGCGTGGAGGCTGGAGGGGTTTTTTTGAAAGAGGGTTGATTTGAATGGGGGG	449 GGGTAGGCAAGTGTTAGCCGATCTCAAAAACTTCTCAAAGGGCAATTGGCTCAACAACAACAAAAATGAAAAATGTTAAAAAATTCAACAACAACAACAATGAAAAAATTCAATACAATAAAAACCCTAGTCGGTAATTGAAAATTTTAAAAAATTTTAAAAAATTTTAAATAAAAACCCTAGTCGGTAATTGAAAAATTTTAAAAAATTTTAAATAAA	451 CCTTITAAACCATGCTAAAAAACTCAAAGCTTGAATGGGGTGGAGATTGTAGGGGTTGGAGCATTTGGATGGA
HP1448	HP0431	HP0431

P	CT	EP	01/	15	428
---	----	----	-----	----	-----

2/066501			PCT/EP01/1542
454 YAKNI.SALAGDNALDPVIGREEEILRVI S EILGRRKKNNPLLIGEAGVGKTSIAEAL 99 ALKIAQKEVPEFLQEYEVYSLDLALMVAG GAKYRGDFEKRLKKTLK EIQQNGRIILF 10 DEIHTLLGTGSSNAGSLDAANILKPVLT DGSLKCLGATTFEEYRSYFEKDKAFNR RFSVIKVEEPSKEACYLI.KKIAPLYEEH HQVRYDESVFKACVDLTSDYMHDKFL PDKAIELLDEVGSRKKISIYKKGKKIGVD DVKETLALKLRIPKMRLSSDKKALLRNL EKSLKNKIFAQAEAISLVSINAIKIQHCGL SAKNKPVGSFLFVGPSGVGKTELAKEL A	56 RLGIQKEIFYISVNEENEKALLNCYPNA KNIAGFFHLETDYVGLGIDRQMACLAV NNGVYVDAGSATTIDLIKEGKHLGGCIL PGLAQYIHAYKKSAKILECIPFKALDSLE VLPKSTRDAVNYGMVLSVIACIQHLAK NQKIYLCGGDAKYLSAFLPHSVCKERL VFDGMEIALKKAGILECK	VGNIGGIFRSAYCLGMGUNLDFAKELA VGNIGGIFRSAYCLGMGUNLDFAKELA YEGINSSLGLMYDLPFSVMPNTLDLIN ELKTSGFLCLGASMQGSSOIENISLKK CALFLGSEHEGLSKKILAKMDTILSVKM RRDFDSLNVSVAAGILMCIKIN AGO SAEIFDKRAIDYESLFSRKNRARNFMP RMPKDSHSQGFFTLSINFEGTMEWSA FGIWLSLLLHQYGTQILRI KGIIDIGSGFL	VSINGVMHVIYPPKHILKDDNGSNLVFI MRHLEREKILNSLKGFKDFLGIKGFETO 462 DFKSRDLPQKLHLDKKLSQTIQPCMQL NASKHYTSTGVREPDKCTKSFKKSAL MSYDLALGYLVSKNKQYGLKAIEILNA WAKELQSVDTYQSEDNII4FYMPYMNM AYWFVKKAFPSPEYEDFIKRMRQ
45	456	450	462
453 AATACGCTAAAAATTTGAGCGCTTTAGCCCAAGACGCTTTAGATCCAGTCATTGGCAGGAGAAGAAGAAGATTTTAA GAGTGATAGAAATTTTAGGGCCCAGAAAAAGAATAACCCGCTTTTAATTGGCCAAGCGGGCGTAGGGAAAACCTC CATCGCTGAAGCTTTGGCTTTAAAAATCGCTCAAAAAGAGGGGGATTTTTGCAAAAAAAA	455 GCGTTTGGGTATTCAAAAGGAAATTTTTTACATTAGCGTGAATGAA	457 TGGCTAAGGTGGAACTGCCCTTAGGGGTTTCTTTAAAGAGGGGTTGCTTAGGAATGGTTGTTTGGGTGGTTATTTTAGGAATGGGTTATTTTAGGAATGGGTTATTTTAGGAATGGGTTATTTTAGGAATGGGTTATTTTAGGAATGGGTTATTTTAGGAATGGGTTATTTTAGGAATGGGTTATGTTTTGAATTGGATTATT	ACATTGGAAGCGGCTTTTGGTGAGTATTAACGGCGTGATGCATGTCATTTACCGGCCTAAGCATATTTTAAAGGATC AAAACGGCTCTAACCTCGTTTTTATCATGCGCCATTTAGAGCGTGAAAAAATCTTAAATTCCTTAAAGGGTTTTAAGGA TTTTCTCGGCATCAAGGGTTTTGAAACCCAATAATTTTTCTATTTATGGATAGCTGTTTGCATTTTGATGGGGAAAAGA ACGATGAAGCTTAAAACCAAAA 461 GGGATTTTAAATCTAGAGATTTGCCCCAAAAACTCCTTCGATAAAAAGCTCTCCCCAAACAATACGCCATGCATG
HP0674	HP0674	HP0553	HP1077

「≥ ∺ ≥ √ = > / ここで 1000201	~ P S	1_ u	30	PCT/EP01/15428
464 NAFVLNPPYSASGNGMVFVEQALEKM QSGYASVIIQSSAGSGKAKEYNVRILEKS HTLLASIKMPLDLFIGKSSVQTHIYVFRVV NEKHDAKQRVKFINFSNDGYARANRK KAKASHNLKDTHNAKERYNEVVDLVHI GQSCLKFLSEDDYYENTIDPKNGSDW NQNKPTDTKPELEDFKRTIADYLSYEV	466 ASGRISMNKEAYDAIINHCVKKGPVLQ TAIIAGIMGAKKTSELIPMCHPIMLNGVD IDILEEKETCSFKLYARVKTQAKTGVEM EALMSVSIGLLTIYDMVKAIDKSMTISG VMLEHKSGGKSGDYNAKK	468 APSÍTKDGVSVAKEIELSČPVANMGAO LVKEVASKTADAAGDGTTTATVLAYSIF KEGLRNITAGANPIEVKRGMDKAAEAII NELKKASKKVGGKEEITQVATISANSD HNIGKLIADAMEKVGKDGVTVEEAKGI EDELDVVEGMQFDRGYLSPYFVTNAE KMTAQLDNAYILLTDKKISSMKDILPLLE KTMKEGKPLLII	470 TGDKVRLGDTDLIAEVEHDYTIYGEELK FGGGKTLREGMSQSNNPSKEELDLIIT NALIVDYTGIYKADIGIKDGKIAGIGKGG NKDMQDGVKNNLSVGPATEALAGEGL	W LAGGID I H 472 KKILVIGDLIADYYLWGKSERLSPEAPV PVLEVQRESKNLGGAANVANNLISLKA KVFLCGVVGDDLEGEHFISALKARGID ASGILIDKTRCTTLKTRIIAGNQOIARVD KEIKDPLNADLRKKLLDFFTEKIQEIDGV ILSDYNKGVLDFELTQAMIALANDHHKL ILCDPKGKDYSKYSHASLITPWRTELEH ALHLKLDSHANLSKALQILKETYHIAMP LVTLSEQGIAFLEKGELVNCPTIAKEVY DVTGAGGDTVIASLTLSSMSLKDAC EFANAAAAVVVGKMGSALASLEEIALIL NQTHP
TAATGCCTTTGTTTTAAACCCGCCTTATTCCGCTAGCGGTAATGGCATGGTGTTTGTGGAGCAGGCTTTAGAAAAAATGCCAAAGGCTTTAGAAAAAATGCCAAAGGCTTTAGAAAAAATGCCAAAGCGGGCGTTTAGGATTTTGGAAAAGCGGGGGGTTTAGGATTTGGAAAAGCGGGGGGTTCAAGCGTTTAGGAAAAGCGGTGAACCCATAGGAAAAGCGGTGAAGGGTTCAAAGCCATAGTTTTTAGGGTCAATGAAAAGCGGTAGCGCTAGGGTGAGGGGGGGTAACGGCGAAAAAGGCCAAAAGGCGAAAGCGGCTAGGGTGAGGGGGGTAGGGGGGGTAGGGGGGGTTTAGTGCAAAAAGGCCAAAGGCGGGCTAGAAAGGCGAATTGGAAAAGGCGAATTGTAAGGGGAATTGGAAAAGGGGAATTGGAAAAGGGGAATTGGAAAAGGGGAATTGGAAAAGGGGAATTGGAAAAGGGGAATTGGAAAAGGGGAATTGGAAAAGGGGAATTGGAAAAGGGGAATTGGAAAAGGGGAATTGGAAAAGGGGAATTGGAAAAGGGGAATTAAGAAAAGGGGATTGGAAACGAAACGGGATTGGAAACGAAACGGGATTGGAAACGAAAGCGGAATGATTTAAAAGAGAACGAAACGGGATTAGAAAGGAAGCGAAAGCGAAAGCGAATTAAAAAAACGGGAATTAAAAAGAAGAAGCGAAAACGGAATTAAAAAAAGGAAACGAAAGCGAAAACGGAATTAAAAAAACGGAATTAAAAAAACGGAATTAAAAAAGGAACGAAACGAAACGAAAACGAAAACGGAAAACGAAAACGAAAACGAAAACGAAAACGAAAACGAAAACGAAAACGAAAACGAAAACGAAAAACGAAAAACGGAATTAAAAAAAA	400 MGCAAGCGGTCGTATCAGCATGAATAAAGGGCTTATGACGCTATTATCAATCGTCGTCGAAAAGGGTCCGGTGT TACAGACTGCTATTATTGCTGGAATTATGGGGGGCTAAAAAGCAAGC	46/ ICCAAGCATCACTAAAGATGGCGTGAGCGTGGCTAAAGGATTGAATTAAGTTGCCGGTAGCTAACATGGGCG CTCAACTCGTTAAAGAAGTGGCGAAAACCGCTGATGCTGCCGGCGCGCGC	469 ACAGGCGATAAAGTGAGATTGGGCGATACAGACTTGATCGCTGAAGTAGAACATGACTACACCATTTATGGCGAAGA GCTTAAATTCGGTGGCGGTAAAACCCTGAGAGAGAGGCATGGCAATCCAACAACCTAGCAAAGAAGAATTGGAT CTAATCACTAACGCTTAATCGTGGATTACACCGGTATTTAAAGCGGATATTGGTATTAAAGATGGCAAAATC GCTGGCATTGGTAAAGGCGGTAACAAAGACATGCAAGATGCGGTTAAAACAATCTTAGCGTAGGTCCTGCTAACTGA AGCCTTAGCCGGTGAAGACTTGATCGTAACTGCAAGATGAAACAATCTTAGCGTAGGTCCTGCTAACTGA	471 AAAAAATCTTAGTCATTGGCGATCTGATTGTGGGGGGAAGAGCGAACGGCTTTCGCTGATGTGCCTGAAGGCCTTTAGTGTGGGGGAAGAGCGAACGGCTTTTGGCCTGATAACCTCATTTTAAAAGTTCATTAGCGGAGGGCGAGCGGCTAATGTGGCCTTTAAAAGCCTTTAAAAGCTTAAAAGCTTAAAAGCTTAAAAGCTTTAAAAGCTTTAAAAGCTTTAAAAGCTTTAAAAGCCTAATTTGGCGCAATTTGAAAGCCCAAAAGCTTTAAAAGCCAAATTTTAAAAAACCCGTTGAAACCCGTTTAAAAGCCGCATTTAAGCAAAAAATTTTAACAAAAAAATTTTAACAAAAAAATTTTAACAAAAAA
GCTAGCGGTAATGGCATG AATCAAGCGCCGGCGGGG AAGCCTTAGATTAT ACGCTAAGCAAAGGTGA AGCCACAATTTCAAAGAC CATGTTTGAAATTTCTAGG ACAAACCCACTGACCCA	GGCTTATGACGCTATTATC SGCTAAAAGACAAGCG/ SAAAAAGAGACTTGTAGTT VATGAGTGTGAGCATAGGC GATGTTGGAGCATAAAAGG GATGTTGGAGATAAAAGGTTAGGGATAGGATAGAAGGATAAAAGGATAAAACGATAAAACGATAAAACGATAAAACGATAAAACGATAAAACGAT	GTGGCTAAAGAGATTGAA CGCTGATGCTGCCGGCG CATCACGGCTGCGGGCTAA WAAAAGCGAGCAAAAAG MAAAAGCGAAACTCATCGCT TTGAAGATGAACTAGATG TGAAAATGACCGCTCAATT GGCTACTAGAAAAACCAT	GACTTGATCGCTGAAGTAK AGAAGGCATGAGCCAATCK ACACCGGTATTTATAAAGC ATGCAAGATGGCGTTAAAA	CTGATTATTATTGEGGG GTGATATTATTGEGGGG SGTGAAGATTTAGGCGGA AGTAAAACCGTTGCAC ATCAAAGACCCTTAAACG TATCCTTTCAGATTACAA ACGAATTAGAGTTTGCG CCGAATTAGAGCATGCGC ACTATCGTATCG
463 TAATGCCTTTGTTTTAAACCCGCCTTATTCCGCTAGCGGTAATGGCATGGTGTTTGTGGGAGCAGGCTTTAGAAAAAAGCGAAAGCGCTTTTGTGTGTG	GIAICAGCAIGAATAAAGA NTATTGCTGGAATTATGG SGATATTGATATTTAGAA GGTAGAATGGAAGCGCT SCATGACAATTAGCGGTGT AGACCAATAATCTAAAGAI ATAGAAGTCTAAAAGATATTA	ACTAAAGATGGCGTGAGC AAGAAGTTGAGGAAA TAAAGAAGGTTTGAGGAA TGCCATTATTAATGAGCTT/ STGCAAACTCCGATCACAA STTGAAGAGCTAAGGGC/ TATTTTGTAACAAACGCTG	ACAGGGGATAAAGTGAGATTGGGCGATACAGACTTGATCGCTGAAGTAGAACATG GCTTAAATTCGGTGGCGGTAAAACCCTGAGAGAAGGCATGAGCCAATCCAACAAC CTAATCATCACTAACGCTTTAATCGTGGATTACACCGGTATTTATAAAGCGGATATT GCTGGCATTGGTAAAGGCGGTAACAAAGACATGCAAGATGGCGTTAAAAAACAATC AGCCTTAGCCGGTGAAGGTTTGATCGTAACTGGTGTGTTGACACAATC	AAAAAATCTTAĞTCATAĞĞCĞATÇTĞATÇĞ CCÇTĞTĞÇCTĞTTTTAĞAĞĞCĞATÇTĞAĞĞĞ CTTTAAAAĞCTAAAĞTTTTTTTATĞTĞĞĞĞ CAAĞAĞĞATTĞAÇĞCTTCAĞĞTATİTTĞA AACCAĞCAAATCĞĞCĞCĞTĞĞATAAĞĞA TYCACAĞAAAAATCCAĞĞCGAĞTTAĞAĞĞ CAAĞCAATĞATÇĞCTCTAĞCCAACAĞ TTTATCAAAAĞCÇCTÇÇAAATCTTAAAAĞAA GCTTTTTAĞAAAAĞĞĞĞĞĞTTAĞTCAATT TACĞĞTĞATÇĞCĞTĞTTTAACĞCTCTTTA GĞCĞĞTĞTĞĞTĞĞTĞĞTĞAAAATĞĞĞĞA ÇACĞCT
463 TAATGCCTTTGT GCAAAGCGGTT, TTGGAAAACAC ATCTATGTTTTT, GCTAGAGCGAA AAGTCGTGGAT ATGCCAAAAACC	499 AGCAAGCGGIC TACAGACTGCTA CTCAATGGGGT GCTAAAACGGG CATTGACAAGA AAAATAGAAAA GGGTTTGTTGTT	467 IGCI CCAAGCATC CTCAACTCGTTA CTTATAGCATTT AAAGCCGCTGAA GGCGACCATTTC GCGTGACCCCT TACCTCTCCCCT AAAAAAATCTCTA	469 ACAGGCGATAAA GCTTAAATTCGG CTAATCATCACTA GCTGGCATTGGT AGCCTTAGCCGGG	471 AAAAAATCTTAG CCCTGTGCCTGT CTTTAAAAGCTAV CAAGAGAAAAA TTCACAGAAAAAA TTCACAGAAAAAA TACCATGCGAGT TTTATCAAAAGCG GCTTTTTAGAAA TACGGTGATCGC GGCGCTGTGGT CACGCT
HP1077	98	HP0436	HP0436	нР0436

~	1
٦	٢
-	٠

WO 0

NOCCE01		PCT/EP01/15428
474 GYALAGSSANFEFRAGIO DI NAGI AL NNDISLGRFVNLKVDAHTANFKGIDTG 99 NGGENTLDFSGYTGKVNINKLITASTNV9 AVKNFNINELVKTNGVSVSETTHFSE 05 AVKNFNINELVKTNGVSVGEYTHFSE 05 DIGSQSRINTVRLETGTRSIFSGGVKFK SGEKLVIDEFYYSPWNYFDARNIKNVEI TRKFASSTPENPWGTSKLMFNNLTLG ONAVMDYSQFSNLTIQCDFINNQGTIN YLVRGGQVATLNVGNAVAMFFSNNVD SATGFYQPLMKINSAQDLIKNKEHVLLK AKIIGYGNVSLGTNSISNVNLIEQFKERL ALYNNNNRMDICVVRNTDDIKACGTAI GNQSMVNNPDNYKYLIGKAWKNIGISK TANGSKISV	NNHVIDGADKIKY IIPGSNE TSATLYO TDSESDLAVIRITKONLPTIKFSDSNDIS VGDLVFAIGNPESVTOGIVSALN KSGIGINSYENFIOTDASINFORSGALI DSRGGLVGINTAIISKTGGNHGIGFAIP SNMWVDTYTQLIKTGKIERGYLGVGLQ DLSGDLQNSYDNKEGAVISVEKDSPA KKAGILWWDLITEVNGKIVKNTNELRN KRAGILWWDLITEVNGKIVKNTNELRN LIGSMLPNGRYTLKVIRDIKKERAFTLTL AERKNPNKKETISAGNGAGGLNGLQ VEDLTGETKRSMRLSDIVVGGVLVSQV NENSPAEQAGFRGGNIITKIEEVEVKSV ADFNHALEKYKGKPKRFLVLDLNGGY RIILVK	GNLFGRELESFCVKIQPKNTRALNSEK LYLKLFQKGVIARISCEFVCFEVFSLNE KDFEKIALVLEEILNKA
		1-4
HP0436	HP0436	HP0436

◥	ľ
_	
	ı

2/066501 [순단등업 > 만 5	∀ ≩	l., ≻ ≤	PCT/E
480 KKDACGFIYEISEFMKAYTALLKKQDRYS VYLLRYLPSRYWASILTTALYVKYPDFDS ALKKLLVSYYYOTWIAGGTITRIKQTSINGS IIKNVKSNKSVETIKELILNSIDSYNTFDC- YLYNLWDSSSVYHSKWVRPVLALANY FMADEEKPHFIAMDAETQVEHILPQTP KRGSQWNADFDKEKREEWVNNIANLT LLKRKKNAHALNGDF	482 SLÍÁSVLLÝAYGTGAÍKGFALTTGÍGILA SIÍTAÍVGTQGÍYÓALLPKLTÓTKSLYFW FGVNKRA	484 EKDIAHARFKGNESMYYEENFYHAGF VLIACNYAALCALNKRHSVYVSNNINFY APLELNOEALIKAQVIQDGVKKAEIKIEA FVLDIQVLEGMIEIVVFÖKKPFKFNFKE E	486 IETELGMRLKAHGSLKKIOKPPKNKFK PPKTTIPKPKEASLRLĎLRGORSEEAL ĎLLDAFLNĎALLGGFEEVLICHGKGSGI LEKFVKEFLKNHPKVVSFSĎAPINLĞ
479 GCAAAAAGAGACGCTTGCGGGTTCATCATGAGATCAGCGAGTTCATGAAAAGCCTATACCGCATTGCTAAAAAAACAAAAAAAA	481 TICTTIGATCGCTTCAGTGTTATTATACGCTTATGGCCACAGGAGCGATTAAAAGGCTTTGCCCTAACTACAGGCATTGG GATTTAGCCCTCTATTATCACCGCTATTGTTGGCACGCAGGGGTTTATCAAGCCCTTTTACCTAAACTCACACACA	483 TGGAAAAGATATAGCCCATGCGCGTTTCAAGGGTAATGAAGCCATGGTGTATGAAGAAATTTTGTGCATGCCGGG TTTGTGCTTATTGCGTGCCCGTTTCAAGGGGTAATGAAAGCCATGGTGTTTCAAGATCTCTAATAACATC AATTTTTATGCCCCCCTAGAATTGAATCAAGAAGCACTCATTAAAGCGCAAGTGATTCAAGAAAAGCT AATTTTTATGCCCCCCTAGAATTGAATCAAGAAGCCTTCATTAAAGCTGATTAAAAAAGCT GAAATAAAAATTGAGGCGTTTTGTGTTAAAGGCGTTTTAGGGCGAATGATAGAATTGTGTTTTAAAAGACCCCTCA GCTTTTAAATTCAATTTTAAAGAAGAGGGGTATTAAATGGTTTTTGTTTTTGTCGTGGATAGTTTTAAAGACCCCTCA GGCACTTCTATGACGCGTTTCTTTTTTTTTT	485 GATAGAAACCGAGCTTGGCATGCGTTTAAAAGCGCATGGGAGTTTGTTGAAAAAATCCAAAAAACCCCCTAAAAACA AATTCAAACCCCCTAAAACAACCATTCCTAAAACCTAAAGAAGCGAGCTTGCGCCTTGATTTAAGGGGGCAACGCGGC GAAGAAGCCCTGGATTTACTAGACGCTTTTTTAAACGACGCGCTTTTAGGGGGGCCTTTGAAGAAGTGCTGATTTGCCA CGGCAAAGGGAGCGGGATTTTTAGAAAAGTTTGTGAAAGAATTTTTAAAAAACCACCCCAAAGTGGTGAGCTTTAGCCG
·			
HP0071	HP0071	HP1402	HP1402

V	
Z	ŗ
_	_

WO 02/066501			PCT/I
488 NOAKVPVIYEENHLIPMGFIHLAFRGG GSLSDKNOLGLAKLFAOVLNEGTKELG AVGFAQLLEGKAISLNVDTSTEDLGITL EFLKEYEDEAITRLKELLKSPNFTQNALG GELFANTPLANALGKESIDFDYLAKLTLK OELFANTPLANAALGTKESIOKIKLDDL KOQFAKVFELNKLVVVI.GGDLKIDOTL KRLNNALNFLPQGKAYTEPPFETSDKK SEKVLYKDTEQAFVYFGAPFKIKDLKQ DLAKSKVMMFVLGGGFGSRLMEKI	490 HLKHVKDLKSFLIHARKINLPFIAKELE CESFEEAKNAMNAGALIVMCDNLSVL ETKEIAAYRDAHYPFVLLEASGNISLESI NAYAKSGVDAISVGALIHQATFIDMHM KMA	492 KKDACGFIYEISEFMKAY TALLKKUDKY VYLLRYLPSRYWASIL TALYVKYPDFD ALKKLLVSYYOTWIAGGTITRIKOTSIN IIKNVKSNKSVETIKELILNSIDSYNTFDQ YLYNLWDSSSVYHSKN VRPVLALANY FMADEEKPHFIAMDAETQVEHILPOTP KRGSQWNADFDKEKREEWVNNIANLT LLKRKKNAHALNGDFDEFRRKYGGKDT SKVISCYOITKELYSNYFIKWNEKSLQE RYK	494 LLG I GSSNAGSLDAANILKPYL I DGSL KCLGATTFEEYRSVEKDKAFNRRFSV IKVEEPSKEACYLILKKIADLYEEHHOV RYDESVFKACVDLTSDYMHOKFLPDK AIELLDEVGSRKKISPKKGKKIGVDDVK ETLALKLKIPKMRLSSDKKALLRNLEKS LKNKIFAQAEAISLVSNAIKIGHCGLSAK NKPVGSFLFVGPSGVGKTELAKELALN L
GCCTTTAGGG AAGGCACTAAA AGCACAGAAG TTAAAATCCCC AGCGATTTGA AGCACTAAAGA SGCACTAAAGA CCAGGTGGT CAAGGTAAAG GCAGGTTCC GCAGGTTCC GCAGGTTCC GCAGGTTCC	GCTAAAATIGA CGATAATITGA GAGCGGAAC ATCCATCAAGC AATATITAGAA ATCAGTTAAAA	TAAAAAACAA TTTATGTCAAA SCAGGATCACG AAGAGCTTATA TTATCATAGCA CGCTATGGATG CGCTTTAAACGG ATCACTAAAGA	TAACGGATGG TTTTAATAGGC CCCCTTTATGA CATGCATGATA AAAGGGCAAA GCAGCGACAA GCTGTCAG GTGGGGCCTA
AAGAAAACCATTIGITGCCTATGGGGTTTATCCATTTAGCCTTTAGGGTTTGGGAAAACCATTTAGGCGAAATTATCGCGCAAGTTTTAAACGAAGGCACTAAATTTGGGGCAAGTTTTAAACGAAGGCACTAAATTTGGGCAAGTTTTAGAAGGCCAGCAAGGAAGG	SCTTTTTAACGCATGCCAGAAAAACTTGCCTTTCACGGCTAAAATTGA AAAACGCCATGAATGCGGAGCGGA	SAGATCAGCGAGITCATGAAAGCCTATACCGCATTGCTAAAAAACAA CCCTCTAGGTATTGGGCCAGCATTTTAACGACTGCCTTTATGTCAA TTGGTGTCTTATTATTACCAAACTTGGATTGCAGGAGGCCCGTTTATGTCAA TTGGTGTCTTATTATTACCAAACTTGGATTGCAGGAGGCCCGTTGATGA SAAAAACGTTAAAAAGCAATAAGAGCGTTGAAACCATCAAAGAGCTTATA SATCAATACCTCTATAACTTATGGGATAGCTCTTCTGTTTATCGCTATGGA AATTATTCATGGCAGATGAAGAAAACCCCATTTTATCGCTATGGATG CAAACGCCCAAAAGAGGCAGTCAATGGAACGCGCATGCTTTAAACGG AGGCAAAGACGCGCATGCTTTAAAAGGAAGA AGGCAAAGACGCGCATGCTTTAAAACGG AGGCAAAGACGCCAAGGGGAAAAA	GGGAGCTTGGATGCGGCGATATATTAAAACCGGTTTTAACGGATGG TTGAAGAATACCGCAGCGTGTTTGAAAAAGACAAGGCTTTTAATAGGC CTAAAGAGGCGTGTTTGATTTTAAAAAAGGCTTTTAATAGGC CTAAAGAGGCATGCGTGATTTAACGAGTGATTACATGCATG
487 TCAATCAAGCTAAAGTCCCTGTGATTTATGAAGAAAACCATTTGTTGCCCTATGGGGTTTATCCATTTAGCCTTTAGGGGGGGG	GCATTTAAGGCATGTGAAAGATCTCAAAAGCTTTTTAACGCATGCCAGAAAAACTTGCCTTTCACGGCTAAAATTGA AATTGAATGCGAAAGCTTTGAAGAGGCCAAAAAGCGCGTTGCGGGAGCGGATATTGTGATGTGCGGTAAATTGA GCGTTTTAGAGACTAAAGAAATTGCCGCTTATAGAGATGCGCATTATCCCTTTGTTTTACTGGAAGCGAGCG	491 GCAAAAAGACGCTTGCGGGTTCATCTATGAGTTCAGCGAGTTCATGAAAGCCTATACCGCATTGCTAAAAAACAAAAAGACGAAAAAGACGATTGCTAAAAAAAA	CCCTTTTAGGCACAGGGAGCAGTAACGCTGGGAGCTTGGATGCGGCGAATATATTAAAACCGGTTTTAACGGATGGGGGGATTTTAGGGGGGGTTTTAACGGGGGGGG
TCAÁTCAAGCTAAAGTCCCTGTGATTTATGAAGAAAAC GGGGTGGGAGCTTAAGCGATAAAAACCAGTTGGGTTT GAGCTTGGTGCGGTGGGGTTTGCCCCAACTTTTAGAGC ATTTGCAAATCACTTTAGAAAAAAGAATACGAAG TAATTTCACGCAAAACGCTTTAGAAAAAGGTCAAAAACCC CTATTTGGCTAAATTGACTTTAAAGCAAGAGCTTTTTG GAGCATTCAAAAAATCAAGCTAGACGATTTGAAACAGC GCTTGGGGGCATTTGAAAATCGATCAAAAAA GCTTGGGGGGTTTTGAAAATCAAGGATTTAAA GTGTATTTTGGTGCCCCTTTAAAATCAAGGATTTAAA	489 GCATTTAAGGCATGTGAAAGATCTCAAAAG AATTGAATGCGAAAGCTTTGAAGAGGCCAA GCGTTTTAGAGACTAAAGAAATTGCCGCTT ATTTCACTAGAGAGCATTAACGCTTACGCT CACTTTATTGACATGCACATGAAAATGGC AGCATTAAAAGATCTTACGCCTGAAAAGAAT	GCAAAAAGACGCTTGCGGGGTTCATCTATG GACCGATACGTCTATTTATTGAGAAAAGCTT TACCCTGATTTGACGCTTTGAAAAAGCTT CGCATCAAGCAACCAGTATCAACATTATC TTGAATAGCATCGACTCTTATAACACCTTT AATGGGTGCGTCCTGTCTTAGCCCTAGCT CCGAAACCCAAGTGGGGAAATATTTGCCAG AAAAAGAAAGAATGATAAAAAATTTATGG GGATTTTGATGAAAAAAGAAATTTATGG	493 CCCTTTTAGGCACAGGGAGCAGTAACGCTI GAGCTTGAAATGTTTAGGAGCGACCACTTT GTTTTCAGTCATAAAAGTTGAAGAGCCACTTT AGAACACCACCAGGTGCGTTATGATGAGAA AATTCTTGCCGGATAAAGCGATTGAATTAT AAAATCGGCGTTGATGATGTGAAAAGAAACC AAAAGCCCTTTTAAGGAATTTGGAAAAAATC CAATGCGATTAAAATCCAGCATTGGGGGCT GTGGGGGGAAAACCAGCATTGCGGGGCT
487	489		493
HP1402	HP1402	HP0071	HP0775

02/066501	12002- I	0=	PC	CT/EF
496 CLDNKARFEMIEHVLDKYKSREIFSPFED KVLLMGFLSFGKMLPDMSVPFFVNKINS9 SDTKAMVLDGESQLKERILKRKNEKIIS9 SDTKAMVLDGESQLKERILKRKNEKIIS9 LNVNFIGEEVLGEEEANARFEKYSQALD KSNYIQYISIKITTIFSQINILDFEYSKKEI VKRLDALYALALEEKKQGMPKFINLD MEEFRDLELTVESFMESIAKFDLNAGIV LQAYIPDSYEYLKKLHAFSKERVLKGLK PIKIRFVKGANME	498 ASVLSALLLVGLGAAPKHSVSANDKRM QDNLVSVIEKQTNKKVRILEIKPLKSSQ DLKMVVIEDPDTKYNIPLVVSKDGNLIIG LSNIFFSNKSDDVQLVAETNOKVQALN ATQČNSAKLNAIFNEIPADYAIELPSTN AANKDKILYIVSDPMCPHCOKELTKLR DHLKENTVRMVVVGWLGVNSAKKAAL	500 KGVFGHDNKEKINALLQEKKRFFIDDN LENKHLDTTMVSEFVGKTRAFIKIQEG CDFDCNYCIIPSVRGRARSFEERKILEQ VGLLCSKGVQEVVLTGTNVGSYGKDR GSNIARLIKKLSQIAGLKRIRIGSLEPNQI NDEFLELLEENCHHIALQHSHDLM LERMNRRNRTKSDRELLETIASKNFAI GTDFIVGHPGESGSVFEKAFKNIESLP LTHIHPFIYSKRKDTPSSI.MTDSVSLED SKKRLNAIKDLIFHKNKAFRQLQLKI.NT PLKALVEVQKDGEFKALDQFFNPIKIKS DKPLRASFLEIKEYEIKERENHAVF	502 SSFANEAPÍDMHGGKSAKIERÓSVENS AQKENSKSAILERLKRLREYSKÖHLKA FÖRLQVÓDFDGRIKPLDTISIEYIH	904 IETELSMKLKARGSLLKKIUKPPKNKFK PPKTTIPKPKEASLRLDLRGGRSEEAL DLLDAFLNDAL
	- C - C - C - C - C - C - C - C - C - C			<u> </u>
ACAATAAAGCCGGTTTGAA AAGTGCTTTTAATGGGGTTTT AAGCGACACGAAAGCGATG WAATCATTTTGAATGTGAAT CTCAAGCCCTAAAATCAAGA TTTGAAATTCTAAA AGGCATGCTAAATTGAA AGGCTTAAATTTGAA	497 GAGCGAGITGTTGAGCGCGTTACTTCTTGTAGGCGTTAGGGGCAGCCCCTAAACATTCAGTTTCAGCTAATGACAAA CGGATGCAGGATAATTTAGTGAGCGTGATTGAAAAACGGACCAATAAAAAGGGTGCGTATTTTAGAAATCAAACTTTA CGGATGCAGGATTTAAAAAATGGTCGTTATTGAAGATCCGGACACTAAATACAATATCCCGCTTGTGGTGAGTAAG AAATCTAGCCAGGATTTAAAAAATGGCAACATATTCTTTAGCAATAAAAAGGGATGATGTGCGATTAGTTGCAGAAACC AATCAAAAAGTTCAAAGCCTTAACGCCACCAACAAAAAAAA	499 TAAAGGGCGTTTTTGGGCATGACAATAAAGAAAAGATTAACGCGCTTTTACAAGAAAAAAGCGTTTTTTTT	501 CTICTICGITTGCTAATGAGGCTCCAATTGACATGCGGGGAAAAGCGCTAAAATTGAGCGAAAGCGTAGAA AATTCCGCCCAAAAAGCAACTCTAAAAGCGCGATTTTAGAGCGTTTGAGCGTTTAGAGAGTATTCCAAAGCCGTAGAA TTAAAAGCCTTTCAAAGGCTTCAAGTCCAGGATTTTGACGGCGTTTGAACCTTTAGACAGTATTGAATAT ATCCATA ATCCATA S03 GATAGAAACCGAGCTTGGCGTTTAAAAGCGGCATGGGAGTTTGTTGAAAAAAAA	AATTCAAACCCCCTAAAACAACCATTCCTAAACCTAAAGAAGCGAGCTTGCGCCTTGATTTAAGGGGGCAACGCAGG GAAGAAGCCCTGGATTTACTAGACGCTTTTTTAAACGACGCGCCTTTT
495 GTGCTTGG GTTTGAAAV TAAAATCAC AAAATGAAA AAAAAACTGAA AAAAAACTGC AAAAACTGC AAAAACTGC AAAAACTGC	497 GAGCGAG CGGATGC AAATCTAG GATGGTA AATCAAAA GATTATGC CCACATTG GCTTGGGG	499 TAAAGGGG ACATTTA CAAGAACT AAAATTT AAAAATTGG TGCATTGG GAATTGTT AAGGACAC TTGATTTTT AAGGACAC AAAAAAAAAA	501 CTTCTTCG AATTCCGC TTAAAAGC ATCCATA 503 GATAGAAA	AATTCAAA(GAAGCAAGC
HP0775	HP0775	НР 0775	HP0775 HP0775	

		ATATTOCOCCUTATATATATATATATATATATATATATATATATATAT	1003	O SIXAM INVOINTIONALIVATIVATION IN INTERIOR
HP0775	202	505 CTCAAACCGAGTTAAATTTAGAAAGATTTAGAAAAAAAAA	000	
		AGGCCATGCAAGAAAAAGGCTCAGACAATGCAGAAAAAAAA		MOEKGSDNAEKNPDVKLPEDIYCKOT 9
		CAAACGGCTTTAGAAAGCATGCTAGAAACAACAGACACTTTCCAAGCAAG		ALESMLE (101FQASCIAIALKSKIKDFL KIDICTI KOLOIVIKEANDU VEELEILOS
		ATCAGAGATI II GALAAAATCCCI ATTGAAACCCI LAAGCCCI LACAAA LAAAALAAAGAGGT LACCCGT LACCCGT LATAAAAAATTAAGAAATTTTGCAAAGTAAGGATGTGAGGGCTTTGTTTAAGGGCTAACGGGGAAGTGTTTAGCGCGCAAGTGTTTAAGAAATTAAGAAAATTAAAAAAAA		KINIETEN COMMENT VETEREILES KHVSASLFKANAQVFSALFNHLSYEKK
		TTTTCAATCATTTGAGTTATGAAAAAAAAGCTCCAAATTTTTGAAAAGCATATCCCCATTAAAGAGTTAAACCGTCTTTA		LOIFEKHIPIKELNRLLDENYPAFNRLIY
		GACGAAAATTATCCGGCGTTTAACCGCTTGATCTATCAGGTTATTTAGATCCTAAATTGGATCATTTTAAAGACGCTC		QVILDPKLDHFKDALTKSNATHSNAQT
		TCACTAAAAGTAACGCTACCCACAGCAACGCGCAAACCTTTTTATTCTAGGGATTAATGAAATCTTGCGCAAAAAAC		FFILGINEILRKKPSKALKYFERSEAVVK DDDESKOPAIEMOYI VSKKKTI EPI S
		CCICIAAAGCGCICAAGIAIIIIGAACGAICAGAAGAGCGCIIIGICAAAGAGCGCCTTTCACAAAGCCCAGCTTTAAATCTCTATAGTCT		GSPALNLYSLYAS
		TTATGCGAGC		
HP0775	507	507 ACAAACCCTTTTACCCACCGCTCAAACCCTTTTAAACCATGCTAAAAAACTCAAAGCTTGAATGGGGTGGAGATTGT	208	508 OTLLPTAGTLLNHAKKT(SLNGVEIVGL
		AGGGTTGGAGCATTTGGATAAAGTGATTTATTTAGATCAAGCCCCCATAGGCAAAACCCCACGAGGCAAGCCCTGCA		EHLUKVIYLDQAPIGKIPKSNPALYIGV
		CTTACACGGGAGTGATGGATGAAATCAGGATTTTTTTTTGCCGAGCAAAAAGAAAG		KGGRCEKCOGDGDIKIEMHFLPDVLV
		CCCCITITION OF THE CONTRACT ON THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT ON		QCDSCKGAKYNPQTLEIKVKGKSIADV
		GAAAGGCAAATCCATTGCCGATGTGTTGAACATGAGCGTGGAAGAGGCTTATGAATTTTTGCTAAATTCCCTAAAAT		LNMSVEEAYEFFAKFPK AVKLKTLMD
		CGCCGTGAAGTTAAAAACGCTTATGGATGTGGGCTTAGGCTATATCACTTTAGGGCAAAACGCTACGACTTTAAGTG		VGLGYITLGONATTLSGGEAORIKLAK
		GGGGGGGGCTCAAAGGATCAAATTAGCTAAAGAATTGAGTAAAAAAGACACAGGCAAAACCCCTTTATATTTTAGAT		ELSKKU GK I LYILDEP I JGLHFEDVNH
		GAGCCTACTACCGGTTTGCATTTTGAAGACGTGAATCATCTTTTACAAGTCTTGCATTCTTTAGTGGCGTTAGGGCAAT		LLQVLHSLVALGNSMLVI
		ICIALGCIAGIGALI	510	510 AVYAPIASRLGMSSIKNELEDKSFYYI
HP0775	SOC .	ICTRACKOUR IN TRACKOUR IN THE	,	YPEEYKNIKEYLHKNKOSILLLKLNAFAS
		CGCTTTTGCGAGCAAGTTAGAAAAAAAAACTTTTTGATAGTGGGTTTAGCCATTCGGATTTTAAACTCGTTACAAGGGT		KLEKKLFDSGFSHSDFKI.VTRVKRPYSI
		GAAACGCCCTTATTCTATCTATCTTAAGATGCAACGAAAGGGCGCGGTTAATATTGATGAAATTTTGGACTTGTTAGC	<u></u>	YLKMORKGAVNIDEILDLLAIRILLKNPI
		<u>CATTAGGATTTTATTGAAAAACCCGATTGATTGCTATAAAAGTTTTAGGGATTATCCATTTGAAATTTCAAACCCATTGTCT</u>		DCYKVLGIIHLNFKPIVSRFKDYIALPKE
		CTCGTTTTAAAGATTACATCGCTTTGCCCCAAAGAAAATGGCTATAAGACGATACACACGACCATTTTGATGAATCTTC TCTTATCAACTGCAGATCGCAC		NGYKTIHTTIFDESSVYE/\QiK
HD0775	511	511 CTT A A GO GOTT THE GAA A C C T C C A A G C G C T T C A A A T C C A G T T T T A G G C T C T A A G A G C C C A A A G C C C A A A G C C A A A G C C A A A G C C A A A G C C A A A G C C A A A C A A A A C C A A A A C C A A A A C C A A A A C A A A A A C A	512	512 LRSFRNPHOSASKSSILGSSSLREPKP
2		ACCTGGCGAAATCGCGCTAGCGCATAACGGCATGCTTTTTTTGATGAATTGCCTCATTTTAAAAAGGATATTTGGA		GEJALAHNGMLFFDELPHFKKDILEALR
-		AGCTTTAAGAGAGCCTTTAGAAAACAATAAATTGGTGGTTTCAAGAGTGCATAGCAAAATTGAATAGGAAAAUUUUTTTTAAAAAAAAAA		EPLEMINTLYV SKY HSNIE, TE I STLT VGA ONPCI GGNI I SATKACR CODREITOYK
		GAGAAATCACGCAGTATAAAAACCGCTTGAGCGAGCCTTTTTTGGATAGGATTGATT		NRLSEPFLDRIDLFVQMEEGNYKDTPS
		GGGAATTATAAAGACACGCCGTCGCATTCTTGGACTTCAAAAGAGATGCATGAATTGGTGTTATTAGCTTTCAAGCAG		HSWTSKEMHELVLLAFKQOKLRKGSV
		CAAAAGTTAAGGAAACAGAGCGTTTTTAATGGTAAGCTTAATGAAGAGCAGATAGAACGATTITTGCCCCTTAAACGT		FNGKLNEEGIERFCPLNAEARKLLEGA VERENI SMRSINKVKKVARTIANI NAC
		GAAGCAAAAAGI (GI 166846CAGGCGGG 1 GAAAGG 1 1 AA I CI CI CON I GOOT GOOT TAA AAGGCGCTGAGTTTAAAAGGCTTTTAGAA		EDIEKSHMLKALSFRKIS
		AGATTICTTAAAAGGATTTTTATAAAGGGAGAAAAATGCAAGAATACCACATTCATAATTTGGATTGCCCTGATTGTGC GTCTAAATTAGAAAGGGATTTAAA		

110077	C42 A A TACOCOTA A D A D A D A D A D A D A D A D A D A		•
C/ /OLL	AGAGGTTTTAAGGAATO	AGAGGGGTTTTAAGGGATGAAGAAGGATGAAGAAGTTAGCAAATGGCTTGGCAAAAAGAAAAGAAAAGCACTGAAGCAGCACCCAAAG	514 NRAKEGFKNVSKWLGKNKSTEAAPKE
_	CONCOUNT TO A CO	SANGANAL CANCARCAGE CI GAAGGATCGCTAAAAGCGAGTTAGAGAAGGATACGAA	RVLSDEEINNRAERIAKSELEKDTKLVS
	TO A A CALL CALL CALL CALL CALL CALL CALL	A LAW A A CARACT A GAAAAAA GCGGATCGCTCAACACGGAAAACTTAGATTCGCACA	SHDQYERMKKSGSLNTENLDSHIQAN 9
	TA A A COTTOCO O A A TO A	AAGAGU GAA ICAAAAA I GCTCCAATTCGTGGGCGCGGATAGGAAGTATATGCCCTAC	SLOELNOKLLOFVGADRKYMPYTKAV 10
	COCCACCET COCCACCOCCACCOCCACCOCCACCACCACCACCACCACC	CONTRACTOR CANDITION OF THE SALE CONTRACTOR OF THE SALE OF THE SAL	OISLNNPNLKDLEVIDTPGVNDPIASRF 1
_	CCAICELICCAGGGA	CCCATICAC TICCAGGGAAGAAGGCACCAAAAGCCTTATTGAAAGATTGCGATGTGGTGTTATCATAAGCTCTTCTAAT	ERTKALLKDCDVVFIISSSNOFI TESDM
	CAGILLIAACGGAGAGATATGAGTTT	CGATATGAGTTTGACAGGGTTTCTAACAAAGAAAGCCTTCAAGAAATTTATTT	SLFDRVSNKESLOEIYFVASOADSAVI
	GCAAGCCAAGCCGATAG	SCAAGCCAAGCGATAGCGCTGTTCTATGAGTGAAGTGGAAAAATCTCGCCACCACCACCCCC	SMSEVEKSRHHL
HP0775	515 GCGAGTTAGAACCCCAG	515 GCGAGTTAGAACCCCAGATCACAGACGCTCTAAAACCCTTAGAATTTATCAAAAGATTTTAAAAGTTGTTTGGATATTG	516 FI FPOITDAI KPI FFIKNEKSCI DIGSGA
	GGAGCGGGGCGGGACT	GGAGGGGGGGGACTCCCTGCTATCCCTTTAGCCCTTGAAAAACCTGAAGTCAAATTCATTC	GI PAIPI AI FKPFVKEII I EPRIKDAAEI
	ATAAAAGAGCGGCTTTTTAAACTACCTT	TTAAACTACCTTAAAAGCGTTTTGCCTTTAAAAAATATTGAAATCATTAAAAAGCGTTTAG	NYI KSVI PI KNIFIIKKRI EDVONI I OVO
	AAGATTATCAAAATCTTTACAAGTGGATT		LITSRAVASSEI IEKSOREI KÜKGVEI
	CCAACGCTTCCTAAAAGATAAGGGGTAT	NTAAGGGGTATTTTTATTCTATAAAGGCGAGCAGTTAAAAGATGAAATCGCTTGTAAAGA	EYKGEO! KOEIACKOTECEMILOKO ACI
	CACTGAATGCTTTATGCA	TCAAAAACGAGTTTATTTACAAATCAAAGGA	YKSK YKSK
HP0775	517 ATTCGCAAGCCTATTTG	517/ATTCGCAAGCCTATTITGACGCTTTGCGAACGATCAGCCGCGCGTTTAAAAGTACCCTCAAACGATGTTTAAAAAG	518 SOAVEDAI PTISPAEKNYPOTMEKYÖL
	ATTIGTATTIGTTAGAAA	ATTIGITATI GETTAGAAATTATCGCATTAGGACAATTAGGCATTAAAAAATCCTTACTCATAGACATTGGCACCCAATG	YLI EIIAI GOI GIKKSI I IDIGTOMIKNYP
	GA) I AAAAA I I ACCCGACTGATCCCAATAT	TGATCCCAATATCCCTGAAGCGTTATACTATGTCGCCAAAGCTTTAGACGAGAACAACCA	TDPNIPEALYYVAKALDENNHYKOAMR
	I I ACAAACAGGCCATGCC	I JACAACAGGCCATGCGTTATTACAAACGCATTCTTTTAGAATACAAGAACTCGCGCTACGCTCCTTTAGCCCAAAT	YYKRILLEYKNSRYAPLAOMRI AIFAAF
	GCG111AGCCA11GAAGC	GUELLI INSECUAL I INVESTIGATION OF THE ANALYSIS OF THE TRANSPARCENT THE TRANSPARCE OF THE TRANSPARCE O	GSDLSNANMLFKEAFSNAKDKESASFI
	CAAAGACAAAGAGAGTGCGAGTGAAATCC	CGAGTGAAATCGCGCTTAATTGGGCTGAAGCAGAGATAAAACTATCAAAATTTTAATAACG	ALNWAEAEINYONFNNAKYLIDKWOS
	TCAATACCICALIGATAAGGIGGICCAAT	AGGIGGICCAATCCAACCCTGATTATATTTCTACGCATAGCGAATCAGCCCTAGACTTGC	NPDYISTHSESALDLLKLLKKNOMNAS
	TOTATOTATOTATOTATOTATOTATOTATOTATOTATOT	CANGILALI BANANAAAAACCAGA I GAATGCAAGGGGGGATTGAGATGATGATGATGATGATG	AIEIAHLLLNODDDLKAKEQALYDI GAI
	TASA A COLO A A GAGG COLO TO TATE A T	SCGCTTTATGATTTAGGAGCGTTGTATGCAAGGATCAAGGACTTTAAAAACGCCCACCTT	YARIKDFKNAHLYNLOYLODHAELDKA
		THE STATE OF THE S	SVVRARDEKALFSMEGNTOEKIAHYDK
	A COUNTY OF THE	TI I CCA I SENESESEA CALGECA GARANA I CGCCCACTA TGACAAA TCATTCAAA TTTCCTAATTTCTAATGA	II ONFPNSNEALKALELKAOLL FENKRY
	A & & TTTO COTT & & C.	ASCULLIAMES I I I ASAA I I GAAASCULATI GAAAACAA GOOTTA I GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	AEVLSMÖKNLPKDSPLIÖKTLNVLAKT
	TO A CONTRACT IC	FOR THE CONTRACTOR I I LOUD I I I BA I COMMANDE CONTRACTOR CONTRACTOR CONTRACTOR I I BA I COMMAND I BA I BA I COMMAND I BA I BA I COMMAND I BA I BA I COMMAND I BA I BA I COMMAND I BA I BA I COMMAND I BA I BA I BA I BA I BA I BA I BA I B	PLENHRCEEALKYLSQITTFEFSPKEEI
	119-446-4411		, QAFDCLYFAS
HPU//S	STELLECAL LAAGGCATGTGAA	319 GCATTTAAGGCATGTGAAAGATGTCAAAAGCTTTTTAACGCATGCCAGAAAAACTTGCCTTTCACGGCTAAAATTGA	520 HLRHVKDLKSFLTHARKNLPFTAKIEIE
	AATTEAATGCCAAAGCTTTBAAGAGCCCA	ANTI DE LA PROPERTIE DE LA PRO	CESFEEAKNAMNAGADIVMCDNLSVL
		AMMILIGUEGU I MINGAGARI GCGCALI MICCCI I TGTTI TACTGGAAGCGAGCGGAAC	ETKEIAAYRDAHYPFVLLEASGNISLESI
	CACTITATEACATECACATECACATEAAAATTACCACATAAAAAAAA		NAYAKSGVDAISVGALIHQATFIDMHM
	AGCATTAAAGATCTTACGCCTGAAAAGAAT	CCTGAAAAGAATGAACTCACGCACCGCCTTCTTATACAACTTGCTTAATCAGTTAAAA	KMA
	AAC		

066501		····	PCT/EP01
522 KKDACGFIYEISEFMKAYTALLKKODRY 90 VYLLRYLPSRYWASIL TTALYVKYPDFD 90 VYLLRYLLVSYYYQTWIAGGTTRRIKQTSIN 60 IIKNVKSNKSVETIKELILNSIDSYNTFDQ YLYNLWDSSVYHSKWVRPVLALANY FMADEEKPHFIAMDAETQVEHILPQTP KRGSQWNADFDKEKREWVNNIANLT LLKRKKNAHALNGDFÜEKRKIYGGKDT SKVISCYDITKELYSNYRKWNEKSLQE RYKSLYNTITPVLHIEGGEDDFEDDFDL E	524 LNLAEDSAPLNHPNACKLSLKNAWTR VLSNHEGLHAQEYAIK?ASKMKLAAKL SFLPQIDLSAFYVYLSN PIKMDFASQKQ PG	SZÓ INELGLIC TRICHANDLI INVIVITAINES VIXYHGNI TIISHENNSI VEGLIIIRELTIP LIDMKKWFYYDSONKNIKDLRPYRIEKE KGEDDIVMICEFSRWTIGVRIYEADRIL SKKWTEMEGSAGLGGSAGNIKLVSR TRYFDGRI VQVVDIEKMLIDVFPWIEDE KHNDLETLSKIHSNQCVLLADDSPSVL KTMQMILDKLGVKHIDI:INGKTLLEHLF NPTTDVSNIGLIITDLEMPEASGFEVIKQ VKNNPLTSKIPIVV	ALIEKGKIKDLISLONGTIRIKEMFLOKOL ALIEKGKIKDLISLONGTIRIKEMFLOKOL EVKLAKAFIGKEVSKLFFKHKNAFGVG GTIRALSKVLMKRFCYPIOSLHGYEIDA HKNLAFIEKIVMLKEDCIRLIGVNEERL DSIRSGALILSVVLEHLYTSLMITSGVG VREGVFLSDLLRHHYF-KFPPNINPSLIS LKDRFLPHEKHSGKVKKECVKLFEALS PLHKIDE
521 GCAAAAAGACCTTGCGGGTTCATCTATGAGATCAGCGAGTTCATGAAAAGCCTATACCGCATTGCTAAAAAACAA GACCGATACGTTTTTTTTTT	523 TTTGAATTTGGCTGAAGACAGCGCGCCTTTGAACCATCCTAACGCTCAAAAACTCTCCTTAAAAACGCTGGACTGGACTAGGACTAGGACTAGGACTAGGACTAGGACTAGGACTAGGACTAGGAGTAGGAGTAGGAGTAGGAGTAGGAGTAGGAGTAGGAGTAGAATTAGCGGCTAGAATTAGGCGCTTTTTATGTGCCTTTATGTGTATTTGAGCGATTAGGATTTTGAGCGCTTTTTATGTGTATCTCTCTAACCCATTAAAATGGATTTTGCCAGCGCGCTTTTTATGTGTATCTCTCTAACCCCATTAAAATGGATTTTGCCAGCGCGCAGCAAAAACAAAACAAAACAAAACAAAAAA	525 ATAACGAGTTACAATTGTTGTTTCAGGCTGGGTAAAACAAGGATTTGTATGTGTGGGTCATTGTGTGTG	527 CGCTCTATGGCGGGATTGCGTGCGCGAATTGTTGTTGCATAAAATTCAGGGATTAATGTTGGCGGCGATTCGCATTAAAGGCGGCGATTCGCATTAAAGGCGAGTGCGGCGTTGATTGGCGCGTTGAAAGGCCATTAAAGGCTTTATCCAAAAGGCGCGTTTGATTGCGAGTGCCCTTTAAAGGCCTTTAAGGCTTTTTTAGAAGAAGGCTTTAGAGGTGCCTTTAAAGGCCTTTAAAAGGCGTTGGGTGGG
HP0775	HP1489	HP1086	HP1086

O 02/066501 O co		1	PCT/EP01/15428
(O 02/066201 (O 02/066201	:1≥	808877795055054	2 0 5 1/21 01/15420

02/066501 a m S	<u>3</u> &	>			150	\ \ \ \ \	J 11 :	٠, نـ	X:	> / n	<u></u>	٠.٧	٠ ــــ	-	لرِ	PC
NAVYNDSANDAGETYEISETW LLKKQDRYVYLLRYLPSRYWA TYKYPDFDALKKLLVSYYYQT ITRIKOTSINIIKNVKSNKSVETII IDSYNTFDQYLYNLWDSSSVYI IPVLALANYFMADEEKPHFIAMII VEHILPQTPKRGSQWNADFDK MVNNIANI TI I KRKKNAHAI NDG	RKIYGGKDTSKVISCYDITKELY WNEKSLQERYKSL	SSIPKDTPLSHNPIFWQVVIHL			KNAPKTALKMONNOOIEVLVDS	SGEALPVYKKVGDKVFSGTFN:	ISRLADKVSSVFVPSVIAISILA!	MPREDEWWNFGIALEVEVSVL ALGLATPMSILVANOKASSLGL	SLEKARLVNTIVFÖKTGTLTNG	EYAKEHNAPLKEMSGVKVKTG	CTDYQGTKEIIKVGNSEFFNPIN	KGVKEHIAQIKNLGINTFLLSGD	GKCAFELGIDGYISNAKPÓDKI	.KEKGOIVMMVGDGLNDAPSL .VVMAKGSDVSVQAADIVSFIN	SAIKLSOATIKNIKENLFWAFC	NSVFIPLACGVLYKANLMLSPAIAGLAN
DAGE AYTAL LTTAL AGGT AGGT KWVR KWVR	TOEK NYRK	-VCS/			ALM	SMLS	SKAE	SCPC	KDAK KAK	¥GZ	GISAK		RENV	KIKELISDVA	IKSV ₹	SVFIP
	`			·	534 0	. ш з	<u>. </u>	<u>> 92</u>	<u>ii o</u>	- 2	<u>il :</u>	<u> </u>	<u> </u>	<u>z ≥</u>	<u> </u>	Z
ATGAAAGCCTATACCGCATTGCTAAAAAACAAGACCGATACGTCTATTTATT	AAGCGI AAAAGGACGCGCATGCTTTAAACGGGGATTTTGATGAAAAAAGAAAATTTATGGAGGCAAAGGACGCGAG CAAAGTGATTAGCTGTTATGACATCACTAAAGAATTGTATAGCAATTATAGGAAGTGGAATGAGAAGTCCCTCCAAGA GCGATACAAATCTTTGT	S31 GTITAGAAGACGTTTTATCCAGCATTCCTAAAGATACGCCCTTATCGCATAACCCCATTTTTGGCAAGTGGTGATCC ATTTGGTGTTGGTGTTCAGCGCCTTTTAGCCGCCGTTACCAATAACATCGCTTTTTCGCAAATAAAGCGCATTAAAAGCTTTTTAAAAGCGCATTAAAAGCTTTTTAAAAGCTTTTTAAAAGCGCATTAAAAGCTTTTTAAAAGCTTTTTAAAAGCGCATTAAAAGCTTTTTAAAAGCTTTTTAAAAGCGCATTAAAAAGCTTTTTAAAAGCGCATTAAAAAGCGCATTAAAAGCGCATTAAAAAGCTTTTTAAAAGCGCATTAAAAAGCTTTTTAAAAGCGCAATAAAAAAAA	TTTTTCATGGATTAAAATGCCTTCTTCACGCTTCCCAAATCACTCTATGCCGATACACACAAAAGAAGGAAG	TGATGTATGCAGAGCGCGGATCAATATTGAAACTCCCTAGAAGCGTTAAATTGTCATCAAAACAATCGTTTGCTTGC	533 TGCAAGCCTTGATGAAAAACGCCCCAAAAACCGCCCTTAAAATGCAAAATAACCAACAGATTGAAGTTTTAGTGGATA GGTGGATAGTGGATA GGTGGATA GGTGGATA GGTGGAAATCATAGAGGGCGA	AGGGGAATTAGATGAGAGCATGTTGAGCGGCGAAGCGTTGCCGGTTTATAAAAAAGTCGGCGATAAAGTCTTTTCAG GGACATTCAATAGCCACACGAGTTTTTAATGAAAGCCACGCAAAAAAAA	AAATGATTTATAACGCTCAAAGTTCAAAGGCAGAGATTTCTCGCTTAGCGGATAAGGTTTCAAGCGTGTTTGTGCCCAA GCGTGATCGCTATTTCAAGAGGTTTGTGGTGTGTGTGTGT	GAATCGCTTTAGAAGTGTTTGTATCGGTTTTAGTGATTTCTTGCCCTTGCGCTTTAGGATTGGCTACGCCTATGAGCA	TCAATACGATCGTTTTGATAAAACCGGCACGCTCACTAACGCCTGTCGTTAAAAGCGTTCATTAAAAAGCAAGGCTAG	AATTATTAGAGGTTATTGAGTTTTAGAGTTTTGAAAAGAGTAGCGAACATGTCATCGCTAAAGGGGATTGTAGAAT	ACSCRESSION ACSCRESSION ACCRESSION A	AAAGAAAACGGGATTTTAGTGTTTGTTGGTAGAGCGATCAGTGAAAAAGAAGAAGAAGAAGCTTTTAGGGGCGTTTGTTT	AGANGAL I GCCCAA			
				· ·						<u>·</u>						
		P0071			1P0071				•							
		ATGAAAGCCTATACCGCATTGCTAAAAAACAGCGCGATACGTCTATTTATT		ATGAAAGCTATACCGCATTGCTAAAAAAACAGACCGATACGTCTATHTATTGAGGTATCTCCCCTCTAGGTATTTGCGCATTTTATTACCAGGTATCTCCCCTCTAGGTATTTTATTACCAGGCATTTACCTCAGGTATTTCCCCCTCTAGGTATCTCCCCTCTAGGTATTTATT	ATGAMAGCCTATACCGCATTGCTAAAAAAACAGACCGATAGTCTATTATTGAGGTATTGCCCTATATATA	ATGAAAGCCTATACCGCATTGCTAAAAAACAGACCGATACGTCTATTATTGAGGTATCTCCCCTCTAGGTATTGG GCCAGCATTTAACCACTTGCTAAAAAACCGATCCCTTATTTTTTTT	ATGAMAGCCTATACCGCATTGCTAAAAAACAGACCGATACGTCTATTTATT	ATGAMGCCTATACCGCATTGCTAAAAAACAGACCGATACGTCTATTTATT	ATGAMAGCCTATACCGCATTGGTCAAAAAACCGGTACTATTTTTTGAGGTATCTCCCCTCTAGGTTTTTTTT	ATGANGGCTATAGGGGATTGGTAAAAAACAGGGGGTGTATTTATT	A IGAAAGCCTATACGGCATTGCTAAAAAACCGATTAGTTATTTGTATTTTGTATTTGTATTTTGTATTTTTT	A IGAMAGCIATACOGCATTGCTAAAAAACAGATCGGTAATTATTGGGTATTTTTTTGGTATTTTTTTT	ATGAMGICTIATIACGGGATTGCTAAAAAACAGCGGATTGAGTTTTATTGAGGTTGTCCCCTTATAGGTTGCTATTATTGGGGTTGTTATATTGAGGTTGCCCTTATAGGTTGCTTATATTGGGGTTGTTATATTGAGGTTGCTGCTTATATTGGGTTGCTTTATATTGGTGGTTTTATATTGGTGGTTTTATTGGTGGT	HIGAMACCIATIACCCIATIACCANTACTAMAMACAGCCATACTATTIATICAGGTANTICAGGTATTACTAGGTANTATACTACACTATACTACTACTACTACTACTACTACTACT	AIGAMGCCTANOGGCATTICCTANAMACAGACCGATAGTTATTATGAGGTTTCTATTATGAGGTTTTATATTACAGACTATTAACAGACTATTAACGACTTAACAGACTATTAACGACTTAACAGACTATTAACGACTTAACAGACTATTAACGACTTAACAGACTACTAACAGACTATTATTACTAACGACTTAACACTTATAACGACTTAACACACTACAACACACTACAACACACTACAACACACACACACACACACACACACACACACACACACA	AIGMAGCOTATIOGCATTGCTAAAAAACAGGCGTTTTTTTTTTTTTTTTTTT

				001/15/00
WO 02/066501 ₀	4 4	70 m 7 > 0 > Y	S A S B B B B B B B B B B B B B B B B B	ZU1/13428
11 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		そののなとがに あるに	のののまたのはの出さるとう	5 1

HP0071	535	535 ACTTAAAATTCTGTTAGTGGGGCATTTGATTACGCCCGTCTTTTTATGAGCCATTTTCAAATGTGGCAAGCGTATTT	536 LKILLV	536 LKILLVGHLITPVFFM:SHFQMWQAYFIQ
	3		טטאנט	2 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	_	TEAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	11.1 × 17.7 × 17.1	FOY FVEY AFOVISILIHELKAS
	_	TAXACCACCOCCITATOR ANAMASTOR CONTINUE TO THE C	YSOK	ALSSI VVLLGVSPLLLSNIPYCF
		MANAGECT CLAST HATCH CANADAM CONTROLL CONTROL CONTR	200	MVACETYMONO' NYOFSKEVE
		CAATATCCTTA11G111CA1AGGGG1G1A1GCGCTCA1GG1GG1GGCG11111CAC11ACA1GAGCTA1	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	
	<u></u>	CAATTCTCCAAATTCGTTTCTAAAAACAACATTCCTCGCTCTCATCGCTTTATCAAGCTGTGCGCGTGTGTCAAGCTGTGTGTG	NAME OF THE PERSON OF THE PERS	PLASTLASTORIOVOVILLALASIL
	=	GTGCTAATCTTATCGCTCAGCAGTCTGGAACTGCGTTACTTCTCACCCCTAACTATCATAACCATGCATTTTGCCTTG	LRYFS	LRYFSPLTIITMHFALTLIILFFFLYKAKP
_	-	A COCCETA TO A TOTAL TOTAL TATA TATA A COCCETA A COCCETA TO A TO A COCCETA TO A COC	FDF	
	- '	ACCUTATION OF THE STATE OF THE		
		GOOD TO THE CONTROL OF THE CONTROL O		
		CONCOLI GENOL	G IVO II BOX	ESBLI DVI DOINTOOKIAI VOEDNISEI SBOI A
HP0071	537	537 TTTGCCTTATTTAAGAGACATCGTAACGCAGCAAAAAATCGCCCTTGTAAGACAAAAAAAA	ייין דיין ספט	CHICKOIN I GGNIALVOLOINSI LSINGLA
		ATTAGCCTICATGGCGCAAAGCICCAACGAGIIAGAAAICGCIIIIIAGCCCCICIAIGCIGGAAGCCCAAAAGCI	S CINIL I	SONELEIN OF SMILL SINELING
	-	TTTAAAAGAAGAAAAATTTATGGGATCTTGCACATTCCCTCTGTT11TGAAGCCAATATCCATAAAAAAATTTATGGGATCTTGCAGTGCCTGTA	EKIYG	EKIYGILHIPSHFEANIHKUVPV IIDFYA
		ACGATAGATTTTTATGCGAATTCCAATTACTTTTTGATTTATGGTGCGTTAGCGAATGCGGTGGTGGAGAGCATCAAC	INSNAI	NSNYFLIYGALANAVVESINALNDEIRF
		GCTTTAAATGATGAGGATAAGGTTCAAACGCAATGCCCAAATAGAAGAAGCTGAATTAGGGACAGACGGGATTAAAAT	KRNAC	KRNAQIEEAELGTDGIKIRPIALYNPSE
	_	CAGGCCTATCGCTTTATATAACCCTAGTGAGGGGTATTTGAATTACGCGCTCTCTAGCGTGTTTATTTTGTTTTGCA	GYLN	GYLNYALSSVFIFILHQVMLIASSMFTS
	_ =	CCAGGTGATGCTCATTGCAAGCAGGATGTTTACTAGCTCCAG	S	
U00074	530	ESOLATION AND TRANSPORTED TO THE SECTION AND THE SECOND TO	540 THCN	540 THCNACLWLNOKVLIERLSGVKKVSVN
1 700 1	3	ATTICACCACCACCACCACCACTIGGAATICGTTTTTTTTTT	HILL.	FTTHHLQIVFEKSLNPKEIIQKIESLGYG
		Georgia de Caracter de Caracte	AKIYN	AKIYNAONYTLKAOKEORSYLLTLSVG
		CONTROL OF THE THE CONTROL OF THE TRANSPORT OF THE CONTROL OF THE TRANSPORT OF THE TRANSPOR	FFATM	FFATMNI MFIAIAKYASYGGAN
		2-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1	VO VO	VGAGMDKI MORNI DI VSI ELSI I VI VV
	<u>~_`</u>	G A GGC GGC GGC GGC GGC GGC	148CV	VGREEKGAFYGI KNGVI GMDI SVSEG
	-	AGCI IGI IGGI GI IAGI GGI IGI GGGGGGGGGG	2014	A CAEVYCVVAAAI VCOETVEEASCTII T
	<u>-</u>	CATEGATTIGAGCGTGTCTTTTGGAGCGTATCGGCTGTTATTCCGTTATGGCCATGTTTGAGCGTGTCCCAAGAGACAC	1413A1	
		TTATTTTGAAGCGAGCAGCACGATTCTAACGCTTGTTTTTGGCTCTAAGTTTTTGGAATTAAAAGCCAGGCTGTTTGC	LVFGS	LVFGSKFLELKAKLF/NNEKCLALESHE!
		GAATGAAAAATGTCTGGCCCTAGAATCGCATGAAATCCATAGCGTGATCGTTGTAGAAAATGGCAAGCAA	HSVIV	HSVIVVENGKQTEKHPKDVAIGSVVWV
		AACACCCTAAAGATGTGGCGATAGGCTCTGTTGTTTGGGTGCCAAGCGGGGCTAAAATCGCACTAGATGGCGTGCT	PSGA	PSGAKIALDGVLLNNASVDASLISGEFK
	•	TTTAATAATAGGGGGGGGGGGGGGGGGTGGGGGGGTTGGGGGG	PLELG	PLELGVNDPILGGYVNVGVPFSYQVSA
	. • .	TTTTAGGGGGTTATGTGAATGTGGGCGTGCCTTTTAGCTATCAAGTGAGCGCTAATTTTCAAAACTCACGCCTTTCTG	NOTO	NFONSRLSGLLETLKKSFLEKPLIESSA
		GTTGTTAGAAACTTTAAAAAAGGGTTTTTTAGAAAAGCCCTTAATTGAGAGTAGCGCGAATCAAATTGCGGATTTTT	NOTAD	NQIADIFSKAVLFLAFVSFLLWQFGLGG
		TTCTAAAGCGGTGTTG	NFEKA	NFEKALMVCISVLVIS CPCAFALATPIAL
			VIGVE	VIGVEKNPLIVFKEALFLETLAKVKKIFID
			KTGTL	KTGTLTQKEVLLKEKIIYEEFDGRLLKSL
			LKVRE	LKVREHLAHSAILKSI.DGDEVSLEKIEF
			FAHGE	FAHGLKASYQNETLI.VGSLKFLGSMGV
			DIPMK	DIPMKESANIMVGFAKNETLCALFILEE
			RLKAN	RLKANAKEVVQALQIVKGLELEILSGDN
			ESSVA	ESSVKECAKKLGISNYHAHLTPEDKA(
			TISSY	KGVCAMVGDGNNDALALKQAS
			VSLGF	FKSALSKSACDILLLEEDLSLLK
			KAFDN	KAFDNAGKVYGVVLCNIVLSLIYNAILIF
			VAMLC	3YINPLIASLSNISASSLLVVLN
	1			

٠
•

				O
HP0687	541 A		542 QTL	542 OTLLPTAOTLLNHAKKTOSLNGVEIVC
	₹.	AGGGTTGGAGCATTTGGATAAAGTGATTTAT.TAGATCAAGCCCCCATAGGCAAAACCCCACGAAGCAACCCTGCCA	五	DKVIYLDQAPIGKTPRSNPATYTCN
	<u>ပ</u>	CTTACACGGGAGTGATGGATGAAATCAGGATTTTATTTGCCGAGCAAAAAGAAGCTAAAATTTTAGGCTATAGTGCGA	MD	MDEIRILFAEQKEAKILGYSASRFSFN'9
	Ø	GCCGTTTTAGCTTTAATGTTAAAGGAGGGCGGTGCGAGAAATGCCAAGGCGATGGGGACATTAAAATAGAAATGCA	KG	KGGRCEKCGGDGDIKIEMHFLPDVLV
	<u>U</u>	CTTTTT6CCTGATGTGTTAGTCCAATGCGATAGCTGTAAGGGCGCTAAATACAACCCCCAAACTTTAGAAATCAAGGT	ည်	QCDSCKGAKYNPQTLEIKVKGKSIAD
	<u>ග්</u>	GAAAGGCAAATCCATTGCCGATGTGTTGAACATGAGCGTGGAAGAGGCTTATGAATTTTTTGCTAAATTCCCTAAAAT	N L	LNMSVEEAYEFFAKFPKIAVKLKTLML
	<u>Ö</u>	CGCCGTGAAGTTAAAAACGCTTATGGATGTGGGGCTTAGGCTATATCACTTTAGGGCAAAACGCTACGACTTTAAGTG	VGL	VGLGYITLGQNATTLSGGEAQRIKLAK
	<u>o o</u>	GGGGGGGGGCTCAAAGGATCAAATTAGCTAAAGAATTGAGTAAAAAAGACACAGGCAAAACCCTTTATATTTTAGAT GAGCCTACTAC	ELS ELS	ELSKKDTGKTLYILDEPT
HP0687	543 G	543 GCAAGAAGTGTGCCTTAATGTGAAAAACCACTTTTTGCACAATGAAGAACTGAGCTCTTTAAGTATTATTATTTTAGAA	544 QEV	544 QEVCLNVKNHFLHNEELSSLSIIILEIRL
	∢		PRV	PRVILALLVGASLSGSGVVMQTIFRNPL
	<u> </u>		VD	VDPFLLGISSGAMLGVAMAIAVVESNIA
	Ő	GCGGTAGTGGAGTCTAACATTGCGATTTTGGCGTTTTTTGGGGCGATTTTAGCTAGC	<u>\$</u>	ILAFFGAILASLAVLAMNRVLGNSVLSL
	È	1AGGGTTTTGGGTAATTCCGTCCTTTCGTTGGTGCTTTCAGGGGTGGTGTTGAGCGCGTTTTTAAGCGCCTTAGCCG	NLS	VLSGVVLSAFLSALAGAIKFFVIPQKAQ
	Ö		<u>X</u>	AIVVWLLGSLSLSSYKDCLIAFIGLSLGF
4		<u>AGTIATAAGGATIGCTTGATCGCTTTCATAGGGCTATCTTTAGGCTTTATCCCGCTTTTTGTTAAGGTGGCGCA. </u>	IPLF	PLFLLRWR
HP0687	545 TT	TTGCGGTGGATGGTGAAATCATAGAGGGCGAAGGGGAATTAGATGAGAGCATGTTGAGCGGCGAAGCGTTGCCGG	546 AVD	546 AVDGENEGEGELDESMLSGEALPVYK
	<u> </u>		. <u>K</u> VG	KVGDKVFSGTFNSHTSFLMKATQNNK
	¥.	ACAACAAAAACAGCACCTTGTCTCAAATTATAGAAATGATTTATAACGCTCAAAGTTCAAAGGCAGAGATTTCTCGCTT	NST	NSTLSQ!!EM!YNAQSSKAE!SRLADKVS
	<u>¥</u>		SVF	SVFVPSVIAISILAFVVWLIIAPKPDFWW
	Ĕ	16CACCTAAGCCCGATTTTTGGTGGAATTTTGGAATCGCTTTAGAAGTGTTTGTATCGGTTTTAGTGATTTCTTGCCC	NFG	NFGIALEVFVSVLVISCPCALGLATPMSI
	<u> </u>	TTGCGCTTTAGGATTGGCTACGCCTATGAGCATTTTAGTAGCGAACCAGAAGCGAGTTCTTTAGGGTTATTTTTAA	<u>r</u>	LVANOKASSLGLFFKDAKSLEKARLVN
	<u>¥</u> .	AGACGCTAAAAAGCAAGGCTAGTCAATACGATGCTTTTTGATAAAACCGGCACGCTCACTAACGGCA	TIVE	TIVFDKTGTLTNGKPVVKSVHSKIELLE
	<u>¥ č</u>	AGCCIGICGITAAAAGCGITCATTGTAAAGAAATATTATTAGAGTTATTGAGTTTAGCGCTCAGTATTGAAAGAGTA	เรา	LLSLALSIEKSSEHVIAKGIVEYAKEHNA
4	5	GCGAACATETCECTAXAGGGATTGTAGAATACGCAAAAGAGCTTCCC	2	
HP0687	547 TT	547 TTATTTAGAGGATGCGTTTCAAAATTCATCAAAACCCCTTTAAAAGAGCAAAAAGAGCACCACCTTTAAAAG	548 IYLE	548 IYLEDAFOKFIKTPLKEONSTTLK
HP0687	549 TC	549 TGCTAAAGCCCAAGCAATGCCTATTGTTTTGCATTGCAT	550 AKA	550 AKAGAMPIVLOLHALYNEENNYTOYLL
	<u>E :</u>	TTTAAGCGTGATGTTGCCTTGCATGTGGCTCATTTTATTGCGATTGGCATGCTCAATTTCATTCA	SVM	SVMLPCMWLIFIAIGMLNFICKASNMRE
	<u> </u>	GCGAGAGAGCTTTGATCAGTATTGTAGCGAATGTGTGTGT	IST ITTIS	LLISIVANVCVFSFWGMGMAFYFNLIG
	₹,	<u> AATCICATIGGCATGGAAGGGCATTATGCGCATTTGTCATTGGTCTTTTTGGCGGTAGTTTTA</u>	MEG	MEGHYAHLSLYFLAVYL
HP0687	5516	551 GATAGAGTTTTCGCTCATGGTCTGAAAGCGAGCTATCAAAACGAAACCCTGCTAGTGGGGGAGTTTGAAATTTTTGG	552 IEFF.	552 IEFFAHGLKASYQNETLLVGSLKFLGS
	हें हैं	CAICTIVITIES IS SENTENCED TO THE CONTROL OF THE CANADA SENTENCED TO THE CONTROL OF THE CONTROL O	S L	MGVDIPMKESANIMVGFAKNETLCALFI
	<u> 5</u>	GCGTTATTAAGCGGGGGATAATGAAAGCTCGGTTAAGGAGTGCGCGAAAAAATTAGGGATTTCTAATTATCATGCCT	בונים בינים	LEEKLNANAKEVVUALUNNGLELEILS GÜNFSSVKFCAKKI GISNYHAHI TPFÜ
	<u>ව</u>	CATTTGACCCCTGAAGATAAGGCTCAAACCATCAGCTCTTATAAGGGCGTTTGCGCCGATGGTAGGCGATGGTAG	KAO.	KACTISSYKGVCAMVGDGNNDALALK
	7.	TGATGCGTTAGCCTTAAAACAAGCGAGCGTTTCTTTAGGGTTTGAAAAAGCGCTTTGAGTAAAAGCGCATGCGATA	QAS	QASVSLGFEKSALSKSACDILLLEEDL?
	F	TTTGCTTTTAGAAGAGGATTTGAGTTTGCTAAAAAAAGGGTTTGATAACGCTCAAAAAAAGGTGTTGCT ******************************	T.K	LLKKAFDNAQKVYQVVLQNIVLSLIYN,
	<u>₹ </u>	AAAACATTGATTTTGAGCGCTAGCTCACCCTTAGTGGTCTTAAATTCTTTGAGGTTGAAACGCTCTTAAACAAAC		CIPVAMILG TINPLIAGESMISASSCEV VERS
				P(

1	P	C	Т	Æ.	PΩ	1	1	54	28

G LPGSLNDYSHSGGFFAGVFAWVFKAL VYFLIFWIVILLSLVINIFASIFYTPLVVSY LHQKYYPHVVLEEI:GSILFSIKYFLKSL AFMLLFLAVLTPFYFIPFIGVFGVFFSIV PHFLFFKNTMSLDIASMIFNHGSYGNLL KOHRLKHYRFSFF(YLFSLIPFFNFFAT LLQTLMLTHYFFIFKEKEC	558 IPLITGFGCSVPAYNIATRTLQNYNERLI TLFVIGFMSCSARLIPYVLFVGSFFPSS SAGFVLFCIYILGAVVALVMAKLLKLSV FKGQTESFIMEMPKYRFPSWRMVYFSI YTKSLSYLKKAGTYILVGAILIWFMSQY PKSDAAMKAYKQE SLLVNKDTTLSSEA KEEKLKELKTELDK KNLKNSIVGRGGA YLEKVFSPMDFDW PLSVSLYTGFMAK EVVVSTLGVLFSLGDQNEKSDAFRGIL RKEVSVPSGIAFIVFVMFYIPCFAATITF GREAGGIKFVAYLFIFTTVVAYAFSLIAF YATQILV
	256
555 ATTACCGCAATCTTTGAATGACTATTCCCATTCTCAAGGCTTTTTTGCCGGTGGTTTTTTAAAGCGGTTA GTGTATTTTCTTATTTTTGCACCAAAATATTTTGCGTCCATTTTTTACCCCTTTA GTGTATTTTCTTATTTTTTTTTT	557 TATCCCTTTAATCACCGGTTTTGGCTGCTGGTGCCGGTTACATGGCGACAGGACCTTACAAAACTATAAACGAAC GACTGATCACCGCTTTTTGTGATCGGGTTTATGAGCTGCTCGGCAAGGCTGCCTATTTATGTGCTGTTTTTTTT
P0687	HP0687
	256 2 4 4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7

2/066501=	12-15-24-20	≥ ₹ =	1	PCT/EP01/15428
らなのよび	はれてだがりる	15.85	10 =	1

АТЕСССО САСВОРОВОВОВОВОВОВОВОВОВОВОВОВОВОВОВОВОВОВ	ATGCCCGGATTTGGGTTTATGATCGCAGCGATGGTTTTAACAGGGCAAAATTTAGGGGCAAACAAGCCAAAGATCGC	
563	<u>CACAGAATACGCGCATTTGATTTTAAAAATCTCTATGGGTTTTAATGGGGGTTTTAGGGGATTGTTTTAGTCTTTATTCGCTT</u>	GFGFMIAAMVLTGONLGANKPKIATES
563	AAAGAATTTGCGAGCCTTTTTCTCAAGATGAAGAGTCTTGGAAGTGGCGCGGATCTTATTGATCGCTGTGGCCTT	FSQDEEVLEVARSYLIAVGLSQAPLIG
563		INPIYLLLIHHFKVEFIFVVIASETFLRSF
563	A/IIIIGIAGIGAICGCATCAGAAACTTTTTTGCGCTCATTCATTATAAAGTTTTTTCTAAAGGCATTTGGAAAAG	YYKVFSKGIWKRCGKKA
563	GOOGGEGOOGGCOOGGEGOOGGEGOOGGEGOOGGEGOOGGEGOOGGEGOOGGEGOOGGEGOOGGEGOOGGEGOOGGOOGGEGOOGGEOOGGEGOOGGEOOGGEGOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGOOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGEOOGGOOOGGEOOGGEOOOGGEOOOGGEOOOGGEOOOGGEOOOGGEOOOGGEOOOGGEOOOGGEOOOGGOOOGGEOOOGGEOOOGGEOOOGGEOOOCGCOOOCCCOOCCOOC	
563	GACTTGGTTGGATTTGACAATCACTCTTAATTCTCGCCCACTCTCCATCGCATACGCTTTTTCCACCCCATCAAATTCT	
563	AGGGGGATCTCTTCTAAAGCTTGCATGCGTTTAGCGTATTCTTCATCGCTCTTTCTCCTAGCCCCAGGACGCCCTGC	
563	GCATTGATCACAACCGGATCTTCTTTATGGCGCTTGCACCTCAA	
563	561 CTTTAACCCTAAACCCGTTGTGGGCGGAGCGAGCGGCGCGTTGATAGCGACGATGATAAAAACGGGCGTGGCTAG	562 FNPKPVVGGASGALIATMIKTGVARGI
563	GGGGTTGTATTCTAATGAAGCGGGGTTAGGGAGCTCAGCCATTATTGCCGCGAGCGCTCAAACACGCCACCCGGTG	YSNEAGLGSSAIIAASAQTRHPVRQAL
563	CECCAGECTIAGIGICCATECTCCAAACTITIATIGIAACCTTAATAGTGTGTGTGGGCAACAGCGGGGGGTGATTTA	VSMLQTFIVTLIVCSATASVILMAPEYNT
565		LLPNGEKLSANLLTLKSTEYFLGSLGTV
565	GIATITICI AGGCICA I AGGGACGGIGGIGGIGGITI I TACAACCATGATTTTTGCCTACTCTACCATCATTGGTTG	VIFTTMIFFAYSTIIGWAYYGEKCTEYAF
565	GECTIALIA I GEGEGAAAAA I GCACTIGAA I ACGECCTI I GGT GAAAAAAA GAAATATTACCGCTTGATCTTTTAGC	GEKKVKYYRLIFLASVMVGAMAKIDFV
565	PAGE EL GALGE GEGEGECTAL GEOCHANA I GALLI I GEGEGAATTI AGEGEGATETTETA ACGGEGETTA TEGECTA	WNLADLSNGLMAIPNLIALILLHKVVYS
563	NOCTAIN THE RESIDENCE TO THE RESIDENCE OF THE RESIDENCE O	ETRWYFSKHSNK
563	AAGINAAATGECATGITAAAAAGGECGAGTTTTTGTGAGGTTGTAAAGTGGATACCGCTTCTTAAGGCATAATTTTAGCGCAGTG	
985	563]GATGGTTH AGTCATTTGCCCCCAACTCTTGCTTTTTTTAAAAACTTACAGTCGCTTTTAAAAACTTACAGTCGCTTTTTTTT	Sed MAN WOOD IT EVEKNI EMBASE OF ME
985	TATEGGGGGATTGGGATTGCCTTCGCTTGGGATTTTCCAAATGCACTTGCAAATGCACTTGCAAATGCACTTGCAAAT	SOUTH OF CELETY TRINE WY VELCHINE WAS A TONE OF THE SOUTH
2992		YSGSYNVGIGSGAI FGSIVIHÒI GI GYI
999	CACCAACTAGGGCTAGGATATATTGGCTTTGTGGGTGGGGCTTTAGGTTTGTTGGCGCTCTTTTGGCTTAGATTCAT	GFVGGALGLLALFWLRFITIKFKKT
565	TACGATAAAGTTTAAAAAAACATAAAGGGGTTAAAAGGATTAGCCCAATAAAGGAGAATCCCTTTCGCACTAAAAAC	
565	CATTITITATIGATACCGCTTAATAACCGCACTAACGGATAGATTGTCTCTTTTTATGTTAAAATAGAAAAATTTGTC	•
565	AI AAA I I I AGGI GGGI GI GGTI I AAA I GCTAATAAAAA GATT GATT TGCATAAAGAT CCGATAAGAAAGCT CTTTT	
COC.	IIIIAIIAIIIIAICCCIIIAGCIIIIIACCATIICACIIICACIIICCACTIACTCIATGATAG	
CTATTATO AGCTATA GAGCAAT	GECTITITESTERSCENEATICESCATISTICATION OF THE CONTRACT OF THE C	566 AFGGAIGMGNAAAATITGTARNPGVG
AGCTATA	CTATTATTATTATTATATATATATATATATATATATATA	GKLLTTMFVAMAMIEAQVIYTLVFAIIA
GAGCAAT		LONGLES
	GAGCAATCTCGTGCGAGTTCGAGTCTCGCCCAGTGCACCATTAAGTTTTTTTAAGGAATAAGTGGGTATAATCTCACT	
CTTIGCT	CTTTGCTCTATATACGCCGAAGTGGTGGAATTGGTAGACACGCTAGACTCAAAATCTGGTGGGAGCAATCCCGTG	
2119921	I CGG I I CGAG I CCGACCTI CGGCACCATTAATAG I TAATAGTAATCTITITI CAATCTGCATTI TIATITITI TCAT	

v	٦
v	i
	-

ESNL ESNL ESNL ESNL ESNL ESNL ESNL ESNL	570 QTSNAQTPVTDKKVPLLVVDVWEHAY YIDHKNARPVYLEKFYE HINWHFVSQC YEWAKKEGLGSVDYYINELVHKKA	572 PCVGNMEVELETKENII?YCLGLIKQALE KQMGGRNRQ	476
567 TTCAAAAGATGATGCAAGAAAACCAATACCTTCTCATTGAAGACGCCCTGAAAGATTTGAAAGATTTTAAAAACTTTTAAAAATCAATTGAAGAGTTTCTCAATTCTCAATTGAGAGATTTTTAAAAGCAAGC	AAAAGGGGCAACGCCCAGTTACGGATAAAAAGTGCCGCTTTTAGTGGTGGATGTGTGGGACATTCTCA ATTACATTGACATTGACCATTAAAAACGCCCCGGTTACTTGAAAGTTCTATGAGTGATTGCATTGCATTGCTTTCTCA ATTACATTGACATTGACCATAAAAAAAGAAAAAGAAATTGGAAATTACATTGAATTGCTTCTTTTTTCTACATTGCTTTAAAAAAAA	AACTTACAAAAACAGGGAAGTAGGAACATAGAAACAAAAGAAATATCCCTTATTGTTTGGGATTGATCAAGCGAGCAGGAGCAGCAGGAGCAGCAGGAGCAACAGGCAACAA	573 TGAAGAACTITITGGTGATTITITAAAAATGGAAAATATCACTGAGATTTGTTACAATGGGAACAAGGTTGTTGTTGGTTTACAATGGGTTGTTGTTGGTTTACGTTTACGTTTACGTTTACGTTTACGTTTACGTTTACGTTTATGCGTTTTTTTAAAAATAATGGCGAATTTACGAATTTTTGACAGCAATTTTTGACAGCAATTTTTTTT
HP0687	HP0525	HP0525	HP0525

٠	2
v	٦
_	_

O 02/066501 - O 00	1 . 3	PC
576 EAINYSPSDEIRNRPLFDNLTPLFPDE(S) IKLEYEPTKYTGRMLDLFSPVGKGQR/S) LIVAPPRTGKTELMKELAGGTSNHPESS LIVAPPRTGKTELMKELAGGTSNHPESS ELIILLVDERPEEVTDMQRSVKGQVFSS STFDLPANNHIRAELVLERAKRRVEM GKDVVVLLDSITRLARAYNAVTPSSGK VLSGVDANALHRPKRFFGAARNIEEG GSLTIIATALIETGSRMDEVIFEEFKGTG NSEIVLARNIADRRIYPAFDILKSGTRKD NILLGKDRLTKVWVLRNVMQQMDDIEA	578 YADPSTSKKRADKGLKKVFKDSKKDA CGFIYEISEFMKAYTALLKKQDRYVYLL RYLPSRYWASILTTALYVKYDDFDALK KLLVSYYYQTWIAGGTITRIKQTSINIIKN VKSNIKSVETIKELILNSIDSYNTFDQYLY NLWDSSSVYHSKWVRPVLALANYFMA DEEKPHFIAMDAETQVEHILPOTPKRG SQWNADFDKEKREEWVNNIANLTLK RKKNAHALNGDFDEKRKIYGGKDTSK VISCYDITKELYSNYRKWNEKSLQERY KSLYNTITPVLHIEGGEDDFEDDFD	580 DIKFSTPNOLEGSLNALKNIKLAAFFSKH PDKHNGMEFNEIAKTGIEALYMPGSSD GFDDFRKHLEESIKSFIRAKKNRYGFD KIFDVADIEQEERKVIEWREKERASKO SYKONLQINKIANDLKRDKVVDKRTILS VIDADLDRGFIPPKDLLKGLEKISASLSK DIVIAKOVEKLELSYALIDNIQHNTLDDT LDFTFIVGDSLSVOSLYYTFDLVIDMDR PMSEQFLNHIGELGSFESRERALEWV RLSQAKLIIETPREALKNAQLSQIEEILT GCIFNGAYRLONDLKGNRHGNFK
	OFF A. ESSAGE	579 CAGACATCAACAGCCCAATCAGTTAGAACCATCCCTCAACGCTCTTAAAACCAGCCTAGCCGCTTTTTT CAAAACACCCTGATAAACATCAGTTAGAACTTAATGAAATCCCAAATAGAAGCCTTTATATTATTATTATTATTATTATTATTATTATTATT
HP0525	HP0525	HP0525

ľ		•	
ı		-	۱
	Ξ.	ľ	•

	6	SBI CACCGCAAGAAGAATCATTACCCTTAAAACCCTTAAAAAACCCTAAAGAAGAATCTCATAGTGGGGGACAAACTCCAACAAGAAGAATCTCATAGTGGGGGACAAACTCCCTAAAAACCAAGAAACCAAAACAAAC	582 PQEEIITPKPSKKNPKEESHSGDKLHEOKOEVSLYEPGND KQELKDLFSHLPYKINK/EVSLYEPGND LIDIDGEDSALLIGEKGYIYYKALSYLLF9 WIHPTYGYSIRLEISTFLJNQEKVMDT9 QLQSVIMTVHEVGKGQIAKAPDGVLT*O ALKKLRKAFPNKYVSIKTNLNDEKYIVI*I DFNNE
		CUCUTITAGGUAAGGAGGATTAATTAAAATCAGGGGCCATAAAGGTTTAAAATTCCTCAAAATATCCTCAAAACAACTCACC CAAAAACAAGACTTCACCCCCAGATACGCTTATGTGCACGATATTTTTTCTAATGGTGTTTTATTGGACAAAGCGTTA GTCATTTATTTCAAAGCCCCTTATAGTTTCACTGGCGAAGATGTGTGCGAAATCCAATGCCATGGAAGCCCCTTTTA G	
HP0887	583	583 AAATCATTACTCAAGGCTAGAAGGCTAATGGGGTGATTGTTCTAGCCAAGACATTAACCCAAGCGAGGTGAGAACCTTAAAGCCAAGCTTAAAGCGAAGGTGAGAACCTTAAAAGCTTAAAAGCTTTAAAAAAAGCTTTAAAAAAAGCTTTAAAAAAAA	584 (ITGARKANGVIVLALGDINGLSEVRNA QSFIKNMGQLILYPQRNIDTKDLNDKFG IRLSDTEKHFLENTAVNEYKYLLKNMN DGSSNIIDVSLSSLGNYLQIFSSNSSMV EHIDNLIKHYPKTWREVFVSNKHENFD DKKHLEKVLK
НР0887	285 85 85 85 85 85 85 85 85 85 85 85 85 8	585 AAACGGTGGGCGATGTTTTTGGTGAAAACGGGCTTTTAAACGCGCTAGATCCTACGGAAAGAAA	586 TVGDVFGENGLLNALDPTERKKIDDML LEGIGAHSSGFEKFIVKTI.GIENVENFIN NWYGKQSLSSFANNFVFGGLNQALDK IGSSSDAKDLQNFLDKTTFGDILNQMIE QAPLINKLISWLGPQDLSvLVNIALNSTT N
нР0887	587 FTT 4 0 4 4 7 7 0 8 0 0	TCCAAGCGCACCATCTTAAAAACCTTTTGGAAGCCTTTTATCACCAAAATAAAGAGAGTTTGGGCTTTTTTTCCCCTTA TTTTAGTTTGCGATCTTAAAAACCTTTTGGAAGCCCTTTTTAAAGCAAAACTATTTTTTTT	588 QAHHLKNLLEAFYHONKIESLGFFSPYF SLRSQTPSVSYESALASI.ENYFMALFQ SHFKDDTALQQNFKGLLJAFVSMAKD KRSQIALNAQAKDNAKLITNALLESLSV NFFQSYKISHE JA A A A A A A A

_	
-	7

- 0 0 0 0 0 0		WC
H-088/	588 GGGGI ICTGGAGCCGGGAGGAAAGCCAGCTCTACGGTTTTAACTTTGCAAGCTTCAGAAGGGGATTACTAGCAG TAAAAATGCGGAAATTCTCTTTATGATGGCGCCACGCTCAATTTGGCTTCAAACAGGGTTAAATTAATGGGTAATGT	590 VGSGAGRKASSTVLTLQASEGITSSKIO
	GTGGATGGGCCGTTTGCAATATGTGGGGAGCGTATTTGGCCCCTTCATACAGCACGATAAACACTTCAAAAGTGACAG	GRLQYVGAYLAPSYSTINTSKVTGEVI®
•	Gegraficated Carificated Carcificated Gegestates and Catal Carcas Catal Cata	FNHLTVGDHNAAQAGIIASNKTHIGTLIS
	ACCTAAGGATAAACCTAGTAACACCCACGCAAAATAATGCTAACAACAACCAAC	LWCSAGLNIIAPPEGGYKUKPKUKPSIC
	CACTCAGGITATTAACCCACCCAATAGCGCGCAAAAAACAGAAATTCAACCCACGCAGGTCATTGATGGGCCTTTTG	NSAGKTEIOPTOVIDGPEAGGKDTVVN
	C. I GG I GGCAAAGACACGGTTGCAATATTGATCGCATCAACACTAACGCTGATGGCACGATTAAAGTGGGAGGGTAT	IDRINTNADGTIKVGGYKASLTTNAAHL
	AAAAGU U U HACCACCAAA GCGGCI CA I GCATATCGGCAAAGGCGGTATCAATCTGTCCAATCAAGCGGG	HIGKGGINLSNDASGRTLLVENLTGNIT
	GTATGCCAGGATCAAGGGGAATTTTAAGGTTAAAGGATAAAAAAAA	VDGPLRVNNQVGGYALAGSSANFEFK
	AATAACGATATTAGTTTGGGAAGATTTGTGAATTTAAAAGTGGATGCTCATACAGCTAATTTTAAAGGTATTGATACTG	AGIDIKNGIAIFNNDISLGRFVNLKVD
	GTAATGGTGGTTTCAACACCTTAGATTTTAGTGGCGTTACAGGTAAGGTC	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
HF0887	3911 CAGIAAI I IAI GI GGTAAT GGTAGTAGC GGTAGTAGTAGCACTACT GCTCCGGTTGGCTTATCAACCTTTTAGGG	592 SNLCGNGSSGSSGTTCSGWLINLLGAI
	SCRAIN COCCARCAR GAGCOGGGTT SAN JAA LIGOLOGO GAA TOAT AAAACCGCGGGGTT ATCCAAAATAA TAATGATAGTAGTAGTATTACAAGCGTTT ATCCAAAATAATGATAGTAGTATATTACAAGCGTTT ATCCAAAATAATGATAGTAGTATTACAAGCGGTTT ATCCAAATAATGATAATGATAATGATAATGATAATGATAATAAT	PTNGVSDTNNLINLLTEFIKTAGFIONN DESVETSI TESTONITE ALEGISTICAL
	TTTCAAGCCTTACAAAACGATATTAGCCCTAATGCGATTTTAACCTTGCTCCAAGAGATTACTTCTAACACCACCACCA	DISPINAL DEITSMITTIONESCHIE
	TTCAGTCATTCTCGCAAACCTTACGGCAGCTTTTAGGGGGATAAAACA	QLLGDKT
HP0887	593 GCTCTTTGCAGATATTCCAGAAGCTTTAGAAAACACCCCAAGAATCGCTGATAAATGCGTTTTAGAGATTGATT	594 LFADIPEALENTOEIADKCVLEIDLKDDK
	TECANOLA INVANCA A TECHNOLATION CONTROLLA CONT	KNPPTPPSFKFTKAYAQNEGLNFEDDA
	I SANGAL GALLA TO THE COLUMN AND A COLUMN	SYFAYKAREGLKERLVLVPKEKHDOYK
	TTGTGTGGGGATTTTATCCGTTATGCTAAAGAAATGGGGATTTOTTATAGGCCTAGAAATGCGGAATAGTAAAGAAATGAAAATGAAAATGAAAATGAAAAATGAAAAATGAAAAAA	ERLEKEIEVITNMKFPGYMLIVWDFIRY
	CTTGGTGGCTTTTGCTTTAAAATCACGGATATTGACCCTTTGAATACGATTTGCTCT	DIDPLKYDLL
HP0887	595 GCAATACGACTTTAAGGCGATGTTTACTCCCTTGATCATGCAAGCGCAGTTGAGGAAACATTGATTTTGT	596 OYDFKAMFTPLIMOAQLSLRNIDNFVE
	GGAAAAAGGAGAAAAAAAAAAAAAAAAAAAAAAAAAA	KGSALIDKFDANPYKTIFGERK
	AAACAAATGCTACCAGAGATCAGGAACTTACGATTTGGAATGCGAGTTCTTTTGAAATCACGC	
HP0088	597 ATCAGTGAGGGTTGCAAATGCGTTAAAGAAGGCGATGTGGTTTTGGCAAATACAAAGGCGCAGAAATCGTTTT	598 SEGCKCVKEGDVIAFGKYKGAEIVLDG
	GTAATCATGACCATAAACATGCTAAAGAGCATGAAGCTTGCTGTCATGACAAAAAAAA	TEYMVLELEDILGIVGSGSCCHTGNHD HKHAKFHFACCHDHKKH
	AGGATACAAAATGGCAAAAGAAATTTTCAGATAGCGCGAGAAACCTTTTATTTGAAGGCGTGAGACTCCA	
	1940-0-1 1940-1940-1940-0-4940-0-4949-4-4-4-4-4-4-4-4-4-4-4-	
	AGAAGTAGCGAGCAAAACCGCTGATGCTGCCGGCGATGGCACGACGACGCG	

-PCT	/FP	Λ1	115	428
-r U 1		U L		720

10.02/066501			PCT/EP01
600 RSFDDDDENSVSDS:KKDEDNEEDEE! EERKKVVSEKDKREVEKVGESFKALDS KAKKEWLKALEAPIDEREDELVRSLTL9 AYKROTLKDRIVDLEPTSKLINELVKTIS ETTLKSGDGFEKELIKLEYKLPLFNDT9 LIANHKKILANITNMTKEDIIAQVPEATM VSVYMDLKKLFLTKEASEGFDLAPNK LKEILEQIRRGKLISCRAKNKMAKSNLR LVVSIAKRFTSRGLFFLDLIQEGNIGLM KAVDKFEHEKGFKF STYATVWWIKQAIS RAIADQARTIRIPIHMIDTINRINKVMRK HIQENGKEPDLEVVAEEVGLSLDKVKN VIKVTKEPISLETPVSNDDDGKFGDFV EDKNIVSSIDHIMRFGLLDDESDRTLEEIG KELNVTRERVRQIESSAIKKLRSPQYG RILKNYTRERVRQIESSAIKKLRSPQYG RILKNYTRERVRGIESSAIKKLRSPQYG	GHEKRDVELINT I FAGA GENERAL GENERAL GENERAL GENERAL TANKSOSGELAFREMTMVOKIKAVDK VIDENIRPMLMMDGGDLEILDIKESDDY IDVYIRYMGACDGCMSATTGTLFAIEN ALOEILDRSIRVLPI GEDLNNFIKSVIDEI	ATGSNEIIIAMESDICHLHLMVQYIPRMS ISSIISRIKQITTYRVVRDKRFIPLLQKHF WKEKTFWTDGFFVCSIGEANPETIKAYI ENQG	606 KELNRFNQSGANSIJSHIKDMFADRKTL EEDIKNAYDDLFDYPIDDIEGMTSAIVS MSAMNELVKVSRAINTLKERYNLIRTS NDKKILSLKEKIDIEIGIHKISSMLHOKAK HLHALKNINEPKNPNDLMILEDLIALLDF KIEFKERK
599 AGGAGCTITGATGATGACGATGAAAATAGCGTGAGCGATTCTAAAAAAGATGAGAGAGGAGAGAGA	601 GCTCAATGATTTAAAAAGCGTTGAAGAAATCACTAACTACCAAAGCCGGTGCTTTTTGTAAAAGCTGTGTGTG	603 GCCCATITGATITIAGIGIGIAAATACAGAAAAAGITGITGCAAGGGGGAITIGAACAACITIAATIAAATACACAATAGATTAGAT	605 AAAGAATTAAACCGATTCAATCAAAGCGGTGCCAATAGCGATTCTCATATCAAAGACATGTTTGCGGATCGTAAGACTTAAAGACTTAAAAACCGATTCAATGAAGACTTTTGATTAGACGATTCAAAACGCATTGAAAAGACGCTTTGAAAAAGATTTGAAAAAGACGCTTAAAAAGACGCTTGAAAAGACGCCTTTGAAAAGAACGCTTCAAAAGAACGCTTCAAAAGAAAATTGAAAAAATTGAAAAAATTGAAAAAAATTGAAAAAA
HP0088	HP0088	HP0088	HP0088

٠.	7	٦
	_	
۰	_	۰

	<u> GCGTTTGTGATTTCAGGGTTAGCTAATAGCTCTATCCAAGAAGCCAAACAGCGGGTTGAATCGGCTTTACAAAATAAC</u>	VISGLANSSIGEAKORVOSALONNOFIN
	GATTICACTITICCCGCCTTTAAAAATCACCATCAACCTTTCCCCCTCAGATTTGCCTAAATCCGGGGGTCATTTTGATT TGCTATCGCTCTTTTAATCGCTTTGCAAAAACAAGAGTTGGCTTTTAAAGAGTGGTTTGGGGAGTTAGGGC TTGATGGCAAGAATCAAACCCAATCCTAACAAGAGTTTTTCCCCATTTTTTTT	FPPLKITINLSPSDLPKSGSHFÖLLGN ALGKGELAFKEWFAFGELGLOGKIKPIG PNIFPMLLDIAIKHPHAKIIAPKANEELFG LIPNLQCFFVGHFKEALEILGNPETKAU THTKKLPFKTIELNDKEYYF
TCCAAAGCC AAATGAAAC GCGAGCGT	609 TATCCAAAGCCCTAAAGTTACCACTTATGACTTAAAGCCTGAAATGAGCGCTAAAGAAGTAACCCTTGCGGTGTTAGA GCAAATGAAACTAGGCACGGATTTGATCATTGTGAATTTTGCTAATGGCGATATGGTAGGCGATACGGGGAATTTTG AAGCGAGCGTCAAAGCGGTGGAAGCAGTGGATGCATGTTTAGGGGAAATCCTTTCACTGGCTAAAAAATTGGATTAC GCCATGCTTTTAACCAGCGATC	610 IGSPKVTTYDLKPEMSAKEVTLAVLEQ MKLGTDLIIVNFANGDMVGHTGNFEAS VKAVEAVDACLGEILSLAKKLDYAMLLT
ACTANA ACANA ATCATTGO ATCATTGO ATTATAGA AGATATTT CTAATATA AGCTAAACA ACTAAACA	611 TATCCATTAGGGGGGTATATTCAACCAACAGAAGTAGCATAATCTAAAAGGCCCATTTGATTTTGGTTTTAGTGTAAATACA GAAAAAGTTGTGCCAAGGGGATTTGAACCAACTTTTATTAGGTCTGTTATAGATAG	612 YPLRGYISTNRSKHNILKAHLILVCKYRK KLLGGLINNFIKSVIDEIATÖSNFIIIAME SDIDHLHLMVÖYIPRMSISSIISRIKQITT YRVWRDKRFIPLLÖKHFWKEKTFWTD GFFVCSIGEANPETIKAYIENQG
TTGTGGTG TCCATTGA AATCATGA TGTGGTTA TAATAAGA	613 GTTTGTGGTGCTGTGCGATGGGGCTAAATGCAATCTTGGCGAGGTTTAGAATTGCTAAAAGAAATGAACCATATCT TATCCATTGAGATTGGAAAGATCGCGAAATTAGACAATGTCATGTGTGCCAGGTTTGCCTAAAACCAGGGGGGG AAAATCATGAGAAGGCTTTTGAAATCCATCGCCAAAAAAGAGCCTATCACTCAGGATTTAAGCACGCTAGAAGATGTG AAATGTGGTTAAAGAAATAATGAGCATCGCTCAAATGGAGGTAAAAATCTAAAAAATGCTTTTTAGCCTTTTTAGCCAA	614 FVVLCDGAKCNLGESLELLKEMNHILSI EIGKIAKLDNVMYVPGLPKTRSGKIMR RLLKSIAKKEPITQDLSTLEDVNVVKEIM SIAQMEE
GGGGTATAT GTTGCAAGG GATGGAAGG ATCAACGTTTTG AACTTTTTG ATCAAGGTTA GGGATTTCTC CCCTAAAAT CTTAAGCTG CTTAAGCTG CTTAAGCTC TCATTCCTTG GCTTAGAAT	615 GGGGTATATTICAACCAACAGAAGTAATCTAAAAGCCCATTTGATTTTAGTGTGTAATTACAGAAAAAGTT GTTGCAAGGGGATTTCAACCAACAGAAGTAATCTAAAAGCCCATTTGGATTTTGGAATTTCCATTATTCATTGC GATGGAAAGGGGATTTGAACTTTATTAGTCTTGATTATTCCTAGAAAGAA	616 GYISTNRSKHNLKAHLILVCKYRKKLLO GDLINNFIKSVIDEIATGSNFIIIAMESDID HLHLMWGYIPRMSISSIISRIKGITTYRV WRDKRFIPLLGKHFWKEKTFWTGGFF VCSIGEANPETIKAYIENGG

ス.m.る.r.を	FJJKSOSKI PCT/EP01/15428

AAA 618 GEAAYDNEGTKLVMKYD LNEEGYGNEGAA SRRYEDRGFVAOMGGEAIKDLLEEID CATC TLLQSLKEEVKDTNSDAKKKKLIKRLK CGG VESFLNSGNRPEWMMLTVLPVLPPDIS RGTA CGG RPLVALDGGKFAVSDVNELYRRVINR CGA ATG CALKRLMELGAPEIIVRNEKRMLQEAV TAA KGKQGFFRQNLLGKRVDFSGRSVIVV GDNLKMDFC	620	TCAG 622 GIENKGLNKDKLIELGVLGKSDNDGKT GGG YLRFLDRIMFPIYSPSAQVVGFGGRTL KEKAAKYINSPQSKLFDK:SSLLYGYHL KEKAAKYINSPQSKLFDK:SSLLYGYHL AKEHIYKOKQVIVTEGYLC VILLHOAGF KNAATLGTALTPSHLPLLKGDPEILLS YDGDKAGRNAAYKASLMI AKEORRG GYILFENNLDPADMIANGCIETLKNWLS SCG GONILFENNLDPADMIANGCIETLKNWLS HPMAFIEFVLRRADSYLI.DDPLEKDK ALKEMLGFLKNFSLLLOSE:YPKTEKPNR PORFAHVSSAPSLEFLEKI.VIRYLLEDR SCC SCA GALHVSSAPSLEFLEKI.VIRYLLEDR SCC SLLDLAVGYIHSGVFLHKKGGFEKE LRILLILRYFERQLKEIPKSSLPFSEKMIC-
617 GGCGAAGCCGCTTATGACAATGAAGCCTAAGCTTGTGAATACGATATTTTGAATGAA	619 TAAGGATAGAGGAAAAACCATTATCCATTAAGGGGGTATATTCAACCAAC	621 ACGGCATTGAAAATAAAGGCTTGAATAAGGACAAGCTCATTGAATTAGGCGTGCTAGGCAAGAGGCGATAACGATCAGGACCAGAATTTGAAAAAACCCAAAACAAAACACATAAAACACCAGACCATAAAGCCAGACCATAAAGCAGCCAGAATTTGATTGA
HP0088	HP0088	HP1298

1310 00/06/504				
$WO_02/066501$ $\omega \omega \geq$) w	1>≥> 1	· · · · · · · · · · · · · · ·	PCT/EP01/15428
子 クッロボ クリゴツ	完产品品产	では、これには、	↑Q 出済 スプ L S シ J	1> : </td
にいるはまならかれ	活をたとさ	はなるのとはん	しゅうしょくいん	100 m

H 1298	PASICACION CACCGA AAATGTI ACAAA ATGATI ATGATI ATGAGAG GCGCCAA AAAGCAA AAAGCAA AAAGCAA	bzsicucicia i Guccegeati i Gegiegegegati i Getatada attica gegatea coatagatattega gegegeta de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccio de la infeccio de la infeccio de la infeccio de la infeccio de la infeccio de la infeccica de la infeccio de la infeccio de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccica de la infeccio de la infeccica de la infeccica de la infeccio de la	624 LYGGIACANLLHKNSGITIDIGGGSTEC ALIEKGKIKDLISLDVGTIRIKEMFLDKEN EVKLAKAFIQKEVSKLPFKHKNAFGVVG GTIRALSKVLMKRFCYPIDSLHGYEID, HKNLAFIEKIVMLKEDQLRLLGVNEER DSIRSGALILSVVLEHLKTSLMITSGVG VREGVFLSDLLRHHYHKFPPNINPSLIS LKDRFLPHEKHSQKVKKECVKLFEALS PLHKIDEKYLFHLKIAGELASMGKILSVY LAHKHS	GGGSTEC EMFLDKET CHGYEID GVNEER MITSGVG WINPSLIS MGKILSVY
HP1298	625 CAN AGN CAA(AAG1 AGC1 AGC1 AGC1 AGC1	625 CAAACTTAAACGCACCCAAACCCTTATTIGAATGTTTIGTAGGAGTTAATCTGGCCAAAGCCCAAATATTATTCTAAAAA AGAAGAAAGAGAAAAAGATGATCTTGAAGTTTTTGTAGAAATTATTCTTTTTGAAGAAAAAAAA	626 NLNAPKPLFECFVGVNLAKAKYYSKKE EREKEKMILNFCKIFEIILFEAIQKQPKP DFKNKDELLGDYPNLKNLDSLREVRED FLKRAFKNDEASLGAYVLVLLSCKYFE SVFEKVQEWLDFIARLIALRGHVHKIT	KYYSKKE IOKOPKP ILREVRED LSCKYFE HVHKIT
HP1298	627 AGAR TATE GGGI TTAT TTAT AACA AACA AACA ACCC	627 AGACCAAGAAAGAAGGACTCAAAAAGAAGCTAAACAGCGCCAACAGATCCCTGATCATAAGAAACCTCAA TATGTCTCTGTTGGTAAAGGACTCAAAAAGAAGCTAAACAGCGCCCAACAGATCCCTGATCATAAGAAAGCTTT TATGTCTCTGTTGGTATAGCGCTTTGAAAAGCAGCGCTGTTTGATATAACGACACCTTGGATTACAACAACAACTT GGGGATTGGTTTGGT	628 TKKEAKPLKKEAKÓROGIPĎHKKPQYÝ SVDDTKTOALFDIYDTLNVNDKSFGDW FGNSALKĎKTYLYAMDLLDYNNYLSIE NPIIKTRAMGTYADLIITGSLEQVNGYY NILKALNKRNAKFVLKINENMPYAQATF LRVPKRSĎPNAHTLDKGASIDENKLFE OOKKMYFNYANDVICRPĎĎEVČSPLR ĎEMVAMPTSĎSVTQKPNIIAPYSLY	HKKPQY DKSFGDW DNYLSIE EQVNGYY PYAQATF DENKLFE :VCSPLR
HP1298	629 TCCT TCAA TCAA TGAA TTATI TTAY CTGC CTGC CTATI	629 TCCTAGCGATAGCGCTTGGAGAACTAATCTTGTTGTGCGGACTAATAAAGCCTTGTATCAATTTGATTTTGAGAATAGC TCAAAAAGACAATTTGCTTTGAGAATCTTGATGAGACTAATAGAATAGCCGAAAGACACGAAGTTTGAGCGTTAT TCAAAAAGACAATTTGCTTCAGCGTATCTAACAGTCAATTAGAAAAAGACACGAAGAAAATCTTAACCCACAG TCAAGAGGAGTTAAAAAAGAGAAGAAGAAGAAGAAAAATAAGAGAAAATCTTAACACCACAG CCTACATCAATAGAGTGATGAGGAGCAATGAACAGATTATCAACAAAGAAAAAAAA	630 PSDSAWRTNLVVRTNKALYQFILRIAQ KDNFASAYLTVKLEYPQRHEVSSVIEE ELKKREEAKRQKELIKQENLNTTAYINR VMMASNEQIINKEKIREEKQKIILDQAK ALETQYVHNALKRNPVPRNYNYYQAP EKRSKHIMPSEIFDDGTFTYFGFKNIL QPAIFVVQPDGKLSMTDAAIDPNMTNS GLRWYRVNEIAEKFKLIKDKALVTVINK GYGKNPLTKNYNIKNYGELERVIKKLPL	VESVIEE VSSVIEE VTAYINR VITAYINR VILDOAK VYYOAP GFKWITL VPNMTNS VPNMTNS VYKKLPL
MP1298	631 1GAC TCGG AGGA AGAT	631 IGACTCTTGTGCCTATTTTCCACGATGAAAATTGATTGGGTGGG	632 TLVPIFHDEKLIGWVGGVTHVIDTGSV O PGSMSTGQVQRFGDGYMITCRKTGA DESFKDWLHESQRSVRTPKYWILDEFE TRIAG	ORKTGA CRICTGA WILDER
	•			//

•	T	EP	01	/1:	5428	3
---	---	----	----	-----	------	---

N 1/	•
VV	•

				•
HP1298	659	b39 A4GATGAATAAATTGCGGACAGCGCCAAGTAAGGAACAGCCCAAGCCATTGGGTGAAATGCCCTAAATGTT ATGCGTTAATGTATCATAAGAAGTGTTTAGTAAATACAGCGTGTGTTTGAAATGCCATTACCATTTCGCATTTCGCATTGAAAG	640	640 FKINKLRTAPSKEEQPSHWVKCPKCYN
	<u> </u>	CGGCTGAAAGGATTGAATTTTTATGCGATGTGGGGGGTTTTGAAGAGTTTGACAAGCATTTACGGCCTAATGATCCTT		EMITHEVEST SVCLACHT HFKMKA)
		1AAAT11CG1GGATAAAGAGGGGTATAAACAACGCATTAAAAAATACGAAAAAAGGACTAAACCGCCCAAGCTCAGTGA		VDKESYKORIKKYEKRTNRPSSVISGI
		I CAGCAGA GAGGACA AAAA AAAA AAAAAAAAAAAA		AKINRMPLQIVVFDFSFMGGSLGSVEG
		CAGCGAGTGGGGGGGCTAGGATGCAAGAATCCACTTATTCGCTCAAAAAAAA		EKIVRAINRAVAKREALLIVSASGGARIM
	<u></u>	CCGATTGAGTGAGGCCAAACTCCCTTTCGCTCTTAAGCGATCCCACTTATGGGGGCGTTAGCGCATCTTTTG		GEST TSCMUMAKTSAALNKLSEAKLPF IST SOPTYGGVSASEAST ODI 114 FBCA
	_	CTTTTTAGGGGGTCTCATTATCGCAGAGCCAGGGCGATGATAGGCTTTGCGGGGGCCTAGGGTGATTAAAGCAAAC		MGEAGPRVIKOTIGADI DEGENTAERI
	<u></u>	TATAGGGGGGGATTTGCCTGAGGGCTTTCAAACAGCGGAATTTTTATTAGAGCATGGCTTGATTGA		LEHGLIDMIVHRKDLKKTLSDI JAMMTH
	<u></u>	ACAGGAAGGATTIGAAGAAGACTTTGAGGGATCTCATGGCTATGATGACGCATAAGACTTCAAAGATTTTTAAAGTT TTAACATTGATGGTTGCGTGGTGTTATTCTAT		KTSKIF
HP1298	6410	641 CAAGAAGCGAAGTGGCCAATGACGGGCGAATTGACTTTGAGCGGGAAGTTTTACCCATACGAGGGTTTGAAAGAAA	643	642) DOE VANTOELTI SOCIA DICOLA
		GTTGATCGCTGCTTTTAAAGCCGGCATTAAAACCGCTCTCCTTTCCTGTCAAAAATTACGAAAGGGATTTAGACGAAGAT	7 10	AEKAGIKTAI IDVKNYEDDI DEIDAEVE
-	<u></u>	CCCTGCTGAAGTGCGAGAAAATTTAAACATCGTTGCGGTGAAAAACATCGCTGAAGTGTTAGAAAAAACTTTGCTTTG		FINI NIVAVKNIAEVI EKTI
	<u> </u>	AAATTTGGCATGAAAGCAGCATTATTGGTTTAGGGCCTTATGGGGGGGG		
	-	GGCGTTTTAAAAGCGTTATAGGCTATGATCATAACGCTTTGCATGCTAAATTGGCTTTGACTTTGGGGCTTGTAGATG		
	V V	<u>AATGCGTGGGATTTGAAAAGGATTTTAGAATGCGATGTGATTTTTT</u> GG		
HP1298	643.0	843 CTGATGGGCTAAGCATAGACCCTAAAAGCAAGCAAGTCATTAACGATAGCTTCAATCGTTTTGAAGACGGCACACCC	644	644 DGLSIDPKSKOVINDSFNRFEDGTPPE
	۱ ر	CLOSASASACEGECES I I CECTITITI ECITICA CATA CONTRA A A CACA GECA A GEGECA GESTI		KNGDFAFLLHIIKSLKNTGKGAVILPHG
	<u>- C</u>	CACCCCAT SECOND STATE SECOND S		VLFRGNAEGAIRKNLLTKGYIKGVIGLA
	<i>y</i> (4	COCCECTOR SALVANICATION TO A TANK THE SALVANICATION OF THE SALVANICATION		PNLFYGTSIPACVIVLDKENARARKGVF
		SCHOOL STATE OF STATE		MIDASKDFKKDGNKNRLREODVOKMI
	, <u>1-</u>	1969 Section 11 Control of Contro		DIFNAYKEIPYYSKMVSLEEISANDYNL
_	<u> </u>	TIGITICSCTTTAATCAACACACACACACACACACACACACACACA		NIPRYIDARPESERULFALINSHKASYLP
	<u> </u>	GTGTTTAAAGAGGTTAAAAAGAGGTTTTTAAAAAAAAAA		KNEIKAYAPYFUVFKELKNILFKKSDKE
	<u> </u>		,, .	SYYALK I ECENIKELIIQSSEFQTFHASV
SA . M.O.	A	ATTIATITICA ACTITITICA CONTINUE ACCOMPANDA ACTITION ACTIT	- -	LNAFURLULFETFUHLEPGF
MP0072	645 <u>C</u>	645 CAAACAAAAGGTTTCAAACTATTTTTAGGGGTTTTGCCTAAAAGCTATTCTATGAGCGAAGAAAACAACATTTTAGGC	646 K	646 KOKVSNYFL GVLPKSYSMSFENNII GL
	 - <u>.</u> (TIGIATICATICAGCATTICTTGCTCACTAAAACGAAAACTTAGTGGGCATCCTCCGTTTAGAAGGGGTTAGCTACACC		YDEHFLLTKNENLVGILRI EGVSYTHI S
	<u>u (</u>	CATTIAAGCACAGAGCAATIGCAAGATCTTTTCACCGAGCGCCAGATGGCGTTGGATTCTTTAGAAAAGTCGTGGC		TECLODIFTEROMALDSLEKVVARLVV
	פ פ	GOSTO 1616611AAAAGGCG1AAAA11GA1GACCAACAAAACATTCAATTCTGAATACTTGCAAGCGATTTT	<u>×</u> _	KRRKIDHQQNIQSDSQYLQAILNGFEN
	<u> </u>	TICEASCATA ACAMACAM CAMACAM CAMACAM CAMACAM CAMACAMA	<u>×</u>	KEVYENOYFLVLESTHSLHGVLEHKKK
	<u>- F</u>	FECANOMY CTTTAN MACCITATION WITHOUT THE PROPERTY OF THE PROPER	<u> </u>	SLMHANRENFKDILSYKAHFLOETLKS
	<u> </u>	ACCACACACACATACATACATTACATTACATTACATTA	<u> </u>	LEIOLKNYAPKLLSSKEVLNFYAEYING
	<u>: </u>	TGGCTAGTICTATCACTTTTGAAAAAGATTATTTCATTCAAAAAAAGATTATTAAAAAAAA		OLPLKPLVGGYLSDSYIASSITFEKDYO
	<u>0</u>	CATTAAAGCTTATGAGAGGAAAGGATCACTTCTATAGCGATCGGAGCGCTTTTATACCAAGAAAGGCCTTTAGATAT	<u> </u>	GALLYOFTPI DIFSIFPMSVHKTI SFI FE
	È	TATCTTCTATAGAGCCTATGAGTGTGTGCATAAAACGCTGAGTTTTTTAAAAGAGGGGCCAAGTTTAGCATGTCCAA	, m	ERAKFSMSNLVKNELI FYÖEL VKTKRIÖ
	<u> </u>	TCTCGTTAAAAACGAGCTATTAGAATACCAAGAACTGGTCAAAACCAAACGCCTATCCATGCAAAAATTCGCCCTAAA	S	SMOKFALNILIKAPSLENLDAGTSLVLG
	<u>3 F</u>	CALICLIAICAAAGCCCCCIAGIIIAGAGAAIIIAGACGCICAAACAGCTIGGTTITAGGGCTTTTATTAAAGAAAT	<u> </u>	LLFKENLVGVIETFGLKGGYFSFFPERIG
		ò lòu	Ξ.	LNHRLRFLTSKALACLMVFERON 12

PC	'T /	EP	11/	114	54	28

020001	12 1/1 1/1 1/1 1/1 1/1 1/1 1/1 1/1 1/1 1	-
7/00/4	OFFIRI GAMANU CAUCUUAAAAGAGI I AGAUAAGI I GAI GUI CUACI A GCI GGAGAAI I GGOI AAAAAAGGGAAAGAAAA AGGGATTAAGGTTAAGCTTAAGAAGGGGGTAAGAGGGAATAATAATAACTAATATATAAGAAAGA	A 648 MKLTPKELDKLML 4YAGELAKKRKEFO
	AGACTGCGGCTGAATTGATGCAAGGGCGCACTCTTTTAAAACCGGATGATGGATG	
	GATCCATGAAGTGGGTATTGAAGCGATGTTTCCTGATGGGACAAAACTCGTAACCGTGCATACCCCTATTGAGGCCA	
	ATGGTAAATTAGTTCCTGGTGAGTTGTTCTTAAAAAATGAAGACATCACTATCAACGAAGGCAAAAAAGCCGTTAGCG	
	1GAAAGTTAAAAATGTTGGCGACAGACGGGTTCAAATGGGCTCACACTTCCATTTCTTTGAAGTGAATAGATGCTTAG	
	ACTITGACAGAAAAACTITGGGTAAA	ĞK
HP0072	649 CCC1111GAGCCTGAAATCAATTCCAAGAATTTGCAAGGGGGGCTTTAATGGGATCTATGATGTTATTTAAAGAAAT	920
-	CCA1G1G1GGATT1GCCCACGAGGGCTAGGATCTTAAAACAAATCACGCTCACTTACCAAGATATTGATGGCTCTATCCA	CA DLPTSARILKQITLTYQDIDGSIHSKVVG
	TTCTAAAGTCGTGGGCATTGATAAAGGCATTGATTGGCATTACCCTTTAAAAGCTCTCCCAACACACCCTTGATCCAGC	
	CGCCTTGAAAAACGCTACCAGATCCAAGACTTTGATTTTTAATGGCAAGCAA	
		T VNPYRIVLDTQKGIPLDIYQNMDLNQKF
	CAAAACATGGATTTAAACCAGAAGTTTTTTCTCACATTAAAGTCGGCACGCAC	FSHIKVGTHKDYYINTLILDGKYRYLLEE
	ATTITAGACGGGAATACCGCTATCTTTGGAAAAAAAAAAGGGGGGGTATGAATTGA	
HP0072	651 AAGGAGTICTATCGTGCATGCTTTGGTGGGTTTGAAGACAACTCTATCATCGCGCATTTAGCGAGGGGAGATATGC	C 652 RSSIVHALVEFEDNSIIAHLASADMQLPI
	AN I ACCCATARGO AT GO SAT COM A GO TO THE AGO CONTRATORAGO CONTRAGATO TA TAGA CONTRAGA TO TATA CONTRAGA CONTRAGA TO TATA CONT	_
	AAGCGCGATTAAATTTGAACCCATTAGCATGGAGCGCTACACTTTGTGGTGTTATAAAGACTTACTGCTAGAAAACC	
	CTAAGCTTGGCGTGCTGAATGCGAGCAATGAAGTGGCGATGGAGTTTTTAAACAAGAGATGTTTTGGT	3T ASNEVAMEKFLNKEIAFGGLIQTISQAL
	GGCCTTATCCAAACCATTTCTCAAGCCTTAGAATCATAAGATAAAATGCCTTTCAAGCTCTCTAGTTTAGAAGAGA	3 (ESYDKMPFKLSSLEEVLELDKEVRERF
	CTGGAATTAGACAAAGAAGTTAGGGAGCGTTTTAAAAATGTAGCGGGAGTGTAGTATAATAAGATTTTGCTTCTAATA	
	GCGTTTATTAAAGAGAGTTTTATGGGGTTAAAAAATAAAATCAAGGGTTTTATTAAAGAGAGAATGCCTTTGT	
	GGTTAGATATGTTCGTAGTTTAAAAGGGGCCAAAAACATTTATGATGAAATCAATC	
	GGCTAA	
HP0072	653 CTAAAAGCCCATTTGATTTTAGTGTGTAAATACAGAAAAAGTTGTTGCAAGGGGATTTGAACAACTTTATTAAGTCTG	G 654 LKAHLILVCKYRKKI_LQGDLNNFIKSVID
	TIATAGATGAGATAGCCACCCAAAGCAATTTCATTATCATTGCGATGGAAAGCGATATAGATCATTTGCACTTAATGG	EIATQSNFIIIAMESIJIDHLHLMVQYIPR
	TICAATATTCCTAGAATGTCTATTAGTTCCATTATTTCTAGAATCAAACAGATCACTTATAGAGTTTGGCGTGAT	
	AAGAGAIITATCCCCTTATTGCAAAAACACTTTTGGAAAGAAAAAACTTTTTGGACTGATGGTTTTTTGTTTG	
	CGGTGAGGCTAACCCTGAAACGATCAAGGCGTATATAGAAAATCAAGGTTAATTTTACTCATAGGGTTTTTATAGTTC	
	CTAGCGGAACTAAAGCATTCATCCCAAACACTAAAGATATTTGGGATTTCTGCTTGGGTGGTTTAAAAATTCCATTCTT	<u></u>
	ICTAACAATCTTATTTTAAGCTCTTGTAATTTTTCTAAATTTGGCTTAGGCGATTCCAAAAGCTCTCTATCTTTTGG	
	IAAGATTTCTTTAAACTGGCTTTCTAAAAGATCATAATTACGCATAACTCCATCATCAAACCCCTCTTGTGTGGC	
	GCGIAAAGCATGGATAGATAGGTTGGGGGCCATTTCTTGTTTTGCTGCTTTTAATTGGCTTTAGCTTTTC	
	ACCCALACAGAALAAAAAAAGCICICALITTITCTATTICAATTCACTGATAGGCGAACTATAG	9
	I ASCETUTAGESCITCT CAALICCAAAATTITICTATATTITICATAATCCCTAATTITICCAGTTTTTTTTCTCAC	
	GCT I I CAR GAGCE I I CAGCAAAC I CI CI CAAI CGCI CATI CAAI CI TI CATOTI GTATI	
	IIIIIIIIAGCACAAATTAAAAGTGGGCAATCCCCCTACTTTGATGCGCTCACGCGCATTGTTAGTCGCATC	

١	ć	2
١	3	5

_	ACAACAGCACCCTGAATTTTCAAAGCGTTCTTTTAAATGGTGCTCTAAACCTTTTAGGCAATGGCAGTAACAATCTAG CGATCAACGCTAAAGGGAATTTTAGTTTTGGGTCTAAAGGGATTTTGAATCGTCTTATATGAATCTATTTGGGGGGG	FYANHSOISFTKLATFNSDASFDLSNNO STLNFQSVLLNGALNLLGNGSNNLAIP9 AKGNFSFGSKGILNLSYMNLFGGDKK
	ATAAAAAACTTCCGTTTATGATGTGTTGCAAGCCCAAAATATTGATGGCTTAATGGGGGAATAACGGCTATGAGAGA TCCGTTTTTATGGCATACAGATTGACAAGGCTGATTACTCGTTTGATAACGGCGTTCATTCTTGGAGATTCACTAACC	SVYDVLQAQNIDGLMGNNGYEKIRFYT IQIDKADYSFDNGVHSWRFTNPLNTTE
	USU I CAATAUGAU I GAAAUGA I I ACAGAAACCI I GCATAACAACCGCTTGAAAGTGCAGATCTCTCAAAACGGCGTT TCTAATAATAAGATGTTCAATCTCGCTCCTAGCTTGTATGATTACCAAAAAAACCCTTATAATGAAACCGAGAATTCCT	TITETLHNNRLKYQISQNGVSNNKMFN I ADSI YOYOKNDYNIETENSYNIYTEONY
	ATAATTACACAAGCGATAAGGTTGGCACTTATTATTAACGAGCAATATCAAAGGCTTTAATCAAAACAATAAAACACC	GTYYLTSNIKGFNQNNKTPGTYNAÓN
	CGGGACTTATAACGCGCAAAACCAACCCTTACAAGCCTTACACATTTACAATCAGGCTATCACTAAGCAAGATTTGAA CATGATCGCCAGTTTGGGTAAGGAGTTTTTGCCTAAAATAGCCAAATTTATATCTTTAAGGCGCTT	QPLQALHIYNQAITKQDLNMIASLGKEF
657	GATAAGATAGATATTGACACGCCTAATTGGAGTTTTGTCGCCTCAAGGCTTTTTTGTATGATTTATACCATAAAGTAA	658 DKIDIDTPNWSFVASRI FI YDI YHKVS
	GTGGTTTTACAGGGTATAGGCATTTGAAAGAGTATTTTGAAAACGCTGAAGAAAAGGGCCGCATCCTTAAGGGCTTT	GFTGYRHLKEYFENAEEKGRILKGFKE
	AAGGAAAAATTICAATCTAGAGTTTTTAAATAGCCAGATCAAGCCTGAAAGGGATTTCCAATTCAATTATTTAGGGATTA	KFDLEFLNSDIKPERDFOFNYLGIKTLY
	MANCOTTOTATORICOUTATITOTTANA GARGEORI ANCARCACTOTATIGATITICA CONTRA TATORI TATO	DRYLLKDANNNPIELPQHMFMSIAMFL AQNEOFPNKIAI FFY
629	659 GGGCGTTACCATTTGATCGCCGGTGAAAGGCGCTTAAGAGCGAGC	660 GRYHLIAGERRLRASKLAKMPTIKAIVV
	11G11G1GGATATTGAGGAAGAAAAAATGCGTGAAGTCGCTTTGATTGA	DIEGEKMREVALIENIGREDLNPLELAR
	GGAA GGC AGAIC IA AAAGAATI GCTTGAAAGCTATCAAATGACCCAAGAAGAGAGCTGTCTAAAATCGTTAAAA	SYKELLESYOMTOEELSKIVKKSRAHV
_	ANTOCOCHOUCH INTERPRETATION IN THE FOR	ANIMRELTESSKYONALLEEKITSGHAK
	GGCAGAAACTCAGCGTGCGCCAGACAGAACATTAGCGCCGTGATTTTAAAATAAACGCAAATTTGACAATAAAAAA	DI ARDEKINANEDNKKHGEKOTOTI IA
	CATGETTICAAGCAAACCCAAACGCTCATCGCTGGAGATGAATTAGAGCGCTTGAATCAAAGTTTGTGGGATCATTA	GDELERLNOSLWDHYKLKAALKGNKIV
	CAMBELLAMAGEGGGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	LRCYENSLLEAFMKKMMS
	TGCGAGTTTCAAATATTTTGTAGGATTTTAGGAAAGAAATAGGTTATGAATATGGTTAACGGTTAACGGTTAAATGGCGG	
	TCGTTTTTGTGTTTGTTGTTATTGTTATGGCCGATGAATGTTTGCGTGTATAGGCCTTTGTTGCTTTTATGGATAA	
	CAGACAGECCAGAGAGAGAGAGAGAGAGAGAGAGAAAGAA	
	TI BAGGCTGT CON AAAGAAGCGGCT GAAAAACGCAGAAAAAAAAAAAAAAA	
661	661/AAAAAGCTTTCCACTTTTCAAGAGCTTGTGAGCGTGTATTACGGCATGGTGTTAAACGCAGAAGTGGCTGAAACTTTA	662 KKLSTFOELVSVYYGMVLNAEVAETLE
	GAAGAGGTGGAAAAAAGGCCCATTATAAGCATTTCCAAAACGCTTTGAAAATGCAAAAAGTGGGGCAAATCGCTAGGGT	EVEKGHYKHFQNALKMQKVGQIARVE
	RGRARCCTTAGGCCCTCARGTGCCTTAGAAAGGCCCCATATTAAAGGCCCCATAAAGGCCTTAAGAAGACGTGTAAGAAGTTT	TLGAQVAYDKAHIASVKAKDVLEVSQL
	AVADATOTIC CONTINUES OF THE TITLE TITLE TO CONTINUES OF THE TITLE TO CONTINUES OF THE TITLE TO CONTINUE OF THE TITLE TITLE TITLE TO CONTINUE OF THE TITLE TI	SFNSILSSKDDLVPSSKLEIRTEKNLPD
	TCAAATCTCTAAAGAAAACACGAAATTACAGATCGCTAAATTTCTTGCCCAAGTGAGTTTTTTTGGCTCTTATATT	LSFFVSSTLNSYPVLKTLENGIGISKEN
	<u>GAAGCAAAACAATTCGGTGTTTGAAGACATGATCCCTAGTTGGTTTGTGGGCGTGGCCGGGCGCATGCCTTT</u>	PLANCISCHE COLLEGE COL
	CTCCCACAGGGCGCATTCAAAATACCAAGCGAGCAAATTAGCGGAGTTGCAAGTGAGTAGCGAACAAATCCAGGC	ASKLAEL OVSSEOIOAKKIMELLVIKTÜ
	<u>TAAAAAAACATGGAATTATTAGTGAATAAGACTTATAAAGAGACGCTTTCTTATTTGAAAGAATACAAAAGCTTGCTT</u>	YKETLSYLKEYKSLLSSVELAKENLKLC
	1CTAGCGTGGAATTAGCCAAGGAAAACTTAAAAACTCCAAGAGCAGGCTTTTTACAAGGCTTAAGCACGAACGCTCA	EDAFLOGLSTNAOVIDARNTLSSIVVE 3
	AGICATTIAATGGCGTTAAGCGATCATATTGATTTAT AGCGAATTTAATGGCGTTAAGCGATCATATTGATTTAT	OKSVAYKYIVSLANLMALSDHIDL

ľ		۰	٠	٠
ī	ı		۰	٠
٦	۰	٠	•	•
٠		-		

10000	ERITATE A A CONTROLLE CONT	664 NEGNDLLEEAEEVIKAVASDCEFALAF
- co/04H	CACATTICA A CARACTA A CACATTIC	FEEKRCYIRNHVISEFLHHFNQLEGI
	CASA CONTRACTOR AND AND A TAGGA TAGGA BATTATICA BETT CONTRACT TO THE TAGA BATTATICA BA	TNKKDSMENIQLDVSNTLKIIDKNLKMI9
	I COMMON AND AND AND AND AND AND AND AND AND AN	SFDTLGAVGNVVGGFSMGFGLAAG
	A ICTURAGE FOR THE CONTROL OF THE CO	VGSVGLLAGPTLAIFGALRAEMEK
	CLICAL GEAGE ANALOG AND A CONTROL OF THE CONTROL OF	EDAKAYCSQVEAAVKKAD AMIDNLQA
	CATTO AT A TOTAL CANDA CONTINUE CONTINU	VRKMADLFTRQITKFDALFFSLAQEAIA
	CALLES OF THE CONTROL OF THE CALL OF THE CALL OF THE CONTROL OF THE CALL OF TH	TMKKHNYDFSHYNOKEQDOLATASST
	VALVACATIVE LINES AND ACCEPTABATE AND ACCEPTAB	LKTLGAFLKVPIMDKHQKLNEATQSKL
	AGCTCATGAGGCTACACAAGAGGTAGGCTAGAGTTATGCAAAGGGAGATGAGTAGCCTAGAAGCTAAGCATTATGAT	EFMQREMSSLEAKHYDSVKIKFGLVRR
102001	ICAGE AAAA CAAAA 1 GGA	666 MFGGONFSDFARSRGPSEDLDDILSSI
HPU/65	CALONIA DE LA CALONIA DEL CA	FGKGGFSQRFSQNSQGFSGFNFSNFA
	CECCCTEAAAATTTAGACATAACCGCCGCTTTAAATGTCTCTGTTTTAGACACCCTTTTAGGCAATAAAAACAAGT	PENLDITAALNVSVLDTLLGNKKQVSIN
	CASCATOR ANALYSIS OF THE SECOND AND SECOND A	NETFSLKIPIGVEEGEKIRVRNKGKTGR
	AGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TTRGDLLLEIHIEEDEMYRIYEKDDITQIF
	CERCEACA ACCEPTATE COCCANATO THE SETT ACCOUNT A COCCANA A COCANA A C	DLPLKTALFGGKJEIATWHICTLTLTIPPN
	Transport Anna Contrata Contra Contra Contra Contra Contra Contra Contra Contra Contra Contra Contra Contra Con	TKAMOKFRIKEKGIKNRKTSHVGDLYL
	CAAAAACAGAAAACTTCGCATGTGGGGGATTTGTATTTGCAGGCTCGTTTGATTTTGCCTAAAACTGAAACTGAAACGCTTTC	QARLILPKTETLSNELKALLEKEL
	TAATGAGTTGAAAGCGTTATTAGAAAAGAATTGTAAGGAGGAATC	
020001	EEST CASCATT ATTITATOCOCT TTATATGGGTGGGGCAAGATT CACGATGGTGCGCATT GCGGATTT GATGCAAAAAGATG	668 SIIYPLYMGGARFTMVRIADLMOKDAN
HF00/Z	SAME AND A STATE OF THE AND A	EVYRLKKLSTFOELVSVYYGMVLNAEV
	CACA A CETECT CACA A CA	AETLEEVEKGHYKHFQNALKMQKVGQ
	CASSOCIATOR TO THE STATE OF THE	IARVETLGAQVAYDKAHIASVKAKDVLE
_	CTAAAAAACTTTAAAAAGTTCACAACCTCTCCATTTCAATTAAAAGATTAAAAAGATTAAAAAAAA	VSQLSFNSILSSKDDLVPSSKLEIRTEK
-	A A TTAGAGAT COGCACGGAGAAAAA TOTGCCCGATCTGAGCTTTTTTGTTTCTTCCACGCTCAATTCCTACCGGTTT	NLPDLSFFVSSTLNSYPVLKTLENQIQ
	TA A A CONTITUTE DA DA DA DA DA DA DE COCCAA DE COCAA DE COCCAA DE	SKENTKLOIAKFLPOVSFFGSYIMKON
		NSVFEDMIPSWFVGVAGRMPILSPTGR
	CCGGGCCATGCCTATTCTTCCCACAGGGCGCATTCAAAATACCAAGCGAGCAAATTAGCGGAGTTGCAAGT	IQKYQASKLAELQVSSEQIQAKKNMEL
	GAGTAGGGAACCAAATICCAGGCTAAAAAAAACATGGAATTATTAGTGAATAAGACTTATAAAGACGCTTTCTTATTT	LVNKTYKETLSYLKEYKSLLSSVELAKE
	GAAAAGAATACAAAAAGCTTGCTTTCTAGCGTGGAATTAGCCAAGGAAAACTTAAAAACTCCAAGAGGGGGCTTTTTACA	NLKLOEQAFLOGLSTNAGVIDARNTLS
	AGGCTTAAGCACGAACGCTCAAGTCATTGATGCGAGGAACACGCTTTCTTCTATCGTCGTGGAGCAAAAAAGCGTG	SIVVEQKSVAYKYIVSLANLMALSUHID
	GCTTATAAATACATCGTTTCATTAGCGAATTTAATGGCGTTAAGCGATCATATTGATTTATTATGAATTTGTTATTA	LFYEFVY
	AGGGAAAAAICALGI	

-	•

(0)	677 I CGTAGATGCCCTGAAAGAATTAGAAGAAAAGACTAAAGAACAAGA 678 I CGTAGATTAGAAGAAAAAAGAAAAAGAAAAAGAAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTTAGAAAATTTAGAAAATTTAGAAAATTTAGAAAATTTAGAAAATTTAGAAAATTTAGAAAATTAGAACAAATTAGAACAAATTGAGGAACAAATTAGAACAAATTAGAAAATTAGAAATAGAACAAAGAACAAGGACAAATGGAACAAATTAGAATAAAACAAATTAGAATAAAAAAATTTAGAATAAAAAAATTTAGAATAAAAAA	673 GGGGATTGGGCGAGTTAGCACTTTGGCTTTAAAGGATAATAAACTTTATGCGTTCAGTAAGGAATTTAACA 674 GLGELVISTLALKONKLYAFSKEFNTLL 6CCTTTAGCACAAAAGAAGAAGAAGAAGATTGGCCTTAAAAAATATCGTTAAAAAATATCAGTG 10 NIDPTKEEILEVYGLPKEIKNISAGGFRN 10 CTGGAGGGTTTAGAAAACGATGAGGTTGTGAGGTTAGAAAAAAAGGTTGTGAGGTTAGAAAAAA
AGCACCAACGATT TGGGGAGATTAGG GATTTAAAACCGA AGGCGTTACTTAT GTCGCTCAAATC CAAGCAGACTTAT GGTATGATCAAGA ATGGCTTGTTTTG GAATAAAAACGCT GCCTATTCATGTT TAAAGGTTTTTA TAAAGATTACCAC	CGTAGATGCGCC CGCAAAAAGCACA ACTTAGACCAAA CAACAAGAACAA AGCCCTGTGTCAA AGCCTTGTACAA AGCAAAAGAAGA CTAAAAAAAAGAAGA TGAAATTTTGATA	GGGGATTGGG CGCTTTTAGTC CTGGAGGGTTT
699	677	673
HP0642	HP1173	HP1173

-PCT/EP01/154	128	
---------------	-----	--

0 02/066501	PC
	678 SDAINQDMMLYIERIAKIIQKLPKRVHIN VRGFTDDTPLVKTFIFKSHYELAANRAY RVMKVLIQYGVNPNQLSFSSYGSTNPI APNDSLENRMKNNRVEIFFSTDANDLS KIHSILDNEFNPHKQQE
675 TTCCTTTATTGGTAAAACGCCTGATTTTGGCAACTCTGCACGCCTTATCAAGGGAATTTCAAGGGAATTTTAATCAATTTAATCAATTTAATCAATTTAATCAATTTAATCAATTTAATCAATTTAATTTAAATTAAAA	677 CTTCAGACGATTCAATCAAGACATGATGCTTTATATTGAACGGATCGCTAAAATCATTCAAAAAACCTAAAAAGGG TGCATATTAATGTGAGAGGCTTTACGGATGATACGCCTTTTAGAAAACCCGTTATAAAAGCCGTTATGAATTAGCCG TGCAATTCAATGAGAGGCTTTACGGATGATACGCCTTTATAAAACCCGTTATTAAAAGCCGTTATTATGAATTAGCGAATTGTTTTTTCTTCTTTCT
HP1173	HP1173

2
Ξ,

HP1173 6F99AGCGGGGATAGGGCAAGCGGAAGCGGGGGGGTTTTTGGGGCGATGTCAAGCAGGCATTTTAGCCCCCATTTAGCCCCCCACAGGGCGATTTTAGCCCCCCACAGGGCAATTTTGAAGCCTTTTTTGAAGCCCCCCCC			TTATGC VLOEAQNLLEHRIEPKDITILCATNDD/9 GGAATC LEIKNYLQERLSAIRPSTESSAKLSOFV		GCACAA KVMEQFELYGEPAOSCI ELAVGCEDA		GGCCTT FYDGTEIIR YYRMKNREYADAA		. 685	AAGAAG EHUDANRALMGTNMORQAVPLLRSDA AATGGC PIVGTGIEKIIARDSWGAIKANRAGVVE			TGATAT NEEDANAMENTERNAMENTALINE TRAINING TO TRAINING TRAINING TRAINING TRAINING TRAINING TRAINING TRAINING TRAININ							ITKNNE! FOKKY! DEFEREK! SII EKOD!	LPNGVIKKVKLYIATKRKLKVGDKMAĞ	RHGNKGIVSNIVPVADMPYTADGEPVD	IVLNPLGVPSRMNIGOILEMHLGLVGKE	ANAIMEENT THAI FUNDELL FYAK	DWSKGVKMAIPVFEGISGEKFYKLFEL	AKIAMDGKMDLYDGRTGEKMRERVNV	684			10000		
83 683	39CAAAGCGAAATGGCACACAGCGTGTTTTTTGTGGGAATGGCAAATG	AGCICITIGITICAAGAGAGAGAGATITITAGCACGATATTAGGAATTAACCACCACGAGAAATTAACCACCACGAGATAATTAACACACCACGAGAGATTAAACAACACACTAAATAAA	3GTCTTACAAGAAGCTCAAAACCTTTTAGAACATCGTATTGAGCCTAAAGATATTACCATT GACGCTTTAGAAATCAAAAATTATTTGCAAGAGCGTTTGAGTGCGATTCGCCCAAGCAC	GTCTCAATTTGTAGAGTCTAAAATCATTAAGAACGCTTTAGAATACGCTCTAGCGGAAGA	GAGCGTGGCAGGCTTTGTGTGGAAGGTGATGGAGCAATTTGAGCTTTATGGAGAGCCT	TAGCGGTTGGGTGCGAAGATGCCGATGGATTTTAGAAAATTAGAGACTAAAGCGATCGCTTC	NGGCGCGCAGATCATGACCATTCACAAATCTAAAGGCATGCAATTCCCTTATGTGATGGT AGCCTAATTCAAGCCATTCCAATCAACTCCTTGAAGAATATGACGGCACAGAGCTTCTT(NAAAATCGTGAGGTCGTAGATAAAGATTACGCTAG	CAAAGTAACCTTAATGGATTTAAGCTCTAGCATGCTAGTGGGGGGTAGCCGCATCGTCA	TGTAGGCACGGGGATTGAAAAATTATTGCTAGGGATTCTTGGGGGGGG	GAAAAAATTGATTCTAAAAATATTTATATTTTAGGCGAAAGCAAAGAAGAAGAAGCCTATATTC	AAAACTTGCGCACCAACCAAAACACCGGTTTCAATCAAGTCCCTATCGTTAAAGTGGGG 3CAAATCATCGCTGATGGCCCTAGCCATGGATGGAGGCGAATAGGAGGAAAAAA	CCTTGGAATGGCTATAACTTTGAAGACGCGATCGTGGTGAGTGA	CACATTTATGAAAAAGAAGTGGATGCTAGGGAGCTTAAGCATGGTGTGGAAGAATTTAC	GAAAGAAGAAGCGCTCGCTCATCTTGATGAAAGCGGGATCGTTAAAGTCGGTACTTATC	TTGGTGGGCAAAACTTCTCCTAAAGGCGAGATTAAAAGCACGCCTGAAGAGCGGCTTTT	ATAAAGCCGGCCATGTGGTCAATAAGAGTTTGTATTGCCCTCCCAGTTTGGAAGGCACG	!!CAC!AAAAAGGC!A!GAGAAGACGCGCGAG!!!GAGGGCGCGTT;GAAGAAAAA.	SCATTTEATURE TEACCATECTURALAGAAGAATTETTECECETAGETURETURETURE TO TO TO THE SECTION OF THE SECTION								1GAGITTGCTGAAACGCTCATAGAAAGCGTGAGAAAAAAACTGCAAAAATTAGGGGGATT	TTTGGGATTTAGAAGAAGCCCTTAGACGCTACTATAGTTCGCCTATCAGTGAATTGGAATT AATGAGAGCTTTTTTAATTCTTCTATCGTCAAAAGCTAAGCCAATTAAAAAGCAA	CGCCAACCTATCTATTATCCAT GCTTTACGCGCCACACAAGAGGGGTTTGAAGATGATG	ATCTTTTAGAAAGCCAGTTTAAAGAAATCTTACCAAAGAAGATAGAGAGCTTTTGGAAT	AMECCAMATTTAGAMAMTTAGEGETTGGATGGTTTAGTTCCGCTAGGAACTATAAAAACCCTATGAGTAAAATTTAAC AATCCCAAATATCTTTAGTGTTTGGGATGATGCTTTAGTTCCGCTAGGAACTATAAAAACCCTATGAGTAAAATTAAC	
			GCCACTAATGAC	TAGCGCAAAATT	CCCTAAAAAGA	AGCTGTTTGGAA	AACGCTTGGGCA		681	CGACGCTCCCAT	GCAGGCGTTGTA	TATTCTTTGCAAA	GTGGCGTTCATG	TTTCACTTCCACC	ATATTCCTGATGT	GCTGGCATGATT	CTATTTTGGGGA	CACCITATACTTACT	AGGGATTTTAGGA								683	ATATAGAAAAT	AACAAGAATGCC	ATGCGTAATTATG	AATCCCAAATATC	

-PCT	EP(1/1	542	28

HP1051	685 CGCAT	685 CGCATTATTGCAAAAAGCCCTCAAACTCTACGCTCTTTAAAGCCTTTAGAATTGAATGTGAGCATAGCCTCTAGCTT	686 ALLOKALKLYALLKPLELNVSIASSFSKO
	TTCTA	TCTAAAATAGGGAATTTGTTTGGTAGGGAATTAGAATCCTTTTGCGTGAAAATCCAGCCCAAAAACACCGTGCTTT	GNLFGRELESFCVKIQPKNTRALNSEI
	AAATAC	<u>AAATAGTGAGAAACTTTATTTAAAGCTTTTCCAAAAAGGCGTTATCGCAAGGATTTCATGCGAATTCGTGTGTGT</u>	LYLKLFOKGVIARISCEFVCFEVFSLNE
	GTCTT	GTCTTTAGCTTGAATGAAAAAGATTTTGAAAAAATCGCTCTGGTTTTAGAAGAAATTCTTAATAAAGCTTAAAAATTCG	KDFEKIALVLEEILNKA 5
	CTATA	CTATAATAAAATTICTTTTAAACGCGCCATATCCCCCACAAACGCTAGAGAATGATAGA)1
HP1291	687 ATGGC	887 ATGGCGGGATTGCGTGCGCGAATTTGTTGCATAAAATTCAGGGATCACGATAGATA	688 GGIACANLLHKNSGITIDIGGGSTECALI
	61606	GTGCGCGTTGATTGAAAAAGGCAAGATTAAGGACTTAATCTCGCTTGATGTTGGGACGATTCGCATTAAAGAAATGTT	EKGKIKDLISLDVGTIRIKEMFLDKDLEV
	TTTAG	TTTAGACAAAGACTTAGAGGTCAAATTGGCTAAAGCCTTTATCCAAAAAGAAGTCTCTAAACTGCCCTTTAAACACAA	KLAKAFIQKEVSKLPFKHKNAFGVGGTI
	AAACG	AAACGCCTTTGGGGTGGGGGGGGGACGATCAGAGCGTTGAGTATTGATGAAAACGCTTTTGTTACCCTATTGATT	RALSKVLMKRFCYPIDSLHGYEIDAHK
		CTTTGCATGGCTATGAAATAGATGCACATAAAAATTTAGCGTTCATTGAAAAAATCGTCATGCTCAAAGAAGATCAATT	NLAFIEKIVMLKEDQLRLLGVNEERLDS
	ACGGC	ACGGCTTTTAGGGGTGAATGAAGAGCGTTTGGATAGCATCAGGAGCGGGGGCGTTGATTTTATCAGTCGTTTTGGAG	IRSGALILSVVLEHLKTS_MITSGVGVR
	CATTIA	CATTTAAAAACTTCTTTAATGATCACTAGTGGGGTGGGG	EGVFLSDLLRHHYHKFF'PNINPSLISLK
	TCATTA	TCATTACCATAAATTCCCCCCCCAATATCAACCCCTCTCTCATCTCTTTAAAAGATCGCTTTTTGCCCCATGAAAGCAC	DRFLPHEKHSOKVKKECVKLFEALSPL
	AGCCA	AGCCAAAAGGTCAAAAAAGAATGCGTGAAATTGTTTGAAGCCTTATCGCCTTTGCATAAAATAGATGAAAAATACCTT	HKIDEKYLFHLKIAGELASMGKILSVYLA
	LTCCA	TTAAAGATTGCGGGGGAATTAGCGAGCATGGGTAAGATTTTAAGCGTCTATTTAGCCCACAAGCACGCGC	HKHS
HP1291	689 TCTAA	889 TCTAAAACCACCTTATGGCGTGTTGAATCTCGGAGCTAGCGATGATTCTAGAGTGTATAAACGCTTTGATGAGATGAT	690 LKPPYGVLNLGASDDSRVYKRFDEMIY
	CTATT	CTATTTTTTAAATCCTGACTACCAACTCGTTCTTTGCGGAAACTCTAAAAAAGATGAAGAGCTTGCCAATTCCATTCTA	FLNPDYQLVLCGNSKKDEELANSILKR
	AAACG	AAACGCCACAAAAATGCCATTTCTTTAGTCAATCAAACCGGTTTGATAGAATACCTTTATCTTTTAAAGAACGCTAGTT	HKNAISLVNQTGLIEYLYLLKNASFAMG
-	TTGCG	TTGCGATGGGCAATGAGTCTTCCATCACGCATTTGAGCGCTTGTTTGAAAATCCCTTATGCGTTCATAGTCTCTTCGG	NESSITHLSACLKIPYAFIVSSGLSSPRF
	GTCTC	GTCTCTCAAGCCCAAGATTCCACCCCTACCCAAAGGAAGTTGGCCCTAATATCCACATGATCTATCCAAGGGATTTT	HPYPKEVGPNIHMIYPRDFQKIISRSSD
	CAAAA	CAAAAAATTTCTAGGTCTAGCGACTGGATGTTTAAAGCCATGACTATGCCACCGCCAGTGGATTTTGTGAAC	WMFKAMTMPHPPVDFVNPQDIISAIKR
	CCGCA	CCGCAAGATATTATTAGCGCCATTAAACGTTTTGCGCCCCATCTCTTGAAAGAAGATGCGCCATCTAATACCAACGAA	FAPHLLKEDAPSNTNETTYFERV
	ACAAC	ACAACCTATTTTGAACGAGTTTGATTGCGTTATAAGTTTTTAGAGGATAACTTCAGCTTTAGATTGTAAAAGCATAAAA	
	AGGAA	AGGAATTITGTAACCACCACCACTAATTGAAAGCTTCTTTTCGCACAACCACATTTTTAAGAGAGCAGAATGTCTTGGAA	•
	TTTTG	TTTTGAAAACGCTCACTCATTAGCGTATTTATTGCCCATTTATCTATTTCTTGTAAAATACGAGTTTATTTTAGCGTA	
	AAGAA	AAGAAATTGATGATCAGTCTCCATAGAAAAAGCCCCTTACATTCCCTACCCCCTAGCTCTTTATGAAAATTAGAGCAA	
70070	CCACA COACA	CCACACACACACACACACACACACACACACACACACAC	REPARENTE SEEMKANTAII KKODRY
167144		GOCCOATOCATITATION OF THE TOTAL TOTA	VYLLRYLPSRYWASILTIALYVKYPDFD
	TACC	TACCTE ATTTE ACCOUNT GAS AS A SECOND CONTROL OF THE ACCOUNT GOOD CONTROL OF THE ACCOUN	ALKKILVSYYYOTWIAGISTITRIKOTSIN
	CGCAT	CGCATCAAGCAAACCAGTATCAACATTATCAAAAACGTTAAAAAGCAATAAGAGGGTTGAAAACCATCAAAGAGGCTTATATA	IIKNVKSNKSVETIKELIL1\S\DSYNTFDQ
	TTGAAT	TIGAATAGCATCGACTCTTATAACACCTTTGATCAATACCTCTATAACTTATGGGATAGCTCTTCTGTTTATCATAGCA	YI YNI WDSSSVYHSKWVRPVLALANY
	AATGG	AATGGGTGCGTGCTGTTTTTGACCCTAGCTAATTATTTCATGGCAGATGAAAACCCCATTTTATCGCTATGGATG	FMADEEKPHFIAMDAETQVEHILPQTP
	CCGAA	CCGAAACCCAAGTATTTTGCCACAACGCCAAAAGAGAGAG	KRGSOWNADEDKEKREEWVNNIANLT
	AAAAAG	<u>AAAAAGAGAATGGGTAAATATCGCGAATTTAACCTTTTAAAGCGTAAAAAGAACGCGCATGCTTTAAACGG</u>	LLKRKKNAHALNGDFDEKRKIYGGKDT
	GGATTI	GGATTTTGATGAAAAAAGAAAAATTTATGGAGGCAAAGACACGAGCAAAGTGATTAGCTGTTATGACATCACTAAAGA	
	ATTGTA	ATTGTATAGCAATTATAGGAAGTGGAATGAGAAGTCCCTCCC	RYKSLYNTITPVLHIEGGEDDFEDDFD 7
	ТСТТТ	TGTTTTACACATAGAGGGCAAGAAGATGATTTTGAAGATGATTTTGATCT	

172

HP1291	693 TAC	693 TACAGACGGCTATGTTAAAGTCTCTTTAGTGGCTGATGAAAGAGAATTGTTATTAGATCAGGTCTTACAAGAAGCTCA	694 TDGYVKVSLVADERELLLDQVLQEAC
	AA LAA	AAACCTTTTAGAACATCGTATTGAGGCCTAAAGATATTACCATTTTATGCGCCACTAATGACGACGCCTTTAGAAATCAAA	LLEHRIEPKDITILCATNDDALEIKNYL(7)
	₹	AAAATCATTAAGAACGCTTTAGAATACGCTCTAGCGGAAGAACCTTACAAGCTTTTATAAAGCACAGGCGTTTTAAAAA	EKLSAIKPS I ESSAKLSGFVESKIIKN) OF PARI AFFPYKPFYKHSVI KI AGYI HOS
	<u>στ</u>	CTCGCTGGATACTTGCATGATGCGATCGCTTTAGCTGGTTTTAACCCTAAAAAGAGAGGCGTGGCAGGCTTTGT	AIALAGENPKKESVAGEVWKVMEDEL
	GT.	GTGGAAGGTGATGGAGCAATTTGAGCTTTATGGAGAGCCTGCACAAAGCTGTTTGGAATTAGCGGTTGGGTGCGAA	YGEPAQSCLELAVGCEDADGFLEKLET
	Y C	GATGCCGATGCATTTTAGAAAATTAGAGACTAAAGCGATCGCTTCTTCCCATTCAAAAGGCGCGCAGATCATGAC	KAIASSHSKGAQIMTIHKSKGMQFPYVI
	<u> </u>	CALICACAAATCTAAAGGCATGCAATTCCCTTATGTGATCGTGTGCGAACGCTTGGGCCAAGCCTAATTCAAGCCATTC	VCERLGKPNSSHSNQLLEEYDGTELLR
	3 <u>5</u>	CAMICACITECAGE AT GACGCCACAGE CACAGE CONTINUE CONTINUE AT GAAAAT COT GAAAAT COT GAAAAT COT GAAAAT COT GAAGAT COT A GACGGT COT A GACGGT COT A GAAAAT A COT TAAAAAT A COT TAAAAAT A COT TAAAAAA TAAAAAAAAAA	LYYRMKNREVVDKDYARALDKEEAAK
-	2	AXABAT ACGCT AGGCT IAGACAAAGAAGCGGCCAAAGA CATGAAGATTAATGTGTATTATGTGGCATT	DHEEINVYYVAFTRAELGLIVVAKDKKE
-	101	CACTAGGGALGAGTTAGGGTCTGTGTGTGTTTAGGAGGAGGGAAAGAAAAGAAAG	SKKESKNKTMREKLDLVPLEEGEIAPVI
	ATA	**************************************	DSOVEKNINDOENIEGIALUKOLEKE
	₹ ¥	AAAGAATAACGACCAG	AYNIPKOSVI FYI NYHHGEYGI DYOAI
			EESLELFENDAEIOALFKNLPLKGEAAF
_			LFGGVVSRIDVLLWDRGGNLYVLDYKS
	_		SQNYQQSHKAQVSHYAEFLKTQAPHF
	100		KIOAGIIYAHKRILLEKLWV
HP0084	150 150 150 150 150 150 150 150 150 150	BSS/CGATGAGCCGGATTTGGATTACGCTAACATGAGCGCTGAAGAAGTGGAAGCAGAGATTGAACGCCTGCTGCAACAAA	696 DEPDLDYANMSAEEVEAEIERLLNKRO
) o	CGCCAAGCCCGAAGAGCGCAAGAGGGGCTCAAAAAAAGGAAGG	EADKERRACKKOEAKPKOEVTPTKET
		TOGNICO CONTROL PARAGEMENTO IN THE PROPERTY OF THE PROPERTY OF THE PARAGEMENT OF THE	PKAPK IETKAKAKADTEENKAPSIGVE
_	AGG		IQIVENUKRIDHIMINLIGELVLGKIRI
_	ACC	ACCORDING TO THE TATAL TO ACCOUNT A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL TO A TO THE TATAL THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL THE	IRIYODVEERYDGEKFLEELNUVVSSIS
	999	GGGTAAGGTGTTCAATAAATTCCCTCGCATGGTAAGGGATTTGAGCCGGAATTAGGCAACTAAGCAACAAGAAATAGAAAAAAAA	AVI I DLOLAVMK TRMOPVGKVFNKFP
	TIST.	TIGA GGGCGAAGAAACCGAATTA AAACAAATCCAACAACAACAACAACAATTA CAACAATTA AAAAAAAA	MWVRDLORELGROELIEGEE I ELDROI
	TCA	T.CATGCGATCATGGGATTGAGCCTTTAGAAGA	
HP0084	711 769	TTTCCGCATGAAAGCGCCTGAAAGGATTGAATTTTTATGCGATGTGGGGAGTTTTGAAGAGTTTGACAAGCATTTAC	698 FRMKAAERIEFLCDVGSFEEFDKHLRP
	9	GGCCTAATGATCCTTTAAATTTCGTGGATAAAGAGGCTATAAACAACGCATTAAAAAATACGAAAAAAGGACTAACC	NDPLNFVDKESYKQRIKKYEKRTNRPS
	ည္သ	GCCCAAGCTCAGTGATCAGCGGTGAGGCTAAAATCAACCGCATGCCTTTGCAGATCGTGTTTTGATTTTAGCTTT	SVISGEAKINRMPLQIVVFDFSFMGGSL
	9 K	A I GGGGGGGAGT I TAGGCTCT GTGGAGGGCGAAAAGATCGTAAGAGCAATCAATCGCGCGGGTCGCTAAAAGAAA	GSVEGEKIVRAINRAVAKREALLIVSAS
	36	SC STATISTICA SC SA SESSES SESSES SESSES SESSES SESSES SESSES	GGARMQESTYSLMOMAKTSAALNRLS
	1	GTACCCCCCATTITITION IS A STREET OF THE STREE	EAKLPFISLLSDPTYGGVSASFAFLGDL
-	150		IIAEPGAMIGFAGPRVIKOTIGADLPEGF
-	TTG	OCIONA I PASCAMON AGGOGGA GOMENTO CONTROPO E EL CAMON DE LA CONTROPO DEL CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DEL CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DEL CONTROPO DEL CONTROPO DEL CONTROPO DE LA CONTROPO DE LA CONTROPO DEL CONTROPO DE LA CONTROPO DE LA CONTROPO DE LA CONTROPO DEL CONTROPO DE LA CONTROPO DEL CONTROPORTROPO DEL CONTROPO DEL CONTROPO DEL CONTROPO DEL CONTROPO DEL CONTROPO DEL CONTROPORMO DEL CONTROPORMO DEL CONTROPORMO DEL CONTROPORMO DEL CONTROPORMO DEL CONTROPORMO DEL CONTROPIO DEL CONTROPORMO DEL CONTROPORMO DEL CONTROPORMO DEL CONTROPORMO DEL CONTRO	GTAEFLLEHGLIDMIVHIRKDLKKTLSDL JAMM
HP0134	921 669 713	699 TCGTGCGTAAAAGATGGGGTCCATTTAGAATGGGTGGCCCTTGGGTATAAAGTGCCTGCTTTCAAGCATAAAGATCAA	700 VHKDGVHLEWVALGYKVPAFKHKDQ
	S S S	οι εφούς του πουστικό πουστικό πουστικό πουστικό πουστικό πουστικό πουστικό πουστικό πουστικό πουστικό πουστικό ΑΓΩ CTTEGETTE ΤΕ ΑΒΩ ΤΗ ΤΕ ΤΕ ΑΒΩ ΤΗ ΤΕ ΑΒΩ ΤΕ ΑΒΩ ΤΕ ΑΒΩ ΤΕ ΑΒΩ ΤΕ ΑΒΩ ΤΕ ΑΒΩ ΤΕ ΑΒΩ ΤΕ ΑΒΩ ΤΕ ΑΒΩ ΤΕ ΑΒΩ ΤΕ	ALDALSRLLGEGKSSWLOSELVDKKR
	1001	TCCTAATGTCAAAGCCGAAGCCTTACAAAAAGAATCGTAGCGCTTTTAGAAAAGGTGAAAAAGGCGAAATCACTCA	VKAFAI OKFIVALI FKI KKRFITOAFI I
	AGC	AGCGGAATTAGACAAGCTCAAAATCAATCAAAAAGCTGACTTTATTTCTAATTTAGAAAGTTCTAGCGATGTTGCGGG	KLKINOKADFISNLESSSDVAGLFADY
	- 646 - 646	GCTTTTTCGGACTATTTTGGATGATGAAACGATATTTAAAGGCTTGACGGATTACCAGCGACAATTTTTGGATTTAAAAGGT GAGCGATTTGGTGCGTGTGAGGATGAATATTTAAAGAACAACCAATCAAACAACAACAATAAAAAAAA	VÁNDIGELTÓYORÁFLOLKVSÓLVRVÍ
1	?		

τ		7
	٠.	
•		7

02/066501====		PCT/EP01/1542
702 FHKI.LAEKIGDIASI/VGVRDNOLIGYGI.COMICLIGATED WIGLNGTGDKSGSKFTMQSISNMI.ESNEWSIGSNETMQSISNMI.ESNEWSIGSKTMQSISNMI.ESNEWSIGSKTWASIQGGTLVMTPL.SOMAVIGANIYALAQGAIVSGNSNNI.LSANGTINGATIEREVSYDLFHKNAMTLSLKNPNI.FKNAIQVQNTLNKVFGNKVAIALDPKTIQITRPERFSMVEFI.ALVQEIPINYSAKNKIIVDEKSGTIVSGVDIMVHPVVVTSQDITTKITKDPLNDSKNTQDLDNNMSLDTAHNTLSSNGKNITIASVVKALQKIGVSAKGMVSILQALKKSGAISAEMEII.	704 LYGGIACANILHKNISGITIDIGGGSTEC ALIEKGKIKDLISLDVGTIRIKEMFLDKDL EVKLAKAFIQKEVSKLPFKHKNAFGVG GTIRALSKVLMKRFCYPIDSLHGYEIDA HKNLAFIEKIVMLKIEDQLRLLGVNEERL DSIRSGALILSVVLEHLKTSLMITSGVG VREGVFLSDLLRHIYHKFPPNINPSLIS LKDRFLPHEKHSQIKVKKECVKLFEALS PLHKIDEKYLFHLKIAGELASMGKILSVY LAHKHS	706 CYKFSQKMFALIQKKRQIRENLKNRPN PLDTKNSPKERLSSVTEEIISKKLEE SKETPEGKHDGERLSSVTEEIISKKLEE LKAKNNKGN
T01 CCTTTCACAAGCTTTTGGCCGAAAAATAGGCGATATAGCCAGCGTGGTGGCGGTAAGGGATAACCAGCTGATTGG TTATGGGCTTGTGATTGGCTTAAATGGCACACGGGATAAATCCGGCTCAAAATTCACCATGCAATCCATTTCTAACAT TTATGGGCTTGTGATTGGCAAAATCTCTGCAGATGATATTAAAATCTAAAAATGTCGCTGCAGTGCAATCCATTACAGG GCTAGAGGCGTTGCAAAATCTCTGCAGATGATATTAAAATTCTTCTATTGGGGATGCAAAATCCATTCAAGG GCTAGAGGCCTTTGCAAAAGCGGCGATAAAATTGATATTCACATTTTTTTT	703 CGCTCTATGGCGGGATTGCGAATTTGTTGCATAAAAATTCAGGGATCACGATAGATA	705 AATGCTATAAGTTCAGCCAAAAAATGTTTGCACTCATTCAAAAAAAA
	20	70
HP0325	HP0325	HP0325

71017		707 4 4 4 4 4	OTO A COLOUTE	
TOWN CASE I I TROUGH TO CHANGE AND COCK TO THANAGARD AND COCK AND	6750AL	CGAA	GIGAACACCCI AGCGI I ICCI ACAAAAAGGCCATI TCCCAACAAAAGATTCAAGCTAAAATTGAAGAATTAGG ACTATGAAAACGCCATTATTGAAGGCAAGATTGTAGGCAAGAATAAAGGGGGTTATATCGTGGAGTCTCAAG	708 KGEHPSVSYKKAISQQKIQAKIEELGI YENAIIEGKIVGKNKGGYIVESQGVEY
CAMCITIGAGGITTCTAAGGAATTGTTAGAGGCAAGAGGGGGTTTAGGGGTTTCAATTGTAGAAAAAAGAGCCCTTTTGGAATTGTTAGAAAAAAAA		1909 1707	GATTOSTRIPECTOCOCOTOCOCTTAAAGAATGACGAAACCATATOGGCAAACGGTTAAAGGCG	LSRSHSSLKNDANHIGKRVKACIIRVE
CATTITETRAMACINAGEGGGGATTGAGGGTTTGGTCATIATICTGAATCAGCCATAGGGGATCGGTATCCTTC CATAAAGGGGGGGGGG		CAACI	TGAGGTTTCTAAGGAATTGTTAGAAGCCACAGAGCCGGTGTTAGGGGTTGTGCGCCAGATCACCCTTTTGG	ENHSINISKKKFFEVNOKKULEVSKE FATEPVI GVVROITPEGIEVEAKRIEG
MANAMAGGACCATRAAAAGGGCATTAGGGGATTTGAAGCAAGCTTAAAACCCGGATACCCCTTTAACTACTACATACA		CATT	TGTAGAAGCTAAGGGGATTGAGGGCTTGGTCCATTATTCTGAAATCAGCCATAAGGGACCAGTCAATCCTG	VHYSEISHKGPVNPEKYYKEGDEVYVK
CUCHANANGGENTRAGGECTATION TO CONTRAGGENT CONTRAGGENT TO CONTRAGGEN		AAAA	ACTACAAAGAGGGCGATGAAGTCTATGTCAAAGCCATCGCTTATGATGCAGAAAAAAGGCGCTTTCACTCT	AIAYDAEKRRLSLSIKATIEDPWEEIQD
I CITICGGATAAAATOCOCCITACAATCAGCGGGGGCAGGAGTTTGATTTGAAATC TOTTGGGATAAAATOCOCCCTAACAATCTTGAGCGTGGGGCAGGATTTGATTT		SCA	AAAGCGACIATAGAAGACCCATGGGAAGAGAGATTCAAGACAAGCTAAAAACCCGGATACGCCATTAAGGTAGTG	KLKPGYAIKWVSNIEHYGVFVDIGNDI
CAGTICAAGATITTIAAGAGCCAAATGATTTIAAGAGTTTAACGGATTTTGGGCCTTTTTAACTGTTTAAAATTTTTAAGAGTTTTAAAGTTTTAAAGTTTTAACGGATTTTGGGCCTTTTTAAAATTTTTAAAGTTTTTAAAAATTAAGGATTTTAAAAATTTTTT		A2121	CAACATIGAAGA TATGGGGG G TIGTGGGAATGATGAAGGCTTTTGCATGTTCTGAAATC	EGFLHVSEISWDKNVSHPNNYLSVGQ
CANGINGGEGRATETTTAGAAGGCATAAGGTTTAGGGGTTTTAGGGGGTTTTAAGGGGGGTTGAAGATTGGGGGG		212	SECRETARY OF THE SECRET	EIDVKIIDIDPKNRRLRVSLKQLTNRPFD
TOB CANGENTAGE CONTRICTOR AND THE CONTRICT OF		S E A S	AXXXXXII CGCCGCCTTXXGGGCTTTCTTTXXXGCXXCTCXCTTXXCAGGCCTTTTTXXXXXXXXTTTXAGAGGCCTTTTXXXXXXXXXX	VFESKHQVGDVLEGKVATLTDFGAFI
709 CAAACTTAAAGGGACCGAACCCTATTTGAAGGTTTATTGTAAGTTTATTGTCAAGGCCAAATGTTTTTGTAAAGGCCAAATGTTTTTTGTAAAGGGAATTTTGTAAAGGCAAATTTTTTTT		ATGG	TTGCTCCACATCACGACGCTTTTTGGGATAAAGATAAAAATGCAAAGACCACTATAAAATTGGCGATGTGA	IGDVIKVKILK
AGAMGAAGGGAAAAAGAGAAAAGAGTTTTGAAATTTTGTAAGATATTTTGAAAATTTGAATTTTTT	IP0325	709 CAAAC	TTAAACGCACCCAAACCCTTATTTGAATGTTTTGTAGGAGTTAATCTGGCCAAAGCCAAATATTATTCTAAAAA	710 NI NAPKPI FECEVGVNI AKAKYVSKKF
CANCCAMAGCCIGATITIA ANAMATANA GEOGRAPHATICITA AGGINATION AND CHANGE CONTINUA AGGINA AND CANAMATICA AND CANAMATI		AGAAC	AAAGAGAAAAAGAAAAGATGTTTGAATTTTGTAAGATATTTGAAATTATT	EREKEKMILNFCKIFEIILFEAIOKOPKP
ANGIGINAGO CONTROLLI II INGAANGAGO II INAGAATGATGAAGCAGTTTGGGAAGGTTGTGTTTGGCTTGGCTTGAGGAGGTGTTGCTTTGAGGGTGTTGCTTTGAGGGTGTTTGAAAAGAGAGAG	-	CAACC	AAAGCCTGATTTTAAAAATAAAGACGAGCTTTTAGGGGATTATCCTTAAAAAATTTAGATTCTTTAAGAG	DFKNKDELLGDYPNLKNLDSLREVRED
THI TCTTCAAGATTAGCTCCTTAATGGCTAAAATCTGCTCGTATCAATCTGCTGTGGCGTTGTGGCTTATTATCTTTATAC THI TCTTCAAGATTAGCTAATGGCTAAAAGCCTCTATAAATTGTTACTGTGGCGCTTATTACTTTTATTAC GCACTCCAAAAAGGCTTTAAAACCTCTAAAAGCCCTCTATAAATTGTTACAAGCGCTTATGCCTTGCTGCTTCCT GCACTCAAAAAAGGCTTTTAAAACCTTTTAGAAAACCAATTTTAGAGCTTTAAAAGCGTTTCTATCCAACTTCCTATGCCTTATTTAGAAAACTTGCAAAATTTGGATTATTTTAGAAAACTTGCAAAATTTGGATTATTTTTAGAAAACTTGCAAAATTTGGATTATTTTTTAGGCCTTTATTAGGTTTTTTTT		AAGIC	A SECRAFACTITITIES AND A SECRET TARGET OF THE SECRET OF TH	FLKRAFKNDEASLGAYVLVLLSCKYFE
711 ICITICAAGCTTACGCCCCCTAAAGCCTCGTCGTTCGATCAATCTGAGGCTGTTATATCTTATCTTATCCTTATGCTCTAAAAACACACCCCCTAAAAATCTTACATGCTTACAGCCCCCCTAAAAACACTTATGCAAAAACACACCCCCTAAAAATCTTACATGCTTACAGCCTTCAAAAAACACACTTACAAAAACACTTTATGAAAACCTTTTTAGAAAACATTTTAGAAAACATTTTAGAAAACATTTTAGAAAACATTTTAGAAAACATTTTAGAAAACATTTTAGAAAACATTTTAGAAAACATTTTAGAAAACATTTTAGAAAACATTTTAGAAAACATTTTAGAAAACATTTTAGAAAACATTTTAGAAAACATTTTAGAAAACATTTAGAAAACATTTAGAAAACATTTAGAAAACATTTAGAAAACATTTATATTAGAAAACATTTATAGAAAACATTTATAGAAAACATTATAGAAAACATTATAGAAAACATTATATATTATATTAGAAAACATTATATATA	-	AGCIL	IAAGIAIIIIGAGAGGGGGGTGAAAAGTTGAAAATGGCTAGATTTATCGCTAGGCTTATTGCTTTGAGA	SVFEKVQEWLDFIARLIALRGHVHKIT
TITTIAGICCCTATATTICAAACCTICTAAAATCTATAAATCTATAAGCTTGGGCTGAAAAACCGGCTTCTTATACTTTAAATCTTTATCTTTATCTTTACTCTTTAAAACCATTCAAAACCATTAAAACCAATAAAACCAATAAAACCAAATTTTAAATTTTTAGCCTTATACTCCTTATACTCCTTATTACTCCTATTACTCCTATTACTCCTC	10000	311	ISTSCANON I AND I A	
THINGSCOND AND THE CARACTER CONTRACTOR OF THE CONTRACT CONTRACTOR OF THE CONTRACT CO	F0325			712 FOAYAPLMAKICSYOSKFVSAFYLYTO
AGCCTTGCCTTTTAAACGTTTTTGAAAACATGGTTTTTTTAAAACGATTCCCAAAATATGACTTTCCCCACCCCCCCC			I CONTRACTOR AND ALTA ANALOGY AT TOTAL TOT	LKKELKTSKDTLYKLLHALEKORILFLV
CCCATGATAACGGGATTITTATCTTGGGGGAAATTCTTATGATTTTTTAAACATTTATGGTTTTTTTT		AGCC	TTGGCTTTTAAAAAACGTTTTTGAAAAACAACGTTTTTTTAAAAAACAATTAAAAAATAAAAAAAA	PNFENNK I KLYLCUFALPYSLIPSPSI
CCCCATTITITAGAAAAACAGCTITIATGGTGCCATAATTICATTGTTTTTTTTTT		CCCAT	34TAACGGGGTATTITATCTTGCGCGAAAATTCTACCAACAACTCATCGCCCCAACAACAACAACAAAAAAAA	
CTATTICAGCACCATACCCCCTACAACCCCTTAATTICATTGATTITICATTGGATATTCAATCTATTITICATTGGATAACCCCTACAACCCCTACAACCCCTACAACCCCTACAACCCCTTAATTATT		4000	THIS AGA A A A CAREFORD A CAREFOR	TICKENO I NICALIANAFY I PRIFICE COL
TAGENTIA DESCRIPTION OF THE CONTROLL OF THE CO		CTATT	CALCASA ANTACCICIONE DE LOS CONTRACTOR DE LA LIBERTA DEL LIBERTA DEL LIBERTA DELLA LIB	WCHKHGFLNIIVVSINAPISA I NI PYKI
TAGENTITION OF THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL T		TANT	<u> </u>	CNFIDFSCDIGSICV
TGAGAAATGCTACCCTAAAAGCGTAGGGTGTTTTTATGCTAAAAGAAGGAAG		TAAAA	TITI AATTGATTATTAATATTTTTTTTTTTTTTTTTTTT	
GAAGAAATTAAGITTCTGCGCCTTGTTATCC. 713 CTTGCGGGTTCATGAGATCATGAAAGCCTATACCGCATTGCTAAAAAAACAAGACCGATACGTC 714 TATTTATTGGGGTTCATGAGATCATGAGATTCATGAAAGCCTATACCGCATTGCTAAAAAAACAAGACCGATATTTG 715 CTTGCGGGTTCATCTCTCCCCTCTAGGTATTGGGCCCATTTTAACGAGACGCCTTTATGTCAAATACCTGATTTTG 8 CGCTTTGAAAAAGCTTTTGGTGTCTTATTATTACCAAACTTGGATTGCAGGAGGCACGATCACGCCATCAAAAGCAAAAAACGTTAAAAAGCAAAAAAAA	•	TGAGA	AATGCTACCTACCTAAAGCGTAGGGTGTTTTTTTTTTTT	
713 CTTGCGGGTTCATGAGATCAGCGAGTTCATGAAAGCCTATACCGCATTGCTAAAAAAACAAGACCGATACGTC 714 TATTTATTGATGACCTCTAGGTATTGGGCCAGCATTTAACGACTGCCCTTTATGTCAAATACCCTGATTTTG ACGCTTTGAAAAAGCTTTTGGTGTCTTATTATTACCAAACTTGGATTGCAGGAGGCACGATCACCCTGATTTTG ACGCTTTGAAAAAGCTTTTGGTGTCTTAATTAACCAAACTTGGATTGCAAAGAGGCGTCATATATTGAATAGCATCG ACGCTTTATAACACTTTATCAAAAACGTTAAAAGCAATAAGAACCATTGAAACAAGAGGGTGCGTCC TGTCTTATAACACTTTTGCCAATAACTCTAAAACTTATGGGATAGCTTTTATCGCTATGGCAAATGGGTGCGTCC TGTCTTAGCCCTAGCTAATTATTCAAGAGAGAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA		GAAAA	ATTAAGTTCTGCGCCTTGTTATCC	
	P0325		3GGTTCATCTATGAGATCAGCGAGTTCATGAAAGCCTATACCGCATTGCTAAAAAAAA	714 CGFIYEISEFMKAYTALLKKODRYVYLL
		TATT	TTGAGGTATCTCCCCTCTAGGTATTGGGCCAGCATTTTAACGACTGCCCTTTATGTCAAATACCCTGATTTTG	RYLPSRYWASILTTALYVKYPDFDALK
	-	ACGCT	TGAAAAGCTTTTGGTGTCTTATTATTACCAAACTTGGATTGCAGGGGGGGG	KLLVSYYYQTWIAGĞTITRIKQTSINIIKN
		CCAGT	NECACATTATCAAAAACGTTAAAAAGCAATAAGAGCGTTGAAACCATCAAAGAGCTTATATTGAATAGCATCG	VKSNKSVETIKELILNSIDSYNTFDQYLY
	-	ACIO	A I AACACCI I I GAI CAATACCI CI ATAGGATAGCI CI TCT GTTT AT CATAGCAAATGGGTGCGTCC	NLWDSSSVYHSKWVRPVLALANYFMA
		JOB GO	AGCCCIAGCIAAIIAIIICAIGGCAGAIGAAGAGAAACCCCATTTIATGGCTATGGATGCGAAACCCAAGT ATATTTTGCGAAAAACGCCAAAAAAAAGAGAGAAAAAAAA	DEEKPHFIAMDAETÖVEHILPÖTPKRG
		GGGTA	AATATTEGEGAATTTAACCCTTTTAAAGCGTAAAAAGAAGAAGCGCGCATGCTTTAAACCGGGGATTTTCAAA	DYWIND TO THE TERM VINIBIAL LELY
		AAAGA	AAATTTATGGAGGCAAAGACACGAGCAAAGTGATTAGCTGTTATGACATCACTAAAGAATTGTATAGCAATT	VISCYDITKEI YSNYRKWNEKSI OERY
		ATAGG	AGTGGAATGAGAAGTCCCTCCAAGAGCGATACAAATCTTTGTATAACACTATCACGCCTGTTTTACACATAG CAAGAAGATGATTTTGAAGATGAT	KSLYNTITPVLHIEGÓEÓDFEDÓ

ч	_
r	•
	-

	CACCACAGGAGGCCCAGAGGGCGAGAGTTGATGGCTTGCATTATAATTTTGTCACCAACAACAACAACAACAACAACAACAACAACAACAA	i i i i i i i i i i i i i i i i i i i
	SCALAGAAAAGGGCAGTITITAGAATGGGCAATCGTGCATAACCACTATTGCAGGCACCTCTAAAAAGGGGCAGAACAAGACAAGACAAGACAAGAAGACAATTGCATTGCAGAAGAATCCTGTAAGACAAGAAAAGGAAATCGTGTAGAAAAGCATTGCAAGGGGCATGAGAAAAGCCTTAAAAAGGGGCATTACCTTTAAAAGGGGCATTACCTTAAAAAGGGGGATTTTAAAGGGGGGATTCTAAAGAGGATTTTAAAAAGGGGGGGG	RKPREGEVDGLHYNFVSEEEFKQGIE/Z GQFLEWAIVHNHYYGTSKIPVEKALKI9 GKIVIFDIDVQGHEILKKHYPNACSVFI-9 TKNOEILKERLLLRGTIJSKETIEKRLINIO YKEMQCLESFDYLIINI:DLEKSKEIILSIA KTLVHRLKAFNFEKICKAWKNETL
HP0419	CTTTGGGGGTAGAGGATTTGCATGAAAATACCCTAACGCTTTTGATGTCATTTTTTGCTTAGGGGTGCTATACCACA GAAAAAGCCCGCTAGAGGCTTTAAAAGCCTTGTATCACGCTTTTGAAAATAAAAGGGGGGGG	718 LGVEDLHEKYPNAFDVIFCLGVLYHRK SPLEALKALYHALKIKGELVLDTLIIDSP LDIALCPKKTYAKMKNVYFIPSVSALKG WCERVGFENFELSVLKTTPKEGRKTD FILGGSLEDFLDKTDPSKTLEGYDAPLR
HP0419 7190	719 GCGTTTGGGTATTCAAAGGAATTTTTACATTAGCGTGAATGAA	720 RLGIQKEIFYISVNEENEKALLINCYPNA KNIAGFFHLETDYVGLGIDRQMACLAV NNGVVVDAGSAITIDLIKEGKHLGGCIL PGLAQYIHAYKKSAKILEQPFKALDSLE VLPKSTRDAVNYGMVLSVIACIOHLAK NQKIYLCGGDAKYLSAI:LPHSVCKERL VFDGMEIALKKAGILECK
7	TTCATTTAGAAAACCGTGAAGAAATGAAAAGCCCTTTTGAATTGTTACCCTAACGCTAAAAATATTGCAGGGTTT TTCATTTAGAAAACCGACTATGTAGGGTTTGGGATAGACCGGCAAATGGCGTAAATAATAGGGGTTT GGTGGATGCCGGGAGTGCGATTACGATAGATTTAATCAAGGCGCAAATTTTAGGGGGTGTATTTTACCCGGTT TAGCCCAATATTCATGCGTATAAAAAAAAAGGGCTAAAATTTTAGAGCCTTAGAGGCCTTTCAAGGTTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGAAAAATCTTTTGGGGGGGTGTTTTTAGAGAGTTTTTAGAGCGTTTTTAGAGGGGCGTTTTTAGAGAGTTTTTAGAGCGTTTTTAGAGGGGCGTTTTTAGAGGGGGGGTTTTTAGAGGGGGGGTTTTTAGAGGGGCGGTTTTTAGAGGGGGGGTTTTTAGAGGGGGGGTTTTTAGAGGGGGG	722 FYISVNEENEKALLNGY PNAKNIAGFFH LETDYVGLGIDROMACI AVNNGVNVD AGSAITIDLIKEGKHLGECILPGLAQYIH AYKKSAKILEQPFKALDSIEVLPKSTRD AVNYGMVLSVIACIQHLAKNQKIYLGG GDAKYI SAEI PHSVCKEDI VEDAMEN
723	T23 TGAAGTGAGCATCACGCAAAAAAGCGGGGATTATGGAGCGGATTTATAGAAAAAGAGGGCCATCAAGTGGGCG GTTCAAGTGAGCGCATCACGCAAAAAGGGGGGATTATGGAGCGGGATTTATAGAAAAAGGGGCCATCAAGTGGGCG TGCGAAAAAGCTTGCGCATAAAGTTTGCCCCAAAGCCGTTCAAGAGGTGGTCTTTCTAAAGCTTATAGGCT TGCGAAAAAGCTTGCGTGAGCTTTTGCCCAAAGCGGCTCAAAAACTGGCTCAAGCTAATGCTTACCCAAAGTGCT AGTTCTTTTAAAATTTGTCGTAATTGCATGCGCTAATTGCCAAAATTTAGCGTCAATTTCTGCTTGGATAAGGGGAT TTAATGATTCAGTCTGTTCGCATCAAAAATTTAAGAAATTTTAAGGACACTAAAATTGTTTACGAAACTTAATAT TATCACCGGCCAAAACAATGCGGGCAAATTGTTAGAAACACTAAAATTGTTAATGTTTATTAGAAACATTAGTTAATAT ATGCACTAATGTTAGAAATTTATGACAAAATTGTTAGAAAGCGTTTAATATTATTAGAAAATGCAAAATTGTTAATTATTAGACCCTTAACAACTTAATGTTTATTATTAGACAACTAAGGACCTTAAAATTGTTAATTATTATTAGACAACTAAAGAAATTGTTAATGTTTATTATTAGACAACTAAGGACCTTTAGAAATTGATTATTATTATTAGACAACAACTAAAGAATTGATTATTATTATTAGACACTAAGGACCTTTAGAAAATCCAAAAATTGTTAATTATTATTAGACAACAACAACTAAGAACTTAATGTTTATTATTATTAGACAACAACAACAACAACAACAACAACAACAACAACAAC	LKKAGILE 724 EVSITÖKSGDYGADLIIEKDGIKWAVQV KRYSHKVSPKAIDEVVSSKAYYACEKA CVITNSYFTQAAQKLAQANEVLLIDRDE WVRFLNEKR
HP0410 725 C4 GG GG GG GG GG GG GG GG GG GG GG GG GG	725 CACGAATAAAGAGGGTAAAAAACATTATCGCTAACCGCCGTAACGCTTCTATTTTAGTGGTAGAGCTAAGATTAAAGC GCCTTTTGATGGGGAATTACGCATTGAAACGGTTTATGAAGAAGTCGTTGTGTTGGTGGTAGAAATGGCGATCAAGAAG CTAAATTTGATGGGGAATTAGGCATATTGTCAAGGCTTTATGAAGAGCGTTGGCGGTGGCGTTGGCGGGAAG GTGTATTTGCCTTATGCTAGTGGGCATAATGGCGAATTAGCCGGCGTTGGCGGTAGATTGAGGGGAAA TGTGCCTA	726 TNKEGKNIIANRRNASILIVVEPKIKAPFIL GELRIETVYEEVVVSVKNGDGEAKFVIS RRSDIVKPSELAGVGGKIEGKVYLPY,85 SGHKVHKGGSIADIIQEGWNVP

ي			
S			
	•		
		۰,	

02/066	501	1	PCT/EP01/15428
728 SSDNPLADEPDLDYANMSAEEVEAEIES RLLNKROEADKERRAQKKQEAKPKGES VTPTKETPKAPKTETK	730 LKNWLSHPMAFIEFVLRRMADSYLLDC PLEKDKALKEMI GFLKNFSLLLQSEYK PLIATLLQAPLHVLGIRERVSFQPFYPK TEKPNRPORFAHVSSAPSLEFLEKLVI RYLLEDRSLLDLAVGYIHSGVFLHKKQ EFDALCQEKLDDPKLVALLLDANLPLK KGGFEKELRLILRYFERQLKEIPKSSL PFSEKMICLKKARQAIMKLKQGELVAI	732 NASSLTIĞERLYRHEISRLÖVKTDETLK LIKEAKKRLNYNDDIRDVLQGLLNIVPD SITINSIEIDDĞSVVVSĞKTPSKEAFYFL FÖNKLNPMFDYSRAEFFPLSDGWFNF VSTNFSNSLLIKNPESIK	KNININVNEKLAGFGKEEVMTNEVSAF LASCKDGGTLPNAGVTSNTWGAGCAY VGETISALTNSIAHFGTDEDDIDDAENI ADTLUNFKSRYSELGNTYNSITTALSKY PNADSLONIVSKKNNPYSPOGIETNY YLNONSYNOIOTINDELGRNPFRKVGI VNSÖTNNGAMNGIGIQVGYKÖFFGÖK SDVWTYGFGADALYNFINDKATNFLGK SDVWTYGFGADALYNFINDKATNFLGK ATVNNVYNAKMNVANFÖFLFNIMGVRMS NICASKKKGSDHAAOHGIELGLKIPTIN TNYYSFMGAELKYRRLYSVYLNYVFAY
727 ATCAAGCGATAACCCGCTAGCCGATGAGCCGGATTTGGATTACGCTAACATGAGCGCTGAAGAGGAGGGGGGGG	729 CCTTAAAAAATTGGCTATCGCACCCCATGGCTTTATTGAGTTTTTTAAAAAACTTTTCCTTGCTTTTTAGGAAAATTGGCGATTCCTTTTAGAAAAATTGGAAAAAGGAAAAGGATTAAAAAAGGATTAGAAAAGGAATTAGAAAAGGATTAGAAAGGGATTACCTTGCTTTTTACAAAGGGATTACCAAAAGGATTTTCAGGCCAGTTTTCAGGCCAGTTTTCAGGCCAAAAGGCATTTTCAGGCCAAAAGGCATTTTTTTT	731 ACAACGCGTCCAGTTTGACGATCCAAGAAAGGCTCTACCGCCATGAAATCAGCCCGCTTACAGGGTTAAAGAAGGCTGATGAA ACCTTAAAACTCATTAAAGAAAGCGTTTGAATTATAACGATGATATACGAGATGTTTGCAAGGGCTTTTG ACCTTAAAACTCATTAAAGAAAGCCGTTTGAAATAGACCAAGAGCGTGGTTTTGCAAGGGCTTTTG AATATTGTCCATCACTCACTATTAATAGCATTGAAATAGACCAAGCGCAAAGCGGTGGTTATGCGGAATTTTTCCCTTT AAGCGATGGGTGGTTTAATTTTTGTTTCAAAAACAACTTAAAAAAACCCCTTTAAAGAAACCCCTTTTAAAAAAAA	733 GAAAAACAATAATĞITAACGAGAAATTAĞCAGGATİTGĞGAAGAAGAAĞTAATGACCAATİTTĞITTAGCGCCÇT TTTGGCAAGCAGTAATAATĞITAACGAGAAATTAĞCAGGGATİTTGGGAAGAAGAAGAACAATAACGAAGAGCGGGTTGCGGG TTTGGCAAGCTGCAAAGATGCAACCAACGCATCGCTCACTTTGGCACTTGGGGGGGG
2	2	<i>K</i>	73
HP1067	HP0650	HP0650	НР 0650

HP0650	735	735 AAAAACAAATAGAGCCTGGCGCCTAAAACCTATCTTTTAAACAACGGCGCTGGCGGCGCTAGAGCGTTATTAAACCTTT TAGATTTGAGCGCTAAAATAGAAGATCCTATCACTTTAAAAACGCTACAATCCTTACGGCCTCATAGCCTAAATGATG GATCTTATAGCGATGATACGCATTATAACCTTACTAGCGCGTTAATCAAATCTTTAAGAGGGAGCGATGAAAACGCTT CCATCTATTATCTGGCGCGCTTGATTGCTGGCGGGGGAAAACCCGGAATTTATCGCCAGAAGGCTGGTGATTTTGCG AGCGAAGATATTGGTAACGCTAACCCGAACGCCCTTAATTTAGCCGCATCTTGTTTGCTTTGCTAACGCTAACGCTAACGCCAATGCGTGATTTATCTGGCAAGTCTAACGCCAAGTCTATAGGC TACCCTGAAGCGCCAACGCCAATGCGTGATTTATCTGGCTTGTTCGCCCAAGTCTAACGCGCTTATAGA GCGATCAAGCGCGATCGGTTC	736 KQIEPGAKTYLLNNSA GDARALLNI, S SAKIEDPITLKTLQSLRPHSLNDGSY S DTHYNLTSALIKSLRG;3DENASIYYL, S LIAGGENPEFIARRLVI FASEDIGNAN, S NALNLAASCLFAVKQI(3YPEARILSC; VIYLACSPKSNTAYRA NQALDCV
НР0650	737	737 CTTTATAGATGCGCGTTTGTTTGGGCGAACGGCTGAAATCGCTAACCAGTATTTGAGCAAGGGTTCAAGCGTTTTGA TAGAAGGGCCTTTGACTTATGAGAGTTGGATGGATCAAACGGGCAAAAAAAA	738 FIDARLFGRTAEIANQYLSKGSSVLIEG RLTYESWMDQTGKKNSRHTITADSLQ FMDKKSDNPQANAMCIDSIMHENSNNA YPANHNAPSQDPFNQAYAQNAYAKEN LQAQPSKYQNSVPEINIDEEEIPF
НР0650	739	GACCGTITTAGCTAATGAGCAAGTCATTGATGGGAGGTGTTGGCGTTGCGAAGGTTATTCAAAAAGAACTCT ATCAATATTTGAAGATCACAAAATTACGCTGAAGAATTGCTAAAAGACTTTAGGGGTTTTAGAAGATCATTGGCTTC TCAAGTCCTAATCATGCAAAAAAAACTGGATAGGAAAATCTAGCGGGTTGCAATTTGGTTTTAAAATCGCTGATGAGTG CTTGAAAGCTTGCAATGCAA	740 TVLANEQVIDGRCWRI:DTEVIQKELYQ YYLKITNYAEELLKDLEALEDHWPSQV LIMQKNWIGKSSGLQFGFKIADECLKA CNGIQEIEVFTTRADTI YGVTYIAIAPEH PLVEHAIKQVSQEVSKMIKAILNTTQRE RALEKKGAFLGIYAIHFLTKQKIPVWVA NFALANYGSGALMGVI?ACDERDFEFA NLYHIP
HP0776	741	741 GTGCATGTTTGATGGCTATACGCATTATTTGAATTTGGTGCTTGTCAATTGCCCCATAGAGCTCTCTGGTGTGCGGAGA ATGCCATTGAAGAAAGCGAAGGGGTGGGTGGGGGGGGGG	742 CMFDGYTHYLNLVLVNCPIELSGVREC IEESEGVDGAVSETASSHLCVKALAKG S
HP0776	743	743 ATGGCGGGATTGCGTGCGCGAATTTGTTGCATAAAAATTCAGGGATCACGATAGATA	744 GGIACANLLHKNSGITIDIGGGSTECALI EKGKIKDLISLDVGTIRIKEMFLDKDLEV KLAKAFIQKEVSKLPFYHKNAFGVGGTI RALSKVLMKRFCYPIDSLHGYEIDAHK NLAFIEKIVMLKEDQLFLLGVNEERLDS IRSGALILSVVLEHLKT3LMITSGVGVR EGVFLSDLLRHHYHKFPPNINPSLISLK DRFLPHEKHSQKVKKIECVKLFEALSPL HKIDEKYLFHLKI
нР0776	745	745 ATTCTTCTTTACAAAGCGAACACATCCACCCTTGTCCCGGAAGCGATGCTTAGGGCAAGCGCAGTG 745 ATTCTTCTTTACAAAGCGAACACATCAATTCCCCCCTTGTCCAGAAGCGCTTTAGGGCAAGCGCCATG AAAAAGAAAGAAAGGAATTTAGGTTTTTACCTTTGAAAAACCGCCTTTGGGAATTATCTCTAATTC TATTTGTGAGTTTAGGCGAATTTATAGAAAAATTCCCTAACCGCCCTTTACCGCCCCTATGTAGAATTCAATTCAATTTAGGGCAAAATGAAATTGCCGTAACCGCACTAGAAATGAAAAACGCCACAAGCCTGAGGGCGTAGAAATGAAAAAACGCCACAAGCCTGAGGGCGTGAAATGAAAAAGGGCAAAATGAGAAATGAGAATGAAAAAACGCCACAAGCCTGAGGGCTTGGTATTTAGAAAAGGGATAGAAAAAGAAAAGAAATGACTTTAGAAAAAGGGATAGAAAAAGAAAAAGAAATGACTTTAGAAAAAGGGATAGAAAAAAAA	746 SSLOSEHINSPLVPEA WIALGOAHWI-LI KEYVLASFYFDEYIKRFGTKDNVDYL'THE CONTROL STANDARD SINSIVSI LKLOSHYYAFKNHSKIOGERISNSIVSI EFIEKYPNSRYRPYVEYMQIKFILGOPL LNRAIANVYKKRHKPEGVRYLERID'T TLEKETKPKPSHMPWYVLIFDW

12 2 2 11 2	7	PCT/EP01
O PLNKLDEKPTRSASLWDITCDSDGEI/ FDSTKPLFLHDIDIDEEFYFLVG/ YQEVLGMKHNLFTHPTEFSVVFDEKC DYEVEDICEAGTILDVLDDLÖYDTKEIR RLLKOKIEDNNOLDMEEKKEIMGRLY MLSENGYLRTIS	ZIKEVLESAMDLITENORKGSLEVTGIPT GFVOLDNYTSGFNKGSLVIIGARPSMC KTSLMMNMVLSALNDDRGVAVFSLEN SAEQLALRALSDLTSINMHDLESGRLD DDQWENLAKCFDHLSQKKLFFYDKSY VRIEQIRLQLRKLKSQHKELGIAFIDYLC LMSGSKATKERHEQIAEISRELKTLARE EGIFIALVQLNRSLENRDDKRPILSDIK	754 PNTTAKKOYTKYSEKOLFNLIHOLERKI KKMONDRISFKEKMAKELEKRDÖNFK DKIDALNELLOKISOAFDDKRDCCLGH EIPNIETQOAMRDALNGINLTQIDSLDD FTNELKRENSKGFENVCFSV
	75	757
749 CCCTTGAATAAATTAGATGAAAAGCCCACCAGGAGTGCGAGCTTGTGGGATATTACTTGCGATAGCGATGGGGAAAT CGCTTTTGATTCACGCAGCCCTTGTTTTTGCACGATATGATATAGATGAAGAAGAAGAATATTGC CGCTTTTGATTCAGGAAGCCCTTGTTTTTGCACGATATTAGATATAGAGAAGAAGAAGAAGAAGAAGAAGCTTTTGATTCAGCCACCCTACGGAATTTAGCGTTTTTGATTTTGATGCCTACGGAATTTAGACGTTTTTGAAAGAAGAAATCGAAAACGAAAAATTGAAGCCCAAACGAAATTGAAACCAACC	751 IATTAAAGAAGTGCTTGAAAGCGCAATGGATCTCATTACAGAAACCAAAGGGGGGGG	753 GCCTAACACCACCGCCAAAAAAGACTACACAAATACAGCGAAAAACAGCTTTTTAATTTAATTTAATCATCATCATCAGCGCGAAAAACAGCTTTTTTAATTTAATTTAATCATCATCAATTAGAGCGCGAAAAACAGCTTTTTTAAGAAAAATGCAAAAAAAGGGATCAAAACAAAAAAAA
4PQ897	1P0897	нР0895 -
	749 CCCTT GAAT AAATTA GAAGAAA GCCCACCAGGAGT TGCGGATATTA CTTGCGATAGCGATAGGGAAAT CGCTTTTGATTCCACGAAGCCCTTGTTTTGCACGAGTATAGATATAGGAGAATTTTTTTT	749 CCCTTGAATAAATTAGATGAAAAGCCCACCAGGAGTGCCGACTTGTGGGATATTACTTGCGGATAGCGATGGGGAAAT CGCTTTGATTCACAAAGCCCTTGTTTTTGCACAATTAGATATAGATTATCACGCACCCTACGGAATTTTAGCGTTCTTTTTA GTGGAAGGCGATTTAGAAGCAAAACCAAATTGAGACCAAACCGAATTAGCGGTTGGATAGCGTTTTTGAT GAAAAAGGCGATTTAGAAGTGGAAGCATATTTGTGAAACCAAACCGAATTAGACTAGACAATTGAATGATTTT GAAAAAGGCGATTTAGACTTAGAAAATTGAGACAAACCAAACCAAACCAAACTAGAAATTGACTTTTAAAAGAAAAATTGAAATTGAGATTTTAGACATTAGACATGAAAAATTCAAATTGAAATTGACATTTAGACAAAAAAATTAAAAAAAA

ς		П
5	•	٠,
-		
•	-	-

VO 02/066501	·		_	
756 ADPSTSKKRADKGLKKVFKDSKKDAC GFIYEISEFMKAYTALLKKODRYVYLLR YLPSRYWASILTTALYVKYPDFDALKKL YLSRYWASILTTALYVKYPDFDALKKL LVSYYYOTWAGGTITRIKOTSINIIKNV KSWEYTIKELILNSIDSYNTFDQYLYN LWDSSSVYHSKWYFPVLALANYFMAD EEKPHFIAMDAETQVEHILPQTPKRGS QWNAADFDKEKREEWNNIIANLTLLKR KKNAHALNGDFDEKIRKIYGGKDTSKVI SCYDITKELYSNYRKWNEKSLQERYKS LYNTITPVLHIEGQEDDFEDDELE	758 LNLKKSFÖKDFDKLLINGFDDSVLNEVI LTLRKKEPLDPOFODHALKGKWKPFR ECHIKPDVLLVYLVKCIDELILLRLGSHS ELF	760 KYSKKQLFNLIHQLEF:KIKKMQNDRISF KEKMAKELEKRDQNF:KDKIDALNELLQ	HISUAF GLKKVFKDSKKDACGFIYEISEFMKAYT ALLKKDDRYVYLLRYLPSRYWASILTA LYVKYPDFDALKKLLVSYYYOTWIAGG TITRIKOTSINIIKNWKSINKSVETIKELILN SIDSYNTFDAYTYNLWDSSSYYHSKW VRPVLALANYFMADEIJRPHFIAMDAET QVEHILPGTPKRGSCIVINADFDKEKRE EWVNNIANLTLKRKKNAHALNGDFDE KRKIYGGKDTSKVISCYDITKELYSNYR KWNEKSLQERYKSLYNTITPV	764 AFALPIINNLKNNHTIEALVITPTRELAM QISDEIFKLGKHTRTKTVCVYGGQSVK KQCEFIKKNPQVMIATI?GRLLDHLKNE
37	75	76	792	764
755 CGCTGATCCTAGCACTTCTAAAAAGAGAGCCGATAAGGGATTAAAAAAGGGTGTTCAAAAAAACAGGCAAAAAAGACGCTT GCGGGTTCATGAGATCAGCGAGTTCATGAAAAAAGACCGATACCTTATACCGATTTTGCAAAAAAACCATTATGACCGATATTTGAC GCGGGTTCATTGAAAAACCTTTATTGCAGCAACTTGGATTGCAGGAGCCGATCAGCAAC GCTTTGAAAAAGCTTTTGGTGTTTATTACCAAACTTGAATGCCTCATTATTGAAAAACCATCAAGCAAC GCTTTGAACAATTATCAAAAACGTTAATTACCAAACTTGAATGCGTTCATATTGAATAGCATCGA GCTTTGAACATTATCAAAAACGTTAAAAAGCAATAAGGATGAAACCATCAAAGAACCATCAAACAAC GTCTTATAACACTTTGATAACACTTAAAAACTTATGAAAAAGCGTGAAGCGTTTATCGCTATGAAAAAGCGTGAAGGAATGAGAATGAGCAACCCAAATTATGAAAAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	757 CTCAATCTTAAAAAATCTTTCAAAAAGATTTTGATAAATTGCTTTTGAATGGGTTTGATGATGGCGTTTTGAATGAA	759 AAAATACAGCAAAAAACAGCTTTTTAATTTAATCCATCAATTAGAGCGAAAAATCAAAAAGGTGCAAAATGGATAGAATT TCTTTTAAAGAAAAAATGGCTAAAGAATTGGAAAAAAGGGATCAAAAACTTTAAGGATAAAATAGACGCGTTAAATGAA CTCTTGCAAAAAATCAGTCAAGCTTTTG	761 AGGGATTAAAAAGGTGTTCAAAGACGAGAAAAGGCCTTGCGGGTTCATCTATGAGATCAGCGAGTTCATGAAA GCCTATACCGCATTGCTAAAAAAACAAGACCGATACGTCTATTTTTGAGGTATCTCCCCTCTAGGTATTGGGCCAGC ATTTAACGACTGCCCTTTATGCAAATACCCTGATTTTGACGCTTTTGAAAAGCTTTTGGTGTCTTATTATTACCAA CTTGGATTGCAGGAGCACGATCACGCGCATCAAAGCAACAGTATCAAAAACGTTAAAAAGCAATAAA CTTGGATTGCAGGAGCACGATCACGCGCATCAAAGCAACAGTTATCAAAAACGTTAAAAACCATTAT GGGATAGCACCATTTTATCATAGCAAATGGGTGCGTCTTTTAGCCCTAGCTAAATTATTTCATGGCAGATGAAG AGAAACCCATTTTATCGCTATGGATGCGAAACCAAGTGGAGCATTTTTGCCAAAAGAAGAGGCGCAGT AAAAAGAACCGTTTTAATCGCTATGGATGCGAAACCAAGTGGGAGAATTATTTGCCCAAAAGAGGCGT CAATGGAACGCGCATTTTAAACGGGGATTTTGATGAAAAAAAGAAAATTATTGCCAAAAGGGCGT AAAAAGAACCATCAAAAAAAAAA	763 CCGCTTTCGCTCTGCCCATTATCAACAACCTTAAAAACAACCACCATAGAAGCCCTAGTGATCACGCCCACCAGA GAATTAGCCATAGAATTAGCGATGAGATTTTCAAATTGGGCAAACCACCAGGACTAAAAACGGTGTGGGAATTGGGCAAACCACCAGGACTAAAAACCGTGTGGGAGCGTTAAAAAGCAATGCGAATTCATTAAGAAAAATCCCCAAGTGATGGTACGCTACACAGGGAAGGCTGC TCGATCACTTAAAAAAGCAATGCGAATCATTAAGAAAAAAAA
HP0895	HP0895	HP0895	HP0895	HP0653

8

2/066501	 -			PCT/EP01/15428
766 NYGTT	768 LKNLDEKAIPTPYMKEPKQDGARTAVY HKDGVHLEWVALGYKVPAFKHKDQVA LDALSRLLGEGKSSWLQSELVDKKRLA SQAFSHNMQLQDESVFLFIAGGNPNV KAEALQKEIVALLEKLKKGEITQAELDK I KINOKAD	770 VFKÖSKKDACGFIYEISEFMKAYTALLK KQDRYVYLLRYLPSRYWASILTTALYV KYPDFDALKKLLVSYYYQTWIAGGTITR IKQTSINIIKNVKSNKSVETIKELILNSIDS YNTFDQYLYNLWDSSSVYHSKWYRPV LALANYFMADEEKPHFIAMDAETQVEH ILPOTPKRGSQWNADFDKEKREEWVN NIANLTLLKRKKNAHALNGDFDEKRKIY GGKDTSKVISCYDITKELYSNYRKWNE KSLGERYKSLYNTITPVLHIEGQED	772 KHYTSTGVREPDKCTKSFKKSALMSY DLALGYLVSKNKQYGLKAIEILNAWAKE LQSVDTYQSEDNINFYMPYMNMAYWF VKKAFPSPEYEDFIKRMRQYSQSALNT NHGAWGILFDVSSALALDDNALL	774 FKROEILNEFYLKNAIKÆLNNAFKKD PSLKDLEKEKELIIQTLFNELTQNHHÖG NPHA
765 AATTATGGGACAACTTAAACCAACGCAAGGGAGTACTATGTTATCAAAAGGCATCATTAAGTTGCTAAACGAACG	767 CCTTAAAAAACCTTGATGAAAAGCTATCCCCACCCCTTACATGAAAGAGCCTAAGCAAGATGGAGCCAGAACGGCA GTCGTCATAAAGATGGGTCCATTTAGAATGGGTGGCCCTTGGGTATAAAGTGCCTGCTTTCAAGCATAAAGATCA AGTCGCCTTAGACGCACTAAGTAGGCTTTTAGGCGAAGGCAAAAGCTCGTGGTTGCAAAGCGAATTAGTGGATAAAA AACGCTTGGCTTCTCAAGCTTTCTCGCACAACATGCAATTACAAGATGAAAGCGTGTTTTTATTCATTGCGGGGGGTA AACGCTTGGCTTCTCAAGCTTACAAAAGAAATCGTAGCGCTTTTAGAAAAGCTGAAAAGGGCGAAATCACTC AAGCGGAATTAGACAAGCTCAAAATCAATCAAAAAGCTGAAAAAGCGCGAAATCACTC	769/AGGTGTTCAAAGACAGCAAAAAAGACGCTTGCGGGTTCATCTATGAGATCAGCGAGTTCATGAAAGCCTATACCGCA TTGCTAAAAAAACAAGACGCATACGTCTATTTATTGAGGTATCTCCCCTCTAGGTATTGGGCCAGCATTTTAACGACT GCCCTTTATGTCAAATACCCTGATTTTGACGCTTTGAAAAAGCTTTTAAAAAAGCTTATAACGACTTGGATTGCAG GAGGCACGATCACGCGCATCAAGCAAACCGTATCAAAAAGCTTTAAAAAGCGTTAAAAGCGTTGAAACCTTGAAAAGCGTTAAAAGAAACCGCATCAAAGCGCTTGAAAAAAAA	771 CAAAACACTACACTTCTACCGGGGTTAGAGACCTGATAAATGCACAAAGAGTTTTAAAAAATCCGCTCTCATGTCCT ATGACTTAGCGCTAGGTTATTGGTGAGTAAGAATAAGCCTTAAAGGCTATAGAAATTTTAAACGCTTGGG CTAAAGAGCTTCAAAGGGTGGATACTTATCAGAGCGAGGATAATATCAATTTTTACATGCCTTATATGAACATGGCTT ATTGGTTTGTCAAAAAGGCGTTCCTAGCCCAGAATATGAAGATTTTTAAGCGGATGCCTTATATGAACATGGCTT ATTGGTTTGTCAAAAAAGGCGTTTCCTAGCCCAGAATATGAAGATTTCCATTAAGCGGATGCGCCAGTATTCTCAATCAG CTCTTAACACTAACCATGGGGCGTTCTTTTTGATGTGAGTTCTGCGCTAGACGATAATGCCCTT	773 ITTTAAGCGTCAAGAAATCTTAAACGAAGAGTATTACCTAAAAATGCCATAAAAGCAGAATTAAATAAGGCTTTCAAA AAAGACCCCTCAAAAAGAATTTAGAAAAAAGAAACTTATCATTCAAACCAGAACTCACACACA
HP0653	HP0653	HP0653	HP0411	HP0411

02/066501			PCT/EP01/2
776 NNHVIDGADKIKVTIPGSNKEYSATLVG TDSESDLAVIRITKDNL PTIK FSDSNDIS VGDLVFAIGNPFGVGESVT GGIVSALN KSGIGINSYENFIQTDASINFGNSGGALI DSRGGLVGINTAIISKTGGNHGIGFAIP SNMVKDTVTQLIKTGKIERGYLGVGLQ DLSGDLQNSYDNKEGAVVISVEKDSPA KKAGILVWDLITEVNGKKVKNTNELRN LIGSMLPNGRVTLKVIRDKKERAFTLTL AERKNPNKKETISAGNGAGGQLNGLQ VEDLTGETKRSMRLSDDVGGVLVSQV NENSPAEQAGFRQGNITKIEEVKSV ADFNHALEKYKGKPRFLVIDLNGGY	RIILVK 778 EQTLKANDLEVKIKSVGNPIKGDNTFIL SPTLKGKALEKAIVRVQFMNIPEMPGM PAMKEMAOVSE	780 EKPKPKPKPITPQSTYGKYYISQSTV LKNATELFAEDNITNLTFYSL TPVYVTA YNQESAEEAGYGDSSLIMIONFLPYNL NNIELSYTDNQGNVSLGVIETIPKOSQ IILPASLFNDPQLNADGFQQLQTTRF SDASTQNLFDKLSKYTTNLQMTYINYN QFSSGNGSGSKPPCPPYENGENCTAK VPPFTSQDAKNLTNL	782 DKIALFDGKTEFLAKDCVEKYGILPSGF TDYGGIVGDSSDNYKGVKGISSKNAKE LLGRLGSLEKIYENLDLAKNLI.SPKMYR ALHDKASAFLSKELATLERGSIKEFDF LSCAFPSENPLLKIKDELKEYJSTISTLR DLENSPTPLILDNAPLLDNTPALDNTPK KSCMIVLESAAPLSAFLEKLEKTNARYF ARLVLDKEKKVLALAFLYEDCGYFLPL EEALFSPFSLEFLQNAFFKMLGHQIG HDLKPLLSFLKAKYQVPLENIRIQDTQII AFLKNPEKYGFDEVLKEVIKEELIPHEK IKDFKTKAEKLELLSVELNALKRLCEYF EKGGLEENLLSLAREIETPFMKVLGM
775 CTAATAACCATGTGATTGATGGCGCGGATAAGATTAAAGTTACCATTCCAGGGAGCAATAAAGATATTCCGCCACCATCAATGCGCACTCTCTAATGATAAGCATCTGCCACGATCAAATGCTCTTTGGCATCTGCCACGATCTGCCACGATCTCTCTTTTCATCTCTCTTCTCTTTTTGGATTTTTGGTGTTTTTGGTGTTTTTGGTAACCCTTTTTGGCGCGAATTTCTTCAACAGCGTTTCCAAAGAATTCTCTTCAACAGCGTTTCAGCGCGCATTTGGTTTTCATTCA	777 GGGAGCAAACCCTAAAAGCTAATGACTTGGAAGTGAAAATCAAATCCGTGGGTAACCCCATTAAAGGCGATAACACT TTCATTCTCAGCCCCACTTTAAAAGGTAAGGCTTTAGAAAAAGCTATCGTTAGGGTGCAGTTTATGATGCCTGAAATG CCCGGCATGCCAGCGATGAAAAGAAATGGCGCAAGTGAGTG	AAGAAAAACCTAAACCTAAAGCCCAAAGCCCATTACCCCTCAAAGCACCTATGGGAAATACTACATCTCCCAAAGCACAAAAAAAA	781 CGATAAAATCGCGCTITTTGATGGCAAAACGGAGTITTTGGCGAAAGATTGCGTGGAAAATACGGGGATTTTGCCGA GTCAATTCACGGATTATCAAGGCATTGTGGGGGGTAATTACAAGGGGGTTAAAGGCATTGGGAGCAA GACGCTAAGGAATTGTTGCAGCGATTAGGGGATAGCAGCGCGATAATTACAAGGCGTTTGGAAAATTTACT GACGCTAAAATGTATCGAGCGATTAGGGACAAGCAAAGCGAAAAATTTAGAAAATTAAGCAAAATTTACT CAGCCCTAAAAATGTATCGAGCCGATTAGGACAAAGCAAAGCGAAAAGCCAAAGCAAAGCCACTTTAGAAA GAGGATGCATTAAAGAATTTGATTTTTTAAGTTGCGCTTTTCCTAGCGAAAACCCCTTTTTGGAAAATTAAAAGAATTTAGAAAACTGAGCCCTA TTAGACAACCCCCGCCTTTGACTTTAAGGGATTTAGAAAAATCCATGCGCTTTTGGGATAAAGAAAAAGTTC CGCGTTTTTAGAAAAACTAGAAAAACTAAGGCAAAAACTTTTTGCGCGTTTTGGGATAAAGAAAAAAATTTTAGAAAAAAAA
HP0411	HP0411	HP0411	HP0411

HP0887	7837 0 4 4 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	783 GGTATGGCAAGCCAAAGCTTGTTTTGCCAATAATTTTGTGCCTGGAGGCTTGAATCAAGCCTTGATAAAATAG GCTCTAGCTCTGATGCAAAGACTTACAGAACTTCTTGGATAAAACGACTTTTGGGGATATTTTAAATCAAATGATTG GCTCTAGCTCTGATGCCAAAGACTCATTTCTTGGTCGCAGGATTTGGGGGATATTTAGTGAATATCGATTAA AACAAGCCCCCTTAATCAAAAACTCATTTCTTGGCTCGCAGGATTTGAGCGTTTTAGTGAATATCGCTTTAA ATAGCATCACTAACCCTAGTAAAGAGCTGACTAGCATTTCTAGGCATAGGTGAAAAAGCGTTAAATGACTTATTAG GCGATGGCGTAGTGAAAAATCATGAGGCAATCAAGGCCAAATGAAAAATCATTGCTGATAAGGC TTTGGAGGCGTTTATCAGCAAGGTTTAGGCCCCCAAATCATTACAAGAATTGAAGAAATTGGGCCATG	784 YGKQSLSSFANNFVPGGLNQALDKIGS SSDAKDLQNFLDKTTFGDILNQMIEQA PLINKLISWLGPQDLSVLVNIALNSITNP SKELTSTISSIGEKALNDLLGDGVVNKI MSNQVLGQMINKIIADKGFGGVYQQGL GSILPQSLQDELKKLGM	JKIGS HEGA SITNP VNKI QQGL
HP0887	785 (0 1 1	785 CCGGGAATATCACCGTTGATGGGCCTTTAAGAGTGAATAATCAAGTGGGTGG	786 GNITVDGPLRVNNQVGGYALAGSSAN FEFKAGTDTKNGTATFNNDISLGRFVN LKVDAHTANFKGIDTGNGGFNTLDFSG VTGKVNINKLI	SSAN RFVN DFSG
HP0887	787	787 GCAATGGGGGGGTACAGGCAGTGGGAATGGCACCAGTCAAATCAACACCAGGCTACCAGATGCTCACAGACG CCAGCGATGGCAATAGGGAATTAGGGAATGGTAGTAGTGGCAATAACGGCTATACGCCATGCAATAGCACCAT CCAGCGATGGGAAATTAGGGAACAATTGTTATGAACCCAACAAAAAAAA	788 NGASGTGSGNGTSQINTAYQMLTDAS DGKLGTYSSSGSNNGYTPCNSTNGS NKTSGNNCYEPNKQQNATTATATTDS NLQKVYNDAQKIANIIASSGNNKGVEN GLKQFFEALKNNSSSLSNLCGNGSSG SSGTTCSGWLINLLGAIPTNGVSDTNN LINLLTFIKTAGFIQNNDSSVSTSLTSA FQAITSAISQFGALQNDISPNAILTLLQ EITSNTTIQSFSOTLRQLLGOKTFFMA QQKLIDAMINAFNQVQNAQNQANNYG SQPVLSQYAAAKSTQHGMSNGLGVGL GY	TDAS TNGS TNGS VEN SSG TILLO TILLO FFMA SVGL
HP0887	789 789 79 4 4 6 0 0 1: 00	789 GCAATACGACTTTAAGGCGATGTTTACTCCCTTGATCATGCAAGCGCAGTTGAGGAAACATTGATAATTTTGT GGAAAAAGGCTTTAAGGAATTTTGATAATTTGACGCTAACCCTATAAAACGATTTTTGGAGAAACATTGATGATAATTTTGT GGAAAAAGGCTCTGCTTTGATAAATTTTGACGCTAACCCCTATAGCTTCATGGTTGCTTGAGGAAATAATCATG AGAGCTACGGCGATAAAAATCTTTCACTCTCATCAGCATTTGAATGCCTTTGCTTCATGCTTGCT	790 ÖYDFKAMFTPLIMOAOLSI RNIDNFVE KGSALIDKFDANPYKTIFGERK	FVE
HP1198	79107 A T A D D	191 CAATGCGATTGAGCAAGATGAAATCACTAAAAAATTGAAGCAGAAGAĞTTGTTAGAGCATGTCCAAAAAAGCGCTGA ATCAAATGAGCGAAAGAGAGCAAATCCTTATCCAGCTTTTGAAGAGTTGAATTTGAGCGAGATTAAAGAGA ATCAAATGAGCGAAATCGCGCATTTCTCAAATCATTAAAGAGTGATTAAAAGGTGCGTAAATCCTTAGGAGTGG TTTTAGGCATTACTGAATCGCGCATTTCTCAAATCATTAAAGAGTGATTAAAAAGGTGCTAAAATCCTTAGGAGTGG ATCATGGCTGATATTTTAAGCCAAGAAAATTGATGCGCTTTTTAGAAGTGTGATAATTCAAAAT GTCCAAAAAAAAGATTATTCCCGCAGGCGCAGCGTAACCCTCTATTCAAACGCCCTAATCGTGTGAGGA GCCAAAAAAAGAAAGGAGTACCATGACAAAATGGCTAGGGAATCTTTTCAAACGCCCTAATCGTGTGAGTAAGGA GCAACTGCCGCTTTTTAGGAGTATCCTGACAAAATGGCCTCTTTTTAGGAGTAATCAAAAAGTCCCTAATCCTGTGTGAGTAACGCCCTAATCCCGCCAAACGCGCAAACGCCCTAATCCTTTTAGGAGTAATCCCGCAAAAATGCCTTATTAGGAGTAATCAAAAAAAA	792 NAIEGDEITKKIEAEELLEHVÖKALNÖM SEREGILIÖLYYFEELNLSEIKEILGITES RISĞIIKEVIKKVRKSLGVDHĞ	NOM

02/066501			PCT/EP01
794 VDEKKGHLILGEVEQDNGVFESSGGR VIFAIGRGKSLLEARNHAYEIAQKVHFE GMFYRKDIGFKVLDLKEYS	796 NAFKNLIRRSAKTTFIYPINSKAVRVIRG RHGDFLNRFKTLYSTSANLTQCAYDKE IASNLADVIVSD	798 HLTDSKGVRVDFKNTILI.TSNVASGAL LEENLSEAEKQKAIKESLRQFFKPEFLN RLDEIISFNALDSHAVINIVGILFENIDKK ALERGINITLDEEAKELIAEAGFDRFYG ARPLKRALYEMVEDKLAIELILEDKVKE NDSVAFVVENNEIVPKIK	800 KL
793 GGTTGATGAAAAAAGGGGTCATTTGATTTTAGGGGAGGTGGAGGATAATGGCGTGTTTGAAAGCAGTGGGGGGGG	795	797 GACATITAACCGATAGGAGGGGGGGGGGGAATTCAAAAACACGGATTTAACCCAGCAATGTGGGCTAGT GGTGCGCTTTTGGAAAATTTGAGGGAGGGAGAAAAGGCGATTAAAGAGAGGCTTGAGGCCAATTCTTTAA GGTGCGCTTTTGAAAAATTTGAGTGAAAACCGGAGAAAAGCGCCTTAAAGAGAGCTTGAGGCAATTCTTTAA GCCGGAATTTTTGAAAACCGCTTAGATGAAAACCCTTGAAAGGCCCTAGATGCTGCTGCTGGGG GATACTTTTTGAAAACCGCTTCAAAAAAGCGCTTGAAAGGGGCATTAATATAAACCCTAGACGAAGAGCAAATTCGTGGG GATACTTTTTGAAAACAGGATTCAAAAAGGCGCTTGAAAAGGCGCGCCTTAAAAGCGCGCGC	799 AAAGCTTTAAAATCCATGAATAAAGTGAATAAAAGGAAAAAAAA
HP1198	HP1065	HP1198	HP1198

•	ŧ	٠	۲
-		3	ı
Ç		ς	į
_			

	TTTAAGAGGCCTT	
	AAGGAĞTTTTAGAAACCCTCACCAAGĞĞÇTTÇAAATCCAGTATTTTAĞĞÇTCAAĞCTCTCTAAĞAĞĞĞĞAAACC TGĞĞĞAAATCĞÇĞÇTAĞÇĞÇATĞÇTTTTTTTTTTATAATĞĞATATTTGAAA	
	GTTTCATAACTTGATTTTAGAGGGAAGTCCAGGGTGTGGGAAAAGCATGATGATGATGGCATGCGTTATATTGCCTT TCCATTAAGCCTGAATGAAATCCTAGAAGAGAAAATTAGGCATTTTAAGGAGAGAAGAGAAATTAGAAGAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAAATTAAAAATTAAAAATTAAAAATTAGAAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAAAAATTAAAAATTAAAAATTAGAAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAAAAATTAAAAATTAAAAATTAAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAAAAATTAAAAATTAAAAATTAAAAATTAAAAATTAAAA	
	ACGCCTAGGTTTTAAAGAAGTTAAGGGGCAAGCTGTCGCTAAAGAGGCTTTGATCGCTAGGCGCTGTGGTGGCTGGC	
	CTITITICGCTIATCCCTAATTTGCAATGCTTTTTTGTGGGGCATTTTAAAGAAGCGTTAGAAATCTTGCAAAACCCTG	
	AACATTTCCCCATGCTTTAGACATTGCCATTAAACACCCCCATGCTAAGATCATTGCGCCTAAGGCCAATGAAGAG	
	AAAAACAAGATTGGCTTTTAAAGAGTGGTTTGCCTTTTGGGGAGTTAGGGCCTTGATGGCAAGATCAAACCCAATCCT	
·	ACCATCAACCTTTCCCCCTCAGATTTGCCTAAATCCGGGAGTCATTTTGATTTGCCTATCGCTTTTAATCGCTTTTGC	
	AGCTCTATCCAAGAAGCCAAACAGCGGGTTCAATCGGCTTTACAAAATAACGATTTCACTTTAAAAAATCAAAAATCAAAAAAAA	
806 KELOKKOKHE	avalchendret.letAdadadadtononadadtono	2001
4 12 12	AAAGGG	
SKVKIEEKR	TACAACTTGACCAAACTGAGAAATTCCGAAAATTCTTTAAGGCGTTTAGGATTCTTCTCTAAAGTCAAAATTGAAGAAA	
KIEVGDMYYINDVIISGNORTSDRIIRRE	ATGTCATTCAGGGAACCAGCGCACGAGGGATCATTAGAAGGGAACTTATTATTAAGACTTAAGAAAGGAACTAATTATTAAGAAGAAAAAAA	
ADKGYAFAVVKPDLDKDEKNGLVKVIY	GCATTTAGGGGGGGTGGCGCAATTTTAGAAACCGAAATCGCCGATAAGGGTTATGCGGTGGTGAAGCCAG	
EKALKVKRKDVFNIEHLRADAGILKTEI	GATTGACAACCCGGTAGTCCCCTTAAAAACCTTAGAAAAAGCGCTTAAAAGTGAAAAGGAAAAGATGTCTTTAATATTGA	
LHYKVKEGIOYRISDILIEIDNPVVPI KTI	ATTITICIACCATGACGCTAAGCTTCATTATAAAGTCAAAGGGGGATCCAATACAGGATTTCAGACATTTTAATAGA	
VYMBRGY! DAHISOEI KTDESTEDAK	ATTCTATGCGTATCCAAGATGTGTATATGCGTAGGGGTTACTTAGACGCTCATATTTCTTCGCCTTTTTTTGAAAACGC	
CONTREGSARLKRRMIESLSANKORDFM	GOMMAN CONTROLL GARAGA G	
VEVRTEKVSEGALLIVFDVNRGDSIYIK	Gearage Gearage George	
TFDEQKLEHAKTALKTALEGQGYYGSV	GECGACACCITITION ISAGCAAAATTAGAGCATGCTAAAAACGCCTTTAAAAACCGCTTTAGAGGGGCAGGGCTATTA	
804 AGVEIKGYGTEKEKDGLKSQMGIKKGD	803 TGCCGGGGTAGAATCAAGGGTTATGGGACTGAAAAGGAAAAAGACGGCTTAAAATCCCAAATGGGGATCAAAAG	HP1198
LIHFASKDALNI	TTTGTGCGAAGAGA	
DICENTIAL CESTADOSCIANIES PANC	GCCTTTAGAATCTTATAGAGACGGCTCGCAACATAAAATTGAACGCCCCAAGGTTTGCCCTATATGTTCGCATGAGC	
INVANITORIUM SEIEVUMIMESOKANIKS	AATTGAAAAAAGGATTGTCATGCTCAGTGATAGGGTCGTTGTCATTAGAGCGGCGGTGTGATCCCTAAAATCATCA	
VGVINGVGRSGAITPVALLEPVEIAGAM	CACACCGGTCGCTCTTTTAGAGCCTGTGGAAATTGCTGGAGCTATGATTAATAGAGCGACCTATAATAAAAAAAA	
KELGYTQKSPKFACAYKFPALEKHTKI	CONTRACTION OF TAXABLE CONTRACTOR AND AND AND AND AND AND AND AND AND AND	
YHTLIREREGFFALLDGMVIVVNELNIQ	AACAAAACCACCACCAAGAAATAGAAGACAATTACCACACCCCTAATTAGAGAAAGGGAGGG	
CLDFIVSLGFSAIQYLSLNKNHQEIEDN	CTITAAATTTTTAAGCTTTAAGGAGTGTTTGGATTTTATCGTCTCGTTAGGTTTTAGCGCCATTCAATACTTAAGCCCTA	
SEITKKRKLOFIPWGVGKHSLNFLSFKE	GAGTITGAGGCAACTTGATAGCGAAATCACTAAAAAGCGTAAAATTGCAATTCATTC	_
OERLNANEPLFANPRNAASGSI ROLD	GATITTGACGCTTTGAATCAAGAGCGCTTAAACGCTAATGAACCCCTATTCGCTAACCCCCAGAAACGCCGCATCAGG	
	CACATCGCTAATATCCCCCACGCTATCGCTTATAGGAAATAGAAATCAGGGGCGAAGTGATCATTCTAAAAAG	_
CRILKAYPSASFVCSPKLDGVSLNLLY		
802 NKNPHLMRMWSLDDVFNQSELQAWL	801/AA1AAAAACCCCCATTTAATGCGGATGTGGAGCTTAGATGATGATGTTCAATCAA	HP1198

/066501				PCT/EP	01/15428
- VIII - 10 CI IV	MDKPNVNPDKLKAECAELGYNPVDW GGEHEFIPVSAKTGDGIDNLLETILIQA GIMELKA 812 EREQTLNQLLAEMDGFGSENAPVIVLA		814 KKHILLENGKEPULEVVAEEVGESLONV KNVIKVTKEPISLETPVGNDIDGKFGD KNOKTKEPISLETPVGNDIDGKFGD QLNEREKAVIRMRFGLLDDI:SDRTLEE IGKELNVTRERVRQIESSAIK:KLRSPQY GRILRNYLRI 816 PNHRYFLFKEEGVYLGVGSITKINFFHK	HGYLGIYKNPFLKNGGETILKALEFIAFE EFQLHSLHLEVMENNFKAIAFYEKNHY ELEGRLKGFISKDKEFIDVLLYYKDKKG YNDQSLLKL 818 NALDYGVCEKCHSKNVIIT(1GNEMRLL	SLEMLAE
B07 ITTAACGCCCATCATTCAAAACAAGAGCGTCGTTTTAGCTGCTCTGATTTCCATAACCCAGAGCTAAAAGAACATG CATGGATAAAACTAACGCTTATGAAAAGCCAAAAAGACCGACAAAATAAAT	809 GATGGGGTGAAGCAGAGTATTGAAGCTTTAGAGCATGCAAAGGCCGCTAATGTGCCTTTGCTTTTTTTT	811 TGAAAGGCAAACCTTAAACCAGCTCTTAGCCGAAATGGTTTTGCGGCCGCAAAAAAGGCGGGGTTTTAGT TAGCCGCAACGAACCGTCGAAATCTTAGATCCGGCGTTTAAAGGCGGCGCTTTGACGGCGCGGGTTTTAGT TAGCCGCAACGAACCGCCCCGAAATCTTAGAAGGCGGTTTTAAAGGCGGCTTTGACGAACTTGCAAGGCGGTTTTAGT TTGCAAGAAGTCGCCAAACTCACTGCAGGCGCTTTCACAGGCGGTTGAAAGGGGGTTTGCAGGCGTTTTAAAAGGAACTGAATGAA	813 GCGCAAACACATTCAAGAAAACGGCAAAGAGCCTGATTTAGAAGTGGTGGTGGTGAAGAAGTGGGGGCTTTCGTTAGATAAACAAAC	815 CACCCAACCACCGCTATTTTTGTTTAAAGAAGGGGCGTTTATTTA	817 TAACGCGCTAGATTATGGGGTGTGTGAGAATTGCCACAGCAAGAATTGTGAGGCGCTTACCAGCAAGAATTGAGCCTTACCAGCAAGAATTGAGCGCTTACAGACATTAGAGACATTAGAGACACTTACAGAAGAAATTGAGAGACATTAGAGAAGAATTTAGAGAAAAAAAA
HP1198	HP1198	HP1198	HP0868	HP0868	HP0868

١	1	•	
¢	5	C	j
	_		

02/066501	1		PCT/EP0
820 MEDYASRTAGALERLDKIVETEGKND OTKLDTENLKIIETLRSKINGNQQKMLD KSKEMSRNFKLDSTKNEIDAIKDLIKKA NEQIANYNEMIKDIEKQKKSCKEQTWK FLVNEFKSDIQEYNKKYCGLEKGINNLE KAISENOFEVKKI EN	822 MRLARGEAU LITERESNGSPKILAI GAQQKGHFELTINFELTYDFKFILA SVLENEKHFKETLNFELTYDFKPTILA CDKHQNYTTTQMAFDFNTPLLQVGHH HAHFLASVLDALQDPHLNHPFIGWW DGSGAYENKIYGAECFYGDLERIEETA RFEEFWLLGGQKAIKEPRRLVLEIALKH QLNKLLKRVQKHFKEDELEIFQQMHDK KIQSIATNSIGRLFDIVAFSLDLTGTISFE AESGQVLENLALQSDEIAFYPFEIKNSV VCLKEFYQAFEKDLGVLEPERIAKKFF NSLVEIITALIVPFKEHWVCSGGVFCN QLLCEQLAKRLRGLKRQYFFHKHFPPN	HASSIPISALMAYFNIPTIIKKG 12 GCOFALKIOKESONRSPFELYSPLKRO 12 PASIEERTOVFRILDMAKKDANKPFL AGKTIATYRILNGGVWILSKNSNPLNCC 13 AGKTIATYRILNGGVWILSKNSNPLNCC 14 AGSKSKAKVRINDLRWVFSÖRLSVLV GYSÖRDFILFILTEGLNTLMAKNYDNL KELNLNPLNYEELSLRALVSGSESINP 11 VLEERTEKTLFVEIKSVFQEEKVFYLL 826 LGPDSAGYRVGTCWKDSGLDTVSVTD CHIVLGYLNPDNFLGGLIKLDVBAKKH IKEOIADPLGISVEDAAAGVIELLDLELK	EYLRSNISAKG 828 KKAALATOKAVLALGLKIFPKSPSLSMT TIVNEHAKELRNLLKEKYOVOFAGGÖE PYKDALIRINHMGIIPVYKSAYALNALEL ALNDLDLREFDGVANATFLKQYYGI
	821 CATGCGTTTGGCTAGGGGGTTTGCCCCCTTTACCTCACCTAAACGCTCTAATGGTTCGCCAAAAAAGGATTT TAGCGCTTGGAGCGCAACAAAAGGGCATTTTAGCTTATTGGATAGCGGAACTTCCATTCTTTTACTCTCTCGCCTTTTT TAGCGCTTTGGAGCGCATTTTAGAAAATGAAAACTTTAAAAACCTTCCATTCTTTAAAAACCTATGATTTTAAA GCGCCATCTTAGCCTTTGCGACAAGCATTCAAAACCTTTTAAAAGCGCTTTTTAAAACCCCCTTGTTG CAAGTCCAGCACCACCATGCCACAGCATTTTAGCGAGCGTCTTAGAAGCCATTGTTACAAGATTAAAATCACCCCTTGTTG CAAGTCCAGCACCACCATGCCACATTTTAGCGAGCGTTTTAGAAAATAAGATTTTAGAGAGCGATTTTAAAAGAGCGATTTTAAAAGAGCGATTTTAAAAGAGCGATTTTAAAAGAGCGATTTTAAAAGAAATTTAAAAGAAATTTAAAAAAAGAATTTAAAAAA		GENTIAGENTAGENTAAGATTTTCCCTAAAGCCCCAAGCTTGAG AGAATTGAGAAACCTTTAAAAGAAAATACCAGGTGCAATTTGCGGG TCGTATCAACCACATGGGGATCATTCCTGTTTATAAAAGCCTTACG ACTTGGATTTAAGGGAATTTGATGGCGTGGCG
HP0868	HP0748	HP0748 HP0748	HP0748

٠
•

2/066501	T	
830 OKGIG	832 VNFNSANITTSLNNSSI/FKGAVSLGG QFNLSNNSSLDFQGSSAITSNTAFNFY DNAFSQSPITFHQALDIKAPLSLGGNLL NPNNSSVLDLKNSQLVI-GDQGSLNIAN IDLLSDLNDNKNRVYNIIQADMNSNWY FRISFFGMHINDGIV	834 GDFSFNAGGNVFVQNS.TFSNANGGTL SFNAGNSLIFAGNNHIAI-TNHAGTLQLL SDQVSNINITTLNSNGLKINAANNNVS VSQGNLFVSASCAQQSDPTTANIANPC ALSAQSTNGASSNNASINNAPIALSNND ESLMVAANDFNFSGNIYANGVVDF
	8	83
B29 CAAAAGGGAATTGGATGATGATTGCAGCGAATAATCTATGCATACAATACCAGGAAAACGAAACGGTCATC AAGCAAGGGAATTGCGCATCAAACGCAAGGACTTGTGTTTCAGGGCCTAGCGGGGAGCGGTAAAAGCCTTCA AAGCAACCATTTAGGATTTAAAACTTTTTAGGGGTTATAAAATTTTAGAGGTTTAGAACTTTTAGAGTTTAGAACTTTTAGAGTTTAGAATTATAAATTATAGGGTTTAAAAATATTTAGGGTTTAGAACTTTTAGAATTATAAAATTTTTAGGGTTTAAAAAATATTTTGGGGTTTAAAAAA	831 GGTTAATTICAATTCAGCGAATATTACTACGAGTTTGAATAATTCCTCTATCGTGTTTAAGGGGGGGG	833 GGGGATTITAGTTTCAACGCACAAGGCAATGTTTTGTGCAAAATTCCACTTTCTGAACGCCAATGGAGGCACGCTC TCTTTTAACGCAGGAAATTCGCCTCATTTTTGCCGGAACCATTGTATTGCATTCACTAACGCCAGCGCTGGAACTCTTCAAT TATTGTCCGATCAAGTTTCTAACATTAACATCACCACGCTTAACGCTTAAGATTAACGCCGCTAAT ACAATGTTCTGTGTCTCAAGGCAATCTGTTTGTCAGCGCTTAGCCGCCAACAAGCGATCCAACTAATA ACAATGTTTCTGTGTCTCAAGGCAATCTGTTTGTCAGCGCTTGCCGCCCCAACAAGCGATCCAACTACAGCTAATA ATTGCAAACCCTTGCGCGCTTAGCGCCCAAAGCACGGCGCTTCTTCTTAATAATGCGTCAAATAACGCCGCAAT CGCCTTGAGTAATAACGATGAAAGGTTGATGGTTGCGCGAATGATTTTTCAGGCAATATTTACGCTAATGG
HP0748	HP0289	HP0289

02/066501	PCT/EP01/154	128
B36 TETITETLHNNRLKVOISONGVSNNKM FNLAPSLYDYQKNPYNETENSYNYTSO KVGTYYLTSNIKGFNQNINKTPGTYNAQ NQPLQALHIYNQAITKQDLNMIASLGKE FLPKIANILLSSGALDNLNSPNSFETLFG IFEKYGITLNQENWKSLLKIINNFSNTTN YDFSQGNLVVGAIKEGQTNTKSVVWF GGEGYKEPCAVGDNTCQMFRQTNLG AKIDAGTDKIFSYLGOGGIEKLFGEKG LGNALSNIIYESLNDNAIPKDLANMIPK DFGSKTLSSLLSPTEVNNLLGVSAFKN AIMEILNSTYGDVFGENGLLNALDPTE RKKIDGMLLEQIQAHSSGFEKFIVKTLG IGNALDKIGSSSDAKDLQNFLDFTF GDILNGMIEQAPLINKLISWLGPQDLSV LVNIALNSITNPSKELTSTISSIGEKALN DLLGDGVVNKIMSNQVLGQMINKIIADK GFGGVYQDGLGSILPOSLIKLC MGSLLGSRGLHNLWQRGNFNAKD YLTNNISSFSNATGGELIKKLG MGSLLGSRGLHNLWQRGNFNAKD YLTNNISTRONOGGELKKLG MGSLLGSRGLHNLWQRGNFNAKD YLTNNISTRONOGGELNFVAKD YLTNNISTRONOGGELKKLG	B38 LRLGGFNGNSFTSYKDSADRTTRVDF NAKNILIDNS-LEINRYGSGAGRKASST VLTLQASEGITSSKNAEISLYDGATLNL ASNSYKLMGNVWMGRLQYVGAYLAP SYSTINTSKYTGEVNFNHLTVGDHNAA QAGIIASNKTHIGTLDLWQSAGLNIIAPP EGGYKDKPKDKPSNTTQNNANNNQQ NSAQNNSNTQVINPPNSAQKTEIQPTQ VIDGPFAGGKDTVVNIDRINTNADGTIK VGGYKASLTTNAAHLHIGKGGINLSNQ ASGRTLLVENLTGNITVDGPLRVNNQV GGYALAGSSANFEFKAGTDTKNGTAT FNNDISLGRFVNLKVDAHTANFKGIDT GNG FSNATGGSLNFVANKSIIFNGDVTIDFS KYOGALIFSANDVSNINITTLNATNGLS I NAGI NINASVOKCEICNSM ANCOTTEM	SS
835 GGACTGAAACGATTACAGAAACCTTGCATAACAAAAACCCTTATAATGAAACGAGAATTCCTAATAATAACAAAAAACACAAAAAACACCGAGAATTACCTAATAATAACAACAAAAAAAA	B37 CTTTGCGCTTGGGCCAATTCAATGGCAATTCTTTCACAAGGCTATAAGGATGCGCTGATCGCACCACCACCACGAGAGTGGAT TTCAACGCTAAAAATTCAATTGAAATTCTTTTTTAGAAATCGTGTGGGGTTCTGGAGCCGGGGGAAAGCC AGCTCTACGGTTTTAACTTTTGCAAGGGATTACTAGCAGTAAAATGCGGGAAATTTCTCTTTATGATGCC AGCTCTACGGTTTTGCAACCACCGCTTAAATTAATGGGTAATGTGGGGAAATTTCTCTTTATGATGGGGAGC GCACCGCTCAATTTGGCCCGTTCAAAATTCAAAGTTCAAAAGTGAAATTTAACCATTTGGCAAAAGC GCATCACAACAACACACACCAGCAGTAATCGCTAGTAAAGGTCAATTTTGGCAAATTTTTGGCCAAAAGC GCGGGACTAACAACAACAACAACAACAACAAGAGCGGTTAAAGGATAATGTAAACACCACAATAGTGGCAAAACAAGAAACAAAC	CCCACAAAAACAGCTCTTC
HP0289	HP0289	

2/066501			PCT/EP01/15
	844 IFDNNNKSANAKTGPATIIAUGTKIKGE LHLDYHLHVDGELEGVVHSKSTVVIGO TGSVVGEIFTNKLVVSGKFTGTVEAEV VEIMPLGHLDGKISSQELVVERKGILIG ETRPKNIQGGALLINEGEKKIENK	846 FNNSASFNFNNSNATTSFVGDFTNAN SNLQIAGNAVFGNSTNGSCINTANFNN TGSVNISGNATFDNVVFNGPTNTSVKG QVTLNNITLKNLNAPLSFGCGTITFNAH SVINIAESITNGNPITLVSSS KEIEYNNA FSKNLWQLINYQGHGASSEKLVSSAG NGVYDVVYSFNNQTYNFQEVFSQNSI SIRRLGVNMVFDYVDMEKSDHLYYQN ALGFMTYMPN ALGFMTYMPN	NSANITTSLNNSSIVFKGAVSLGGOFNL SNNSSLDFGGSSAITSNTAFNFYDNAF SQSPITFHQALDIKAPLSLGGNLLNPNN SSVLDLKNSQLVFGDGGSLNIANIDLLS DLNDNKNRVYNIIQADMNSNWYERISF FGMHINDGIYDAKNQTYSFTNPLNAL KITESFKDNQLSVTLSQIPGIKTLYNIG SEIFNYQKYYNNANGVYSYSDDAGGV
8	8	(
841 GAAATAATGAAAATITTAGTGATTCAAGGGCCTAATTTAAACATGTTAGGACACAGAGACCCAAGGCTTTATGG TATGGTAACCTTAGACAATCCATGAAATCATGCAAACATTTCGTGAAACAAGGCAATTAGAAGTT TATGGTAACCTTAGAATCCATGCAAACTTTCGTGAAACAAGGCCATTATGAAGGGATTATGAAGGGATCATTTCAAACTTCATTGCAAACTCCAAGGCGATCATGCTAGGCGATTATTGAAGGGATCATTTTTCAAACTTTTTGCAATTCATTGCAATTCATGCGATTCATTGCAAGCGGATCATTTTTGAAGGGATCATTTTTGAAGTTTTTTGAAGCGATTTTTTTT	GAGCGGTATTIGCA 843 CAATCTTTGATAACAATAAATCGGCTAATGCAAAAACAGGGACCAGCGACTATCATCGCTCAAGGCACAAAAATAA 843 CAATCTTTGATAACAATAAATCGGCTAATGCAAATGCGGAATTAGAAGGGGTGGTGCATTCTAAAAGCACGTG AGGGGAGCTTCATTTAGATTACCATTTTACCAATTAGAAGGGGTGGTGGCCAAGTTCACTGGCCACGTGGCCACGTGGCCACGTGGCCACGTGGCCACGTGGCCACGTGGCCAAGAGCTTCAGCCCAAGAGCTTGTGGTGGGAAATCTCTAGCGCCAAGAGCTTGTGGTGGGAAGTTGTGGAAATCATGGGGAAATCTGAGCCAAGAGCTTGTGGTGGAAGGGGAAGTTGGAAATCAAGGGGAAATGAAAATTGAAAAAATTGAAAAAATGAAAAATTGAAAAAA		1TTCAATTCAGCGATCAACGATTATGCGAGCTTGATTGCGAGIAAIGGCITICACCTITAAGGGGGGGGGTTTTAGGAGGGGGGGGGTTTTAAGTTTCTATTCCTCTATCGTGTTTAAGGGGGGGG
HP0289	HP0289	HP0289	HP0289

	•
-	•
	•
	٠

2/066501		PCT/EP01
850 LINFKGNTNFNQATLNLRAKNIHINFOG VSTFKQNSTMNLAESSQASFNALKVE GETNFNLNNSSLLNFNGNSVFNAPVSF YANHSQISFTKLATFNSDASFDLSNNS TLNFQSVLLNGALNLGNGSNNLAINA KGNFSFGSKGILNLSYMNLFGGDKKTS VYDVLQAQNIDGLMGNNGYEKIRFYGI QIDKADYSFDNGVHSWRFTNPLNTTET ITETLHNNRLKVQISQNGVSNNKMFNL APSLYDYQKNPYNETENSYNYTSDKV GTYYLTSNIKGFNQNNKTPGTYNAQN OPLQALHIYNQAITKQDLNMIASLGKEF I DKIA	852 LMLKDTHLRHVKDLKSFLTHARKNLPF TAKIEIECESFEEAKNAMNAGADIVMC DNLSVLETKEIAAYRDAHYPFVLLEASG NISLESINAYAKSGVDAISVGALIHQATF IDMHMKMA	854 LVGNGLSGIEATALAKNFSDIKKELNEK FKNFNNNNNGLKNSTEPIYAKVNKKKT GQVASPEEPIYTQVAKKVNAKIDRLNQI ASGLGGVGQAAGFPLKRHDKVDDLSK VGLSASPEPIYATIODLGGFPLKRHDK VDDLSKVGRSRNQELACKIDNLNQAV SEAKAGFFGNLEQTIDKLKDSTKKNVM NLYVESAKKVPASLSAKLDNYAINSHT RINSNIQNGAINEKATGMLTQKNPEWL KLVNDKIVAHNVGSVSLSEYDKIGFNQ KNMKDYSDSFKFSTKLNNAVKDIKSGF THFLANAFSTGYYCLARENAEHGIKNV NTKGGFCKS
849 GCCTTATCAATTTCAAAGGGAATACGAATTTTAATCAAGGCCTCAATTTAAGGGGCTAAAAATATCCATATCAATTT CCAAGGCGTTTCTACCTTTTAAACAAAACTCTACGATGTTTAGCTGAAAGTTCCCAAGCGGGCTTTAACGCTCTTAA CCAAGGCGAATACGCTTTTCAATCTCAATACCTCAAGCTTGTTGAATTTCAATGGCAATAGCGTTTTCAACGCTCCT TGTGATTTTATGCTAATCATCTCAAATTTCTTTCAATTGTTTCAATTGCGACTTTTTAATTCTGACGCTTCTTTTAA GCAACAACAGCACCCTGAATTTTCAAAGCGTTCTTTTAAATGGTGCTCTTAATGGCAATGGCAATGGGGG TAGCGATCAACAGCCTTAAAGGGAATTTTGGTTTTGGGTCTTAAAGGGGATTTTGGGGG GGGATAAAAAACTTCCGTTTTTGGAAGCGTTGTTTGCAAAATATTGATTG	851 ITTAATGCTTAAAGACACGCATTTAAGGCATGTGAAGACTTTTAAAGCCTTTTTAACGCCAGAAAAACTTGCC TTTCACGGCTAAAATTGAATTG	853 CCCTAGTCGGTAATGGGATAGTGGGACTCACCCAAAAATTTTTCGGATATCAAGAAGAATTG AATGAGAAATTTAAAAAATTTCAATAATAATAGGCTCAAAAACGCACCAGAACCCATTTATGCTAAAGTTAATA AAAGAAAACCACAACAATAACAATAATGGACTCAAAAACGCACCAGAACCCATTTATGCTAAAATTG AAAAGAAAACGGACAAGTGCTTGGGTGGAGGCCAATTATACTCAAGAACCCATTTGAAAAGGCATGATAA ACCGACTCAATCAAATAGCAAGTGGTTTGGGTGGTGAGGCCAAGCCATTTACGCTACGGTTGATAAAGGCATGATAA AGTTGATGATCATCAGTAAGGTAGGCTTTCAGCTAGCCTAGGGCCATTTATGGCTACGGTTGATGATCTCGGCGGAC CTTTCCCTTTGAAAAGGATGTTATGATGATCAAGCCTAGGGCGATTGATGAGGAACCTAGGACCTAGAGCGAACGGAACCAAGGCGAACCTAGAGCGAAAGGCGAAAGGCGAAAGGCGAAAGGCGAAAAGGCGAAAAGGCGAAAAGCGGAAGGCGAAAAGGCGAAAAGGCGAAAAGGCGAAAAGGCGAAAAGGCGAAAAGGCGAAAAGGCGAAAAGCGGAAGGCGAAAAGGCGAAAAGGCGAAAAGGCGAAAAGGCGAAAAGGCGAAAAAGCGGAAGGCGAAAAGGCGAAAAAGGCGAAAAAGGCGAAAAAGGCGAAAAAGGCGAAAAAA
HP0289	HP0289	HP0383

٠	Ξ	7
	3	١

2/066501		P(
856 PLSCLLVLRVLILPLLERLSLNKDFKLKP FKAQINAPLKLKGERAHLILGNYSNHQF IPYNNNRYDSGAIQALARVDSIALIDEG VRLVQGEIEILRFEN	858 VFKDSKKDACGFIYEISEFMKAYTALLK KQDRYVYLLRYLPSRYWASILTTALYV KYPDFDALKKLLVSYYYQTWIAGGTITR IKQTSINIIKNVKSNKSVETIKELILNSIDS YNTFDQYLYNLWDSS;3VYHSKWVRPV LALAMPAADEEKPHFIAMDAETQVEH ILPQTPKRGSQWNADF:DKEKREEWVN NIANLTLKRKKNAHALNGDFDEKRKIY GGKDTSKVISCYDITKELYSNYRKWN	860 TFGELVSVYYGMVLNAEVAETLEEVEK GHYKHFQNALKMQKVI3QIARVETLGA QVAYDKAHIASVKAKDVLEVSQLSFNSI LSSKDDLVPSSKLEIRTEKNLPDLSFFV SSTLNSYPVLKTLENQIQISKENTKLQIA KFLPQVSFFGSYIMKQINNSVFEDMIPS WFVGVAGRMPILSPTGRIQKYQASKLA ELQVSSEQIQAKKNMELLVNKTYKETL SYLKEYKSLLSSVELAKENLKLQEQAFL QGLSTNAQVIDARNTLISSIVVEQKSVA YKYIVSLANLMALSDHIDLFYEFVY
B55 ICCTTTAAGTTGCTTATTGGGGTTTTTACGCGTTATTGGAGCGCTTATCCTTGAATAAAGGTTTTAAAAC TAAAACCCTTTAAGGCTCAAATCAATGCAAGTGCCCTTTAAAGCTTAAAGGGGGACGGGCGTTTAATTTTAGGCAACTATT CAAACCCCTTTGATTCATTCCTTACAACAACAACGGCGTATGAATTTTAAGCCTTTGAAAATTAAAAATTGTT CAAACCACCAATTCATTCCTTACAACAACAACCGCTATGAATTGAAATTTTAAGCTTTGAAAATTAAAAATTGTT ATCGCTTTGATTGATGATGAAGGGTTAGTTAGTTCAGGGCGAAATTGAAATTTTAAGGTTTTGAAAATTGTTGTT AACAATGCTATAATGATAAGTTCAAAAACCCCACTCATAAAGGTTCTTTTGGGAAAATTGTTTAAAAGAAAAGAGAATTGTT AAAAAGGTTGCAAAAAGAGAACCTATTTTGGCAAAAATTCTTTAAAGGCTAGAAATTGTTTGAAAAAAAA	857 AGGTGTTCAAAGACAGCAAAAAAGACGCTTGCGGGTTCATCTATGAGCGAGTTCATGAAAGCCTATACCGCA TTGCTAAAAAAACAAGACGGTATTTATTGAGGTATCTCCCCTCTAGGTATTGGGCCAGCATTTTAACGACT TTGCTAAAAAAACAAGAACCGATACGTCTATTTATTGAGACTTTATTATTACCAAACTTGGATTGCAG GCCCTTTATGTCAAATACCCTGATTTTGACACATTTTCAAAAACCTTAATATTACCAAACTTGGATTGCAG GAGGCATCACGCGCATCAAGCAAACCGGTATCAACACTTTTTCAAAAAGCAATAAGAGAGCGTTGAAACC ATCAAAGAGCTTATTGAATAGCATCGACTCTTATAACACCTTTGATCAATACCTCTATAACTTATGGGATAGCTCTT CTGTTTATCATAGCAAATGGGTGCGTCCTGTCTTAGCCCTAGCTAATTTTCATGGCAGATGAAGAAACCCCATT TTATCGCTATGGAAACCCAAGTGGAGCATATTTTGCCACAAAGGGCAGTCAATGGAACCC GGATTTTGACAAAGAAAAGA	859 CACTITICAAGAGCTIGIGAGCGTGTATTACGGCATGGTGTTAAACGCAGAAGTGGCTGAAACTTTAGAAGGGTGG AAAAAGGCCATTATAAGCATTTCCAAAACGCTTTGAAAATGCAAAAAGTGGGGCAAATCGCTAGGGTAGAAACCTTA GGCGCTCAAGTGCCTTATGATAAGCCATTTCCAAGCCTTAAGGCTTAAGAGCTGTTAGAAGTTTCGCAGCTCTC GTTCAATTCCATTTTATCTAGCAAGGACGATTTAGTGCCTTCAAGCAAATTAGAGATCCGCACGGAGAAAATCTGCC GTTCAATTCCATTTTTATCTAGCAAGGACGATTTAGTGCCTTCAAGCAATTTAGAAAATCTGCTCT AAAGAAAACACGAAATTACAGATCGCTAAATTCTTGCCCCAAGTGAGTTTTTTTT
HP0507	HP0507	HP0507

02/066501			PC1/EP01/15	5428
862 QFIGYGNIMAQAILEGAHEILSKRFILEIT GRNPEKIAPFLOEKNIQAQIVPYKDAIDI HQKFVFLLFKPYNLKDFNYQGQAKSVL SALAGVGFKALSDAIDSLHYLKCMPNIA SKFALSSTAVCEKSPMPLISQKALSVIE SFGNCVYGHEELVDASVATNGSALA FLSLVANSLKDAGIREGLANGSALA FLSLVANSLKDAGIREGLELV KMSFKGFAKLLEKERPEMIEQICTPKG ATIEGLSVLEKKGVRGAFIEACHKSVKK MRL	864 LGVDGVSEVASVGGFVKDYEVTLQND SLIRYNLSLEQVANAIKNSNNDTGGGVI LENGFEKIIRSHGYIQSLKDLEEIVVKKE GAIPLKIKDIASVRLTPKPRRGAANLNG DKEVVGGIVMVRYHADTYKVLKAIKEKI ATI	866 GLKKVFKOBKKDAGGFIYEISEFMKAYT ALLKADRYVYLLRYLPSRYWASILTTA LYYKYDPDALKKLLVSYYYQTWIAGG TITRIKQTSINIIKNYKSNKSVETIKELILN SIDSYNTFDQYLYNLWDSSSVYHSKW VRPVLALANYFMADEERPHFIAMDAET QVEHILPQTPKRGSQWNADFDKEKRE EWVNNIANLTLLKRKKNAHALNGDFDE KRKIYGGKDTSKVISCYDITKELYSNYR KWNEKSLQERYKSLYNTITPVLHIEGQ EDDFEDDFDLE	868 PLQALVIELLEEIKTSPHKGTFKAKVLD SKKPRQVLGVYNISPHKKLTLTITHISTA IVYQPLDEKI.SLETTLNPNRPTIPRNTQI VFSSKELKESHPHQMPSLNAPMQKPQ NKPHSSQQPSQNFSYPEPKLGSKNSK NSLLQPLAIPSKISPTNETQ	870 VGNLRDLNPLDFSVDHVDLEWFETRK KIARFKTROGKDIAIRLKDAPKLGLSVG DILFKEEKEIIAVNILDSEVIHIQAKSVAE VAKICYEIGNRHAALYYGESQFEFKTPF EKPTLALLEKLGVONRVLSSKLDSKER
861 TACAATTCATCGGCTATGGGAATATGGCTCAAGCGATTTTAGAAGGCGCTCCATGAAATTTTATCCAAGCGTTTTATTTTT AGAAATTACCGGGCGAAACCCTGAAAAAATCGCCCCTTTTTTAGAAAAAAAA	863 ITTTAGGGGTTGATGGGGTGAGTGAGGTTGCAAGCGTGGGGGGGCCTTTGTAAAAGATTATGAAGTAACGCTTCAAAACCGTTCAAAACCGTTCAAAACCGTTCAAAACCGGTGGGGTTCTCTCTGATACCGGTGGGTTTAGAAAATTATAGAAGTCGCTAACCGGTGGGGTTTAGAAAAATTATAAGATCCCATGCTATTTAGAAAGAA	865 AGGGATTAAAAAAGGTGTTCAAAGACAGCAAAAAGACGCTTGCGGGTTCATCTATGAGATCAGCGAGTTCATGAAAAAGGATCAAAAAAAA	CCCTCTTCAAGCCCTTGTGATCGAGCTTTT CCTTGATTCTAAAAACCAAGACAAGTTTTT CACATATCCACTGCAATCGTCTATCAACCC ACTATCCCTAGAAACACCCAGATTGTTTTT AACTGCCCATGCAAAAACCACAAAAACAAAAAAAAAA	69 TAGTTGGCAATCTAAGGGATTTAAACCCCTTGGATTTCAGCGTGGATCATGTGGATTTGGAATGGTTTGAAACGAGG AAAAAAATGGCTCGTTTTAAAAACCAGGCAAGGCA
8	98	98	967	98
HP1158	HP1158	HP1158	HP1158	HP0068

VO 02/06650			PCT/EP01/15428
LTVSM	872 STGDVSEQIELEGEKGKTSNIETNNGIK VEGEKGKTSNIETNNGIKVEGEGCKTS NTGKDLVKEGKDLVKEGKDLVKEGKD LVKEGKDLVKTGKDFIKYVEJNCGENH NGFFIEKGGIKAGIGIEVEAECKTPKPA KTNGTPIGPKHLPNSKQPRSGRGSKA GELIAYLQKELEFLPYSGKAIAKQVDFY RPSSIAYLELDPRDFKVTEEV/QKENLKI RSKAQAKMLEMRNPQAHLSNSGSLLF VQKIFADVNKEIEAVANTEKKAEKAGY ĠYSKRM	874 ILLYSEIIVAGRVARNELFKFNFLHTKISI LQDEKPIYYDNTILDPKTTDLN NMCMF DGYTHYLNLVLVNCPIELSGV;RECIEES EGVDGAVSETASSHLCVKALJAKGSEPL LHLREKIARILYTQTT 876 KELLNNHFKQRLAFRCNGENI.SAIKKD LPLLTNELNALFVELSKDSHTEFRPFSL	878 LGLSPIKMGLRINPLYSEVTPAÍYNPCS KVSRLGITPSGFEKGVKEHGLEGVSGL HFHTHCEQNADALCRTLEHVEKHFRP YLENMAWVNFGGGHHITKSDYDVNLI QTIKDFKERYHNIEVILEPGEAI 3WQCG FLASVIDIVQNDQEIAILDASFSAHMPD CLEMPYRPSIFKVSVENDEELIEVEKGE NQGA DONLVSVIEKQTNKKVRILEIKFLKSSQ DLKMVNIEDPDTKYNIPLVVSKIJGNLIIG LSNIFFSNKSDDVQLVAETNQKVQALN AANKDKIL YIVSDPMCPHCQKELTKLR DHLKENTVRMVVVGWLGVNSAKKAAL
		878	880
TTTTAAGTTCAAAATTGGATTCCAAAGAACGCTTAACCGTGAGCATGCC		873 ATTGCTCTATAGTGAAATCATIGTCGCAGGGCGAGTGGCGCGCAATGAGTTGAATTCAACCGCTTGCACACCAAAAAAAA	877 ACTT IGAGGCT ANAMATICA 877 ACTT IGAGGCTTAAAATGGGTTTGAGGGATAAACCCTCTCTATAGCGAAGTAACCCCAGGGGTCTATAAC CCATGCTCAAAGTGGGATTACGCATTGCGCATTGCGGATTTGAAAAGGGGGTGAAAGGCTTTAGAGGGATCTATAAC GGGTGAGCGGGTTGCATTTCCATACGCATTGCGAACGCTTGACGCGTTTGTGCCGGACTTTAGAGGCATTGAGAGGGATTTAGAGGCTTTGAGAGGCTTTGAGAGCGATTTTAGAGCCTTGAGAGCGATTTTAGAGCCTTGAGAGCGATTTTAGAGCCTTGAGAGCGATTTTAGAGCCTTGAGAGCGATTTTAGAGCGATTTTAGAGCCTTGAAACGGTTATTTAGAGCCTTGAAAACGATTATAGAAATTTGCTCAAAACGATTAGAAATTGCTCAAAACGATTTTAGAGCCTTGAGAAATTGCTCAAAACGATTTTTAGAGAATTTGCTGAAATTTGCTGAAAACGATTAGAGGGCGGTTTTTAGAGAGTTTTTAGAGAATTTTAGAGAAATTTTAGAGAGTTTTTAGAGAGCTTAGGGGCGGTTAGTTTTAGGGGCGGTTATTTAGGGGCGTTATTTAGAGAATTTTAGAGAATTTAGAGAAATTTAGTGAGCTTATTTAGAGAGCTTAGGGGCGGTTAGGGCGTTAGGGGCGGTTAGGGGCGGTTAGGGGGCGTTAGGGGGGCGTTAGGGGGGGG
	HP0068	HP0069	HP0187

193

۹	c	۲
¢	2	١
-	_	•

2/066501			PCT/EP01/15428
882 GMEFGVKIPAINQRYLRANGADVDYRR LYAFYINYTIGF	884 NGVEIVGLEHLDKVIYLDQAPIGKTPRS NPATYTGVMDEIRILFAEQKEAKILGYS ASRFSFNVKGGRCEKCGDGDIKIEM HFLPDVLVQCDSCKGAKYNPQTLEIKV KGKSIADVLNMSVEEAYEFFAKFPKIAV KLKTLMDVGLGYTLGQNATTLSGGEA QRIKLAKELSKKDTGKTLYILDEPTTGL HFEDVNHLLQVLHSLVAL	886 ÖNYÖLFSSAKEDLKRLĞIĞKEIFYISVN EENEKALLNCYPNAKNIAGFFHLETDY VGLGIDROMACLAVNNGYVYDAGSAIT IDLIKEGKHLGGCILPĞLAQYIHAYKKSA KILEQPFKALDSLEVLPKSTRDAVNYG MVLSVIACIQHLAKNÖKIYLCGGDAKYL SAFLPHSVCKERLVFDGMEIALKKAĞIL ECK	888 TPYLVEDVIJATTLANKHALSILDALKNT LKPLGEVFYQIDESNEEWIILDLGDLMI HLFTEECRKKFDLEGFLNAYKRGLPYQ NA
881 ATGGGATGGAATTTGGCGTGAAAATCCCCGGCTATCAAGGTATTTGAGGGCCCAATGGGGCTGATGGGATTACCAGTTGCAATGCAATTGCAATTGCGATGTGGATTTTACCAGTTGTATTTAGGGCTTTTTACTTTTAGGGCTTTTTACTTTTACCAGTTGTTTTACCAGTTGTTTTTACCAGTTTTTACGTATTCTAACAAGGCTTTTTACTTTTTTTT	883 GAATGGGGTGGAGATTGTAGGGTTGGAGCATTTGGATTAAAGTGATTTATTT	885 ACAAAACTATCAGCTCTTTTCAAGCGCTAAAGAGTTTAAAGCGTTTGGGTATTCAAAAGGGAAATTTTTACATTAGCATTAGCGTGGGGAAATTTTTACATTAGCATAGCGGAAAGGAAATTTTACATTAGCAAAGGAAATTAGAAAGGGAAATGGAAAAGGGAAAATGGAAAAGGGAAAAGGGAAAGGGGAAAGGGGAAAGGGGAAAGGGG	BB7 AAACCCCCTATTTGGTAGAAGATGTCATTATCGCCACCGCGAATAAGCATGCCCTTTCTTT
HP0187	HP0187	HP0187	НР0187

ı
۰
ľ

HP0958	888	899 ITACGCTTITGGGGGGGGGAGAAACCAAGAAGAATTGAAAGCCTAAACAAAAACTCAATGCGTTAGGGTTAAAAT CCAAAAAAATCATCGCTCAGCACCAGTCCTTAAAACCATTTAGTCAAAAACCATCAAGCCATCATGGAAAAGCTTAAAA CCAAAAAAATCATCGCTCAGCACTTTAATGCAACAAGAAAGCGTGAAAGCCTTATAGCGAGTTTATGTTTGCTT TAAAGCGTTTGAAAATCTTAAAAGCTCAAATGTTAGAATTGCAAAAA	900 YAFGGRENQEELKAAKOKLNALGLKS KKIIAQHQSLNHLVKNHOAIMEKLKNAT EEIKRSLMQQESVKDAYSEFMFALKRL KILKAQMLELQK	LNALGLKS IMEKLKNAT EFMFALKRL
HP0958	901	TGAAGTGAGGAAATGGCCTTTAGAGCGGCAAAAGGGTGATGTTTGAATACCTTTTGATCAAAGATTTGAACGATA TGAAGTGAGGATTTGAAACGTTTAGAGGGGCATTAAATCCAAAGGTTTTGATCTTATTCAACCCGCA GCCTAGACTGCGCTAAAAAACTTTTAAAACGTTTTAAACGGCATTTTGAGGGATTTTTAAACCCCTAAAGGCTTATT TGAAGGCTCTAAGTCTAAAGCCTTGGATATTGAAGCGCTTGCGGCAGTTGAGGGAAAAAACTCTCTCAG ATGCACCATTAGAGAGTCTAAAAGCTTGGATATTGAAGCGGCGCTTGCGGCAGTTGAGGGAAAAACTCTCTCAG CAAATTTGAAAACTTTTTTGTGGTGTTTTTTTTTT	902 EVRKWPLEGRKRVMFEYLLIKDLNDSL DCAKKLLKLLNGIKSKVNLILFNPHEGS KFERPSLENARMFADFLNSKGLLCTIR ESKALDIEAACGQLREKKLSQQI	LIKDLNDSL LFNPHEGS SKGLLCTIR SQQI
HP0958	903	903 CCAAAAGGCAATGAACCATCAAGTCTATGACATTGAAACCATGCTCGCTGATAGCGCTTTTAGAGGCATGAAG AAGAGCAAGATTCCTCTAAATACCGGTTTGCCTGAAGATAAAACAGCGATTGAAGGCCAAAGAAAA GAAAAAGAAAAG	904 ÖKVEMNHQVYDIETMLADSAFREHEE EQDSSLNTALPEDKTAIEAKEGEGKEK RKRWYELFKKKPKPKSSMGEFVFDQK ENRIYGKGYCNRYFASYVWQGDRHIGI	SAFREHEE KEGEOKEK SEFVFDOK VOGDRHIGI
HP0067	902	905 GCATTCTTTTGGGCTAGAAACTTACATCCAGCAAAAAAGGTTACCAATAAAGAAAG	906 HSFGLETYIQQKKYTNKESALEYLKAN LSSQFLYTEMLSIKLTYESALQQDLKKI LGVEEVIMLSTSPMELRLANQKLGNRFI KTLQAMNELDMGEFFNAYAQKTKOPT HATSYGVFAASLGIELKKALRHYLYAQ TSNMVINCVKSVPLSQNDGQKILLSLQ SPFNQLIEKTLELDESHLCTASVQNDIK	ALEYLKAN ALGODLKKI VOKTGONRFI VOKTKOPT RHYLYAQ OKILLSLQ ASVONDIK
HP0145	206	TCACTTACATGAGGACCGATAGCTTGAATATCGCTAAAGAGGCTTTTAGAAGAAGCGAGGAATAAGATTTTAAAAGACTAAAGACTTACATGAGGACCGAAGACTTTACATGATATCGCTAAAGGCCTTTAGAAGAGCCAAGAAGCGCCAAGAAGCCCAAGAAGCCCAAGAAG	908 TYMRTDSLNIAKEALEEARNKILKDYGK DYLPPKAKVYSSKNKNAGEAHEAIRPT SIILEPNALKDYLKPEELRLYTLIYKRL ASOMODALFESOSVVVACEKGEFKAS GRKLLFDGYYKILGNDDKOKLLPNLKE NDPIKLEKLESNAHVTEPPARYSEASLI KVLESLGIGRPSTYAPTISLLQNRDYIK VEKKQISALESAFKVIEILEKHFEEIVDS KFSASLEEELDNIAQNKADYQQVLKDF YYPFMDKIEAGKKNIISQKVHEKTGQS CPKCGGELVKKNSRYGEFIACNNYPK CKYVKQTESANDEADQELCEKCGGEM VQKFSRNGAFLACNNYPECKNTKSLK NTPNAKETIEGVKCPECGGDIALKRSK KGSFYGCNNYPKCNFLSNHKPINKRC EKCHYLMSERIYRKKKAHECIKCKERV	AKILKDYGK AHEAIRPT TLIYKRFL EKGEFKAS KLLPNLKE RYSEASLI ONRDYIK HFEEIVDS QOVLKDF HEEIVDS ACNNYPK EKCGGEM KNTKSLK EKCGGEM KNTKSLK EKCGGEM

HP0145	909 CAAAAACGCGG AGCCTATTTGC TTAGAGCTGGT TACAACTCCCC AAATAAGGCTT		910 KNAPYKLDI YLHHLFRAN VKNARNAIL H	910 KNAPYKLDNTPIEENCAC'ACKRYSKA 20 OYLHHLFRAKELTYARLASI.HNLHFYLEL VKNARNAILEKRFLSFKKEFLEKYNSRS 10 OKNARNAILEKRFLSFKKEFLEKYNSRS RNAILEKRFLSFKKEFT 10 OKNARNAILEKRFLSFKKEFT 10 OKNARNAILEKRFLSFKKEFT 10 OKNARNAILEKRFLSFKKEFT 10 OKNARNAILEKRFLSFKKEFT 10 OKNARNAILEKRFLSFKKEFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFLSFKKFT 10 OKNARNAILEKRFKT 10 OKNARNAILEKRFKT 10 OKNARNAILEKRFKT 10 OKNARNAILEKRFKT 10 OKNARNAILEKRFKT 10
HP0145	911 CTTGTATGTTA GCGGCGTGAT TGCAAGAATCCC ATCGCTTCTAA GGCTATTATGC GAAATCATCAA AATGAATGGG ATCAAACGAAC AATGAATGGG ATCAAACGAAC AATGAATGGAAC AGGGCTT	-	912 LYVKWLMK GVMNFLSV GVMNFLSV EILTNSKIKF PKTPNPPK SAKLYLEKI ISTHDFLTA EDAYLNILH KKYQLYE ELKSPFDAI LKAPHFLEK GAHLRYLG GAHLRYLG OAHLRYLG	912 LYVKWLMKRYPTERNRLI.EMISQPES GVMNFLSVVHYLYKNDDIVIDHEIYELQ EILTNSKIKPWKDFSKNLLSLFQYPSNS PKTPNPPKTCALFNAYAKHLDVQSLLK SAKLYLEKMGQKIIDLPFCYDGGYYGKI ISTHDFLTASAYNLALAKANGVSLIFCE EDAYLNILHAKEVLDNNPEIINSVNEKL KKYQLYFEKGVEVYLNEWVNEFLAW ELKSPFDAFLGAEFSRIKRSDHFFNKIH LKAPHFLESFQNYAPLLEVNEVSGLLQ CAHLRYLGIDLGADFLIVF.SLGLFHAFE NLSLKASKVYKRDNDNTPTLFLPQIAL MAMGEKNTQALGLDAHYHKVTFI
HP0145	913 GCGCGGGACTAAACA CAAATAATGCTAACA GCGCAAAAACAGAA TGATCGCATCACACGTI ATTTGCATATCGGCAT GGGAATATCACCGTI TTTTGAGTTTAAAGGCT GAATTAAAAGTGGAT AATGAATTGGTTGTTGTA AATGAATTGGTTGTTGTA AACTGGTTATAGATG AAAATTCGCTTCTCA AAAATTCGCTTCTTCA	913 GCGCGGGACTAAACATTATCGCCCCTCCAGAAGGCGGTTATAAGGATAAACCTAAGGATAAACCTAAGACAACACACAC	SIL AGLINICATORIS NAMINICONIS NAMINICONIS TUNADGTIKVG GGINLSNOAS PLRVNNOVG DTKNGTATFN ANFKGIDTGN NKLITASTNV/ NKLITASTNV/ NKLITASTNV/ NKLITASTNV/ NKLITASTNV/ NKLITASTNV/ NKLITASTNV/ NKLITASTNV/ NKLITASTNV/ NKLITASTNV/ NKLITASTNV/ NKLITASTNV/ NKLITASTNV/ NAFFSNNVO DFINNOGTINV AMFFSNNVO	MANINGONSAQNINSINGONSAGNINA MANINGONSAQNINSINGONSAQNINSINGONSAGNINANINDRIN TINADGTIKVGGYKASLTTINAAHLHIGK GGINLSINGOSGYALAGSSANFEFKAGT DTKNGTATFINDISLGRFVINLKVDAHT ANFKGIDTGNGGFNTLDFSGVTGKVNINKLITASTNVAVKINFININELVYKTNGVS VGEYTHFSEDIGSQSRINTVRLETGTR SIFSGGVKFKSGEKLVIDEFYYSPWNY FDARNINLTLGGNAVMDYSGFSNLTINGONSKINTLTGGNAVMDYSGFSNLTINGONSKINTLTGGNAVMDYSGFSNLTINGONSKINTLYRGGGVATLNVGNAA AMFESINVD
HP0145	915 ATTTGTTAGA AAATTACCCG ACAGGCCATC AGCCATTGAA CAAGAGAGT CTCATTGAT ATTAGAAAAAA CTAAAAAAAAAA	915 ATTTGTTAGAAATTATCGCATTAGGACAATTAGGCATTAAAAAAATCC I ACICAI AGACAI I GGCAATGCCATTAGGACAATTAGGACAATTAGGACAATTAGGACAATGCTTAGGACAAGGCTTAGGACAAGGCTTAGAAACGCCAAATGCGTTACAAAGGCTTAGAACGCCAAATGCGTTTAGAACGCCAAATGCGTTTAGAACGCCAAATGCGTTTAGAACGCTTAAACGCCAAAGAAAAAGAAGAATTTTGAAGCCTTAATTGGACTGAAGGCTTTTTTAAAAAGAAGCTTTTTTAATAAGGCTAAATAGCCTAAATAGCGCTAAATAGCGCTAAATAGCGCTAAATAGCGCTAAATAGGCTAAATAGCGCTAAATAGGCTAAATAGAAAAAAAA	DPNIPEALY YKRILLEYK SDLSNANM LINWAEAEIN PDYISTHSE EIAHLLING EIAHLLING ARKOFKNA VYRARDEK QNFPNSNE	DPNIPEALYYVAKALDENNIHYKOAMRY YKRILLEYKNSRYAPLAGIMRLAIEAAEG SDLSNANMLFKEAFSNAKDKESASEIA LNWAEAEINYQNFNNAKYLIDKYVQSN PDYISTHSESALDLLKLLKKNOMNASAI EIAHLLNQDDDLKAKEGALYDLGALY ARIKOFKNAHLYNLQYLQDHAELDKAS VVRARDEKALFSMEGNTJEKIAHYDKII

C	•	•	•
	t		۰
	٦	_	

930 YRSDLGVNLPLKPENIVDTKMÅTVLGK DNARISTIEHLLSAVHAYGIDNLKISVDN EEIPIMDG	929 TTACCGCTCTGATTTGGGCGTGAATCTCCCCTTAAAACCTGAAAACATCGTGGATACCAAAATGGCAACCGTGTTGG GTAAGGATAATGCTAGGATTCTACGATTGAGCATTTGCTTTCAGCTGTCCATGCGTATGGCATTGACAATCTTAAGA TCTCTGTGGATAACGAAGAAATCCCTATCATGGATGGG
928 SGVNGMQAHQIALDIESNNIANVNT	927 GTCTGGTGTCAATGGGATGCAAGCCCACCAAATCGCTTTGGATATTGAGAGTAATAATATTGCGAATGTGAATACCA
KKEELFLKLNGAITDLSFNEDKAILTTEN Q	TTTAAAATTGAATGGAGCGATCACGGATTTGAGTTTCAATGAAGACAAGGCGAT
GENLLELL OSEEDIKI SALDKÜNDYEDSEDIETTYTIKIĆ	TAAGTATTTAGGGGGTGAAAATTTATTGGAATTGTTG 925 CGAGCCTTTGAAATTGAGGGCTTTAGCTTAAAGATAATGAACTATTAGAAATTACAAAAAAAA
KWEKSANPKFAYKMTHFSNGGDKYLG	TTTTGACTTTGGCAAATGGGGAAAAAGCGCTAATCCTAAATTCGCTTACAAAATGACGCATTTTAGCAATGGGGGGGA
DKFAKLDKPIYYGVFDFGGGTTDFDFG	TACGGGTTTGATAAATTTGCAAAATTAGACAAGCCCATTTATTACGGGGGTGTTTGATTTTGGGGGGGG
924 HUAENIKESFEKGLKKSLPRHVFUDEK TAKMFKVELKASEPCAYAISALKSYGF	ABOCKTICKBOOTBAKKKKKKTICKBAKBABATTTI BAKKKKKBOOTTI BAKKKKKTICOTTACUURBGOOTTI TITTI BAKUGATTI AAAAAACGGOTAAAATGTTCAAAGTGGAATTAAAAGCGAGCGAGCOTTGOGCGTATGCCATTAGCGOTTTAAAAAGC
KGDGSACGIFK	<u>AATAGATAAAGGCGAGCGCGTGCGGGATTTTTAAAAA</u>
EACPWLSNGGAGNVAGGNSLWAGID	CTCTTAATGAAGCATGCCCATGGTTGAGTAATGGTGGTGCAGGCAATGTGGCCCGGTGGCAATAGTTTATGGGCCGG
922 VQPGERWKFPW I NGKFVSVKWVNGK YEEIKEDIKVSNNAQELLKOASTILTTLN	921 JUGTUCAGCCAGGAGAAAGATGGAAATTUCCATGGACTAATGGAAAATTTAAAACAGGCTAGGGGTGAATTTAAAGAACAGGCTAGGGGTGAATTTAAACAAGAAGT ATGAAGAAATTAAAGAAGACATCAAAGTGTCAAATAACGCTCAAGAGCTTTTAAAACAGGCTAGCACTATTTAAAACAGGCTAGCACTATTTAAACCA
EDDFEDÖFÖ	<u>CAAATCTŢTGTATAACACTATCACGCCTGŢŢŢTACACAŢAGAGGGGCCAAGAAGAŢGTŢŢTGAAGATGATŢŢŢGATÇŢ</u>
KWNEKSLÓERYKSLYNTITPVLHIEGO	
KRKIYGGKDTSKVISCYDITKELYSNYR	AAAAAGAACGCGCATGCTTTAAACGGGGATTTTGATGAAAAAAAA
EWVNNIANLTLLKRKKNAHALNGDFDE	CAATGGAACGCGGATTTTGACAAAGAAAAAAGAGAAGAAGAATGGGTAAATAATATCGCGAAATTAAACCCTTTTAAAGGT
QVEHILPQTPKRGSQWNADFDKEKRE	AGAAACCCCATTTTATCGCTATGGATGCCGAAACCCAAGTGGAGCATATTTTGCCACAAACGCCCAAAAGAGGCCAGT
VRPVLALANYFMAĎEEKPHFIAMDAET	<u> GGGATAGCTCTTCTGTTTATCATAGCAAATGGGTGCGTCCTGTCTTAGCCCTAGCTAATTATTTCATGGCAGATGAAG</u>
SIDSYNTFDQYLYNLWDSSSVYHSKW	AGCGTTGAAACCATCAAAGAGCTTATATTGAATAGCATCGACTCTTATAACACCTTTGATCAATACCTCTATAACTTAT
TITRIKOTSINIIKNVKSNKSVETIKELILN	CTTGGATTGCAGGGGGCACGATCACGCGCATCAAGCAAACCAGTATCAACATTATCAAAAACGTTAAAAGCAATAAG
LYVKYPDFDALKKLLVSYYYQTWIAGG	ATTITAACGACTGCCCTITATGTCAAATACCCTGATITTGACGCTTTGAAAAAGCTTTTGGTGTCTTATTATTACCAAA
ALLKKODRYVYLLRYLPSRYWASILTTA	GCCTATACCGCATTGCTAAAAAAAAAAGACCGATACGTCTATTTATT
920 GLKKVFKDSKKDACGFIYEISEFMKAYT	919 AGGGATTAAAAAAGGTGTTCAAAGACGCAAAAAAGACGCTTGCGGGTTCATCTATGAGATCAGCGAGTTCATGAAA
	GCGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
DIDDLSKHTLDKIKHFFETYKDLEPNKW	CACGCATTCCACTACTACTACTTTTTTTTTTTTTTTTTT
NMEDESGMDEKLIALPIDKIDPTHSYVK	GTTGGGGTTTTGAACATGGAAGATGAAGCGGGATGGATGAAAACTAATCGCTCTGCCCATAGATAAGATCGATC
DPVDALYSACIATEANTGEVENTLESDG	TO ANGEGE GOOT ANGEST OF THE GOOD CONTRACT TO CONTRACT TO CONTRACT TO CONTRACT CONTRACT TO
918 ADSLCVVIEISKHSNIKYELDKESGALM	CGCTGATTCTTTGTGCGTGGTGATTGAAATATCCAAGCATTCTAATATCAAGATTGGATTGGATAAAGAAAG

표리숙하등승구	34243014		PC17EP01.	/15428
932 KRFRENAGKNAEYSN-IEASSHHKKEH RPNKKPNNHHKOKHAKTRNYAGELD SNKVEGVTEILHVNERGTLGFHKELKK GVEANNKIQVEHLNPHYKMNLNSKAS VKITPLGGLGEIGGNMINVIETPKSAIVID AGMSFPKEGLFGVDIL PDFSYLHQIKD KIAGIITHAHEDHIGATI?YLFKELQFPLY GTPLSLGLIGSKFDEHGLKYRSYF	934 VFNAQKRLNIANAHLNINDKAGLONSW MNFIVNNGNLNVTNAKFSNOTPHGGF NLKANNITWDKGSVNCGGNFGVDNAD SNGATTISGVTFNNNGTLIYKGGENSA GNSLTLENNTFNSYNINAKAONLIFNNN SFNGGSYSFNDTKNTTFKGTNTLINSD PFSRLKGSVSIENNSVFNIERDLTDKTT YTLLSGNSIKYNNQALAGOCFFKKFME FNPLWWRTRDSIKSG	936 WSQVRKQFDFIPGKTPVCVGVCYIAPY KNQDLIGSSAFAWSLNFGATVVGTLLL GSAQEKANNNGGSIWFGKNNLLYLHG NFNATNIFLTNNFNVGNFNAGGGATIN FNADETLNADGLNYTNFQTVALGLQTS ASQHSWANFNSKLSMEIKNSNFRDFT WGGFNFNSGRITFENTT=SGWTNING ATESGSSYVNMVANTDLIFSNSILGGGI RYDLKANNIIFNNSQMVIIVVGSSINGNTFN	938 RLGIOKEIFYISVNEENEKALINCYPNA KNIAGFFHLETDYVGLGIURQMACLAV NNGVVVDAGSATIDLIKEGKHLGGCIL PGLAQYIHAYKKSAKILECIPFKALDSIE VLPKSTRDAVNYGMVLSVIACIGHLAK NOKIYLCGGDAKYLSAFL?HSVCKERL	VFDGMEI 940 PKPSKKNPKEESHSGDKI.HEIKQELKD LFSHLPYKINKVEVSLYEPGVLLIDIDGE
			938	940
931 AAAGCGTTTCAGAGAAAACGCGCGAAAAA ATCGCCCTAACAAAAACCCAAACCA GATAGCAACAAAGGGGCGTTACG AAAAAGGGCGTTGAAGCGAATAACAAC AGCGAGCGTTAAAATCACGCCTTTAGGC AGCGCGATCGTGATTGATGCGGGCATG TTCCTACTTGCACAAATCAAGGACAAA CGCCTTATTGTTTAAAGAGCTGCAATTC		935 TTTGGAGTCAAGTGAGGAAGTTTGATTCCAGGAAAAACCCCTGTGTGTG	937 GCGTTTGGGTATTCAAAAGGAAATTTTTACATTAGCGTGAAGGAAAATGAAAAAGGCAAAAGGAAATTGTTACCCTTTTGCGTGAAAAAGGCCTTTTGAATTGTTACCCTTTAGCGTGAAAAGGCAAAAGGCAAATTGTTACCCTTTTGCAAAAATGCCGGCTTGTAGGCCTTGGGATAGAATTGAAAAAGCGCTGTTTAGGCGTGGTGGTGGTGGTGGTGCCGGGGTGCCGATTCATCAAAAAAAGCGCTTAAACAAAAGGCCAATAAATTCATGCGTTAAAAAAAA	939 CCCCTAAACCCTCTAAAAAAACCCTAAAAGAATCTCATAGTGGGGACAAACTCCATGAGATTAAACAGGAATTGAAACTGAAATTGAAACTGAAATTGAAACTGAAAACAAAACTGAAAACTGAAAACTGAAAAACAAAAATGAAAAAAAA
HP0595	-IP0621	HP0621	HP0621	00117

HP0181	140	941 GTTAATTTTAATAATTTTTTTAGCATCGGTTTGAATTGAGAAGGGTTATCACAATGAATG	IVCIGLN
HP1391	943	944	944 AIDEVLKIEFLELALGYQLISLADMKOĞ GDLLERIRGIRKKIASDYGFLMPQIRIRD NLQLPPTHYEIKLKGIVIGEGMYMPDKF LAMNTGFVNKEIEGIPTKEPAFGMDAL WIETKNKEEAIIQGYTIIDPSTVIATHTSE LVKKYAEDFITKDEVKS
HP0061	949	TAAAAGAACTGGATGACTTAGATAAAGTTGTTGCTAAAAAAGAGC CCAATAGAGGACTACCAAAAGGTGTCAGGCAATTCAAGCGCAATTC SCGCTTACCCACAATTTTAAGCTGTGGTTATTGGAAATTAAAGGCCAA TCAAAGTTTATCCACCAAAAGGTGTGTTATTGGAAATTAAAGGCAA TGCGCTTGCTATCCACTGCGCCTTTAGTGCAATTAGAAGTGATCTTAG SAATTATAATGCAAAGACGCTTTAGTGCAATTAGAAGTGATTTACCAGC SAATTATAATGAAAAAAAAAAAAAAATTTGAATATTTAAAAAA	946 IKMIDVNĞLLKELDDALDKVVAKKEPÊS FLKPIISPIEDYÖKSVRÖIQAĞFTDAPKF NEEGAYPQFLSCGLLEIKGKNĞASMEF CLPKVYPFPPKSLYIEHEKOGĞFLREM LMRLLSSAPLVQLEVILVDALSLGGIFN LARRLHKDNDFIYÖQRILTESKEIEEAL KHLYEYLKVNLĞEKLAĞYKDFAHYNEE KKDRLPLKALFLSGVDALSQNALYYLE KIMRFGSKNGVLSFVNLESEKNNKSTE DLKRYAECFKÖRTSFERLKYLNIEVIND HGIQSKHMKÖFADKIKAYYEKKKAVKR ELKÖLĞKDEKFWTESSĞFKVSVPVĞW DINHKEVCFEIGNEĞ
HP0061	944)	947 CTATAAAACCCACCGAACAAAAAGGTTTTTTTAAAAGTTTCCTTGATAAGATTTCTAAATTCTTTTTAAGATACAGCCATT 948 IKFTEC 1 CTATAAAAACCCACCAAAAAAGGTTTTTAAAAAGTTTCCTAAAATTTCTTAAGATTTATCAAAGTT 1 TAAGATTTGCAAAAAATCGTATCTCAAGGGGAATGTGCTATGCTATAAAAGTT 1 TAAGATTTGCAAAAATTGTTCCAAAGGGGAATGTGCTATAAAAGGGGGGGG	948 IKPTEQKĞFFKSFLÖKİSKFF

_	
3	١
4	
	E

2/066501	- 	PCT/EP01/15428
950 VFKDSKKDACGFIYEISEFMKAYTALLK KQDRYVYLLRYLPSRYWASILTTALYV KYPDFDALKKLLVSYYYOTWIAGGTITR IKQTSINIIKNVKSNKSVETIKELILNSIDS YNTFDQYLYNLWDSSSVYHSKWVRPV LALANYFMADEEKPHFIAM JAETQVEH ILPQTPKRGSQWNADFDKEIKREEWVN NIANLTLKRKKNAHALNGDFDEKRKIY GGKDTSKVISCYDITKELYSNYRKWNE KSLQERYKSLYNTITPVLHIEGQEDDFE DDFDLE	952 ATSLLLAACSTGDVSEQIELEGEKGKT SNIETNNQIKVEGEKOKTSNIETNNGIK VEGEGOKTSNTGKDLVKEGIKDLVKEG KDLVKEGKDLVKEGKDLVKTGKDFIKY VEGNCGENHNGFFIEKGGIKAGIGEVE AECKTPKPAKTNGTPIQPKHLPNSKQP RSQRGSKAGELIAYLQKELEFLPYSQK AIAKOVDFYRSIAYLAKEN AIAKOVDFYRSIAYLAKEN AIAKOVDFYRSIAY AIAKOVDFYRSIAY AIAKOVDFYRSIAY AIAKOVDFYRSI	954 TNKSGIELANSQIKAEGERGKTEGEKG KANSAIELEGOKOKTITOAJOLIKEGK DFIKETEGNCGENHNGFIKKLGIKGGI AIEVEAECKTPKPAKTNOTPIOPKHLPN SKQPHSQRGSKAGEFIAYLÜKELEFL 956 ALNLPLYRYLGGANALTLPVPMLNIING GTHANNSIDFOEYMIMPLGFESFKEAL RASAEVYHTLKKLLDGKNQI.TSVGDE GGFAPNFSNNVEPLEVISQAIEK 958 VLVDGEKQILKVSGVIRPYDIERNNTIQ SKFLADAKIEYTNLGHLSDSNKKKFAA DAMETQMPY
CCGCA CGACT TGCAG AAACC CCTCTT CCCATT CCCATT AACGC TTGTA TTGTA TTGTA TTGTA		
TIGCTAAAAAAAGGCGATTATGGGGGTTCATCATGAGGATTCATGAGGGTTTTATGGGCCATTACCGCATTACCGCATTACCGCATTACCGCATTACCGCATTACCGCATTACCGCATTACCGCATTACCGCATTACCGCATTACCGCATTACCGCATTACCGCATTACCAGGATTACCAGGACTTTAGCACTTTGCAGAAAAAAAA	951 GCGACAAGTTTATTATTAGCCGCTTGTAGCACTGGTGATGTTAGTGAACAAATAGAACTAGAACAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAA	953 ACAAACAAGAGTGGGATAGAACTCGCTAATAGTCAATAAAAGCAGAACAAGAAAGA
	390	390
	HP1390	HP1390 HP1390

2/066501 밀설방≥ய	R m x 4 k B x * ト * 6 H	2.0	>x < x	PCT/EP01/1542
960 AAAVPKLTIENVKIVNENGESIGEGDILE NSKELALEQLHYKONFENILENKIVNILA PIVGGKNKVVARVNAEFDFSOKKSTKE TFDPNNVVRSEQNLEEKKEGASKKOV GGVPGVVSNIGPVQGLKDNKEPEKYE KSQNTTNYE	962 ENLTNAMSNPQNLSNNKNLSEFIKQQR ENELDQMERLEDMQEQAQANALKQIE ELNKKQAEETIKQRAKDKINIKTDKPQK SPEDNSIELSPSDSAWRTNLVYRTNKA LYQFILRIAQKONFASAYLTVKLEYPQR HEVSSVIEEELKKREEAKRQKELIKQEN LNTTAYINRVMMASNEQIINKEKIREEK QKIILDQAKALETQYVHNALKRNPVPR NYNYYQAPEKRSKHIMPSEIFDDGTFT YFGFKNITLQPAIFVVQPDGKLSMTDA AIDPNMTNSGLRWYRVNEIAEKFKLIKD KALVTVINKGYGKNPLTKNYNIKNYGEL ERVIKKLPLVRDK	964 IGTDINFSYNDTIKGLVVSVKDANGDKV IREIPSKEAVELMORMRDVIGIIFDKRG 1966 VNLVSGNGRRYLKASISLELSNEKLLN EVKVKDTAIKDTIIEILSSKSVEEVVTNK GKNKL	968 DAINQDMMLYIERIAKIIQKLPKRVHINV RGFTDDTPLVKTRFKSHYELAANRAYR VMKVLIQYGVNPNQLSFSSYGSTNPIA PNDSLENRMKNNRVEIFFSTDANDLSK IHSILDNEFNPHKQQE	970 VVGDVNSQKVFELSKKHFESLKNLDEK AIPTPYMKEPKQDGARTAVVHKDGVH LEWVALGYKVPAFKHKDQVALDALSRL LGEGKSSWLQSELVDKKRLASQAFSH NMQLQDESVFLFIAGGNPNVKAEALQK EIVALLEKLKKGEITQAELDKLKINDKAD FISNLESSSVAGLFADYLVQNDIQGLT DYQRQFLDLKV
959 CGCTGCAGCTGTGCCTAAACTCACGATAGAAAATGTGAAAATCGTGAAATGGAAATGGCGAATCAATAGGCGAAGGC GATATACTAGAAAACTCCAAAGAATTAGCCCTAGAGCCAATTGCATTACAAACAA	981 GAAAATCTCACTAACGCTATGAGTAACCCACAAAATTTGAGCAAAAATCTTAGCGAATTTATCAAGCAACAA CGAGAAAATGCTCACTAACACGAACGACTAGAGGACAAGAAAAAAAA	963 CATTGGCACGGATATTAATTTTAGTTATAACGATACGAT	967 AGACGCTATCAATCAAGACATGATGCTTTATATTGAACGGGATCGCTAAAATCATTCAAAAACTCCCTAAAAGGGGTGCA TATTAATGTGAGGGCTTTACGGATGATACGCCTTTAGATAAAACCCGTTTTAAAAGCCATTATGAATTAGCCGCCAA TCGCGCTTATAGGGGTGATGAAAGTCCTTATACAATACGGCGTAAATCCTAACCAATTGTCTTTTTTACGGCCTC TACCAACCCTATCGCGCCTAACGACTCCCTAGAGAACAGAATGAAAAACAATCGTGTGGAAATCTTTTTTTCAACCGA TGCGAACGATTTGAGTAAAAATTCATTCTATTTTAGATAATGAGTTCAATCCCACAAACAGCAAGCA	969 GGTGGTAGGCGATGTCCCAAAAGGTTTTGAATTGAGTAAAAAGCATTTTGAATCCTTAAAAAAACCTTGATGA AAAAGGTATCCCCACCCCTTACATGAAAGGCCTAAGCAAGATGGAGCCAGAACGGCAGTCGTGCATAAAGATGGG GTCCATTTAGAATGGCGCCTTACATGAAAGGCCTAAAGTGCCTTCAAGCATAAAGATCAAGTCGCCTTAGACGCACT AAGTAGGCTTTTAGGCGAAGGCAAAAGCTCGTGGTTGCAAAAGCGAAAAAAAA
HP1390	HP1390	HP1390 HP1390	HP1390	HP1390

ľ	•
¢	=
(`

HP0838	981	981/CCGATAAGGGATTAAAAAAGGTGTTCAAAGACAGCAAAAAAGACGCTTGCGGGTTCATCTATGAGATCAGCGAGTTC)	982 DKGLKKVFKDSKKDACGFIYEISEFMK	₹ :
			AY I ALLKAUDKYVYLLKYLPSKYWASI	7 2
		SCCASCALL CACCACCAC SCCC CONTRACTOR CONTRACT	LIIALYVRYPUFUALKKLLVSYYYQIWI	<u> </u>
•		ACCARACI I GEA I I GERAGGEREGERICACIGECER I CARGECARACICA I I CARACACI I RAZARICE	AGG I I KIKU I SINIIKNVKSNKSVE I IKE	¥ ;
		<u>AATAAGAGCGTTGAAACCATCAAAGAGCTTATTGAATAGCATCGACTCTTATAACACCTTTGATCAATACCTCTATA</u>	LILNSIDSYNTFDQYLYNLWDSSSVYHS	£.
		ACTTATGGGATAGCTCTTCTGTTTATCATAGCAAATGGGTGCGTCCTGTCTTAGCCCTAGCTAATTATTTCATGGCAG	KWVRPVLALANYFMADEEKPHFIAMĎ	Õ
		ATGAAGAGAAACCCCATTTTATCGCTATGGATGCCGAAACCCAAGTGGAGCATATTTTGCCACAAACGCCCAAAAGA	AETQVEHILPQTPKRGSQWNADFDKE	Ĥ
		GGCAGTCAATGGAACGCGGATTTTGACAAAGAAAAAAGAGAAGAAGAATGGGGTAAATAATATCGCGAATTTAACCCTTTTA	KREEWVNNIANLTILKRKKNAHALNGD	69
		AAGCGTAAAAAGAACGCGCATGCTTTAAACGGGGATTTTGATGAAAAAAGAAAAATTTATGGAGGCAAAGACACGAG	FDEKRKIYGGKDTSKVISCYDITKELYS	Z.
		CAAAGTGATTAGCTGTTATGACATCACTAAAGAATTGTATAGCAATTATAGGAAGTGGAATGAGAAGTCCCTCCAAGA	NYRKWNEKSLQERYKSLYNTITPVLH	ェ
		GCGATACAAATCTTTGTATAACACTATCACGCCTGTTTTACACATAGAGGGGCAAGAAGATGATTTTGAAGATGATTT	EGGEDDFEDLE	
		TGATCTAGAATGATTAAAGATTGCCAAGCATCAAAACAACAAGAGGTGATGATGCCTAÀAAAAGGGCTATTAAAGA		
,	. 1	TGTC&AAGAAAAGGATTTTAAAAGACTTCTTAAAAGAAGCGAAAGAGCGCCGCCCTATTGT		
HP1033	983	<u>983 GATATTGCAGAACCAAACCAATCTATTAGCCCTAAATGCCGCTATTGAGGCCGCGCGGGCGG</u>	984 DIAEQTNLLALNAAIEAARAGEHGRGF	بير
		GGTTTGCGGTGGTGGCTGATGAGGTGAGAAACTCGCTGAAAAACCCCAAAAAGCCACTAAAGAAATCGCTGTTGT	AVVADEVRKLAEKTÖKATKEIAVVVKS	S
		CGTTAAAAGCATGCAACAAGAAGCGAACGATATTCAAACCAATACCCACGATATTAATTCTATTGTAAGCTCTATTAA }	MODEANDIOTNTHDINSIVSSIKGDVEE	田
		GGGCGATGTGGAAGAGCTTAAATCCACCGTAAAAATAACATGATTGTTGCGCAAGCGGCAAATACACCATCTACA	LKSTVKNNMIVAQAAKYTIYNINNRVFC	ပ္
		4TATCAATAACCGGGTGTTTGCGGTTTGGCCAAACTTGATGTGTGGTCTTTAAAAACAATCTTTATGGCATGGTTTT	GLAKLDHVVFKNNLYGMVFGLNSFDI	=
		TGGTCTCATTCCTTTGATATA	-	
HP1033	985	<u>885 CCACAACCCCCATTITAAAAAAGACACGCCCTTTAAAGATTTACAAACTCTTGCTAAAGAGCATGATCTCATTGATTAT</u>	986 HNPHFKKDTPFKDLQTLAKEHDLIDYY	≻
:		TACAATTTAGGGGATGTGGATTTGTCAAACAGAGTGGCTTTGGAAGAAATTTTAGCCCTAAAACCATCGCTTTAAGC	NLGDVDLSNRVALEEILALKPSLLSFSA	ΑŠ
		TTTAGCGCGGATAAATTCTTTAACAGTGCGCAAGCGGGCATTATTATGGGGCAAAAAGAACGGGTTGAAGCGTTAAA	DKFFNSAGAGIIMGOKERVEALKNHPL	7
		AAACCACCCCTTTATAGAGTTTTAAAGGGTGGGTAAAATCACGCTCACCTTGCTTTTTTGCAGCCTAAAAGCATGGAT	YRVLRVGKITLTLLFCSLKAWINHQEDI	~
	-	AAATCATCAAGAAGACATTACAATCCATGCGTTATTGAACCAAACTAAAGACGCATTATTGCAAAAAGCCCTCAAACT	TIMALLNOTKDALLOKALKLYALLKPLEI	山
		CTACGCTCTTTTAAAGCCTTTAGAATTGAATGTGAGCCTCTAGCTTTTCTAAAATAGGGAATTTGTTTG	NVSIASSESKIGNLFGRELESFCVKIOP	٥
		GANTTAGATCCTTTTGCGTGAAATCCAGCCCAAAAAGCCGTGCTTTAAATAGTGAGAACTTTATAAAGCTTT	KNTRALNSEKLYLKLFÖKGVIARISCEF	<u> </u>
		TCCAAAAAGGCGTTATCGCAAGGATTTCATGCGAATTCGTGTGAGTCTTTAGCTTGAATGAA	VCFEVFSLNEKDFEKIALVLEEILNKA	
		AAAAAATCGCTCTGGTTTTAGAAGAAATTCTTAATAAAGCTTAAA		
HP1033	286	987/ATGCTCTATGAAAACCCTTTAAACACCCTTGATGGGAAAGCTTACTTTTACCAAGATTTGAGTTTTAAAAAAATCCTAG	988 MLYENPLNTLDGKAYFYQDLSFKKILD	0
		ATTITITAAAACGATTITAGAAAACGACTACTATTATCACAATAACCCTTTCATTTCTATCGTGATCTGAGCCT	FFKTILENDTIYHNNPFIFYRDLHEPLISI	<u>.</u>
		HAATATCI ATTGATGATTTGAGGGTTAATTATGATGGTTAATTATGAGGGTTAATTATGATG	DULKVNYDULKVNYDDLKVNYDDLKV	 >;
		ATTIERGEGE HATTATER EATTER FOR THE SALES TO	NYDDLKVNYDDLKVNYDDL SANXOOL SANXOOL SANXOOL ONAS	۲ ۵
		16A [16A 1		2 9
		AACGC CGCC A AAAC C CAAAACACACAC	DWAKK	<u> </u>
		16C 16C 16C 17C 17C 17C 17C 17C 17C 17C 17		
		AAT IN CONTRACT OF THE CANAGO STATES AND A S		_
		ITITIAAAGACACGATGAGGAAAGGAATTCIITIAGAA		٦

٠		۰
i	÷	
1	:	-
c		u

≥ υ	<i>σ</i> . ο	PCT/EP01/15428
990 HYFSHAHAEIKENSLEMFLNHYFSHVY RLPKKARKRLFRVFVKHCI JIPLKSLVG KTLRLLKLHALAKKILIQLKI LKKS	992 PNAYLDMLYENPLNTLDGKAYFYQDLS FKKILDFFKTILENDTIYHKFSTSFMWE YDLHKPLVSIDDLRVNYDDLRVNYDRL LQNASPLLELSQNTTFKIYRKAYQKSLP LLRAVRKLVKKLGL	994 YGEFLEKEKEGFMVDEQNPYPEEVRF NELRLAEFESVFSANVPLEDLIJKPACAH HALKALEATLKNRDLGFDATIELEDIAK GFIPKGYLWHFDANVLGNVALVREELL LGVKHTKGYLLWK 996 EECGTLLELREKISLFLEPKDIVKTYEN EDFKERCLALFNALTSMDFQAYKDFES FKKEAMRLSQLKGKDFFKPLINLLTGN SHGVELPLIFPYIQS 998 PQIVAKDFLERLGL
989 CACTACTICICGCATGCCCATGCAGAGATCAVAGAAAACTCCCTTGAAATGTTCTTGAACCACTACTTCTCGCATGTT TATAGGCTCCCTAAAAAAGCACGGAAGGACTCTTTAGGGTGTTTGTCAAAAAAATGTTCTTGAACCACTCAAGAG CCTTGTGGGTAAGACTCTTAAAAACTCCTTAAAAACTCCATGCGTAACAAAAAATCCTAATCCAAGAGCTTAAA AAAGAGCTAGAAACTTTTAATCAAACGATTTTTTCATAATCAATC	SUI CCCAAACGCTTATTTAGACATGCTCTATGAAAACCGTTTAAACACCTTTGATGGGAAAGCTTACTTTTACCAAGATTTG AGTITTAAAAAAATCCTAGATTTTTTAAAACGATTTTAGAAAACGATTACGATTTATCACAAATTCTCAACATCTTTCAT AGTITTAAAAAATCCTTGCATAGATTTTTTAGAAAACGATTTGAGGGTTAATTATGAGGGTTAATTA GTGGGGCTTTTACAAAACGCTTCGCCTTTATTAGAACTCTCTCAAAAATTGAGGGTTTATTGAGGGTTAATTA CAAAAATCCTTGCCTTTGTTGCGCGTTGATTATTAGAACTCTCTCCAAAAATTGGGGGGTAATTAGTAGGGGTTATTA CACAAAATCCTTGCCTTTGTTGCGCGTGAGAAGTTGGTTAAAAAATTGGGCCCTAATACAAAATTAGTAGGGGTTTTT CCCTTGCGCTATCATCGCAGACGCTACTTTTTTAAAAACCAGCGATTTGGCCCCTAATACAAAATTAGTAGGGGTCTTT CTCCAAGGGTGCATTGGCGTTTTTTTTTT	993 GTTATGGCGAGTITITAGAAAAAGAGGGGCTTTATGGTAGATGAGCAAAACCCTTATCCGGAAGAAGTCCGC TTTAATGAGTTTAGCGGAATTTGAGAGGCGTTTTAGCGCCATTGTGCCTTTAGAGGATTTAGATGCGAATTGGA TGCGCTCATCATCCTAAAGGCTTTAGAGGCGTAAAAATGGGATTTGGGCATTTGGCGATTTGGGCATTTGGAAA TGCGCTCATCATCCTAAGGCGTTTTAGAAGCCCTTAAAAATGGGATTTTAGGGCATTTTAGGGCATTTGGAAA ACAGATCGCAAAGGCTTTAATGGCGTGAAACACCAGGAAATTTTAGGGCATTTTAGGGCATTTTAGGGCATTTTAGGGCAAAGGTTTTTAGGGCGTTTTAGGGGAAAATTTGGTTAGTTA
HP1033	500	HP0064 HP1032 HP1032

	_
ч	,
C	2
ē	ú

2/066501 W . >	10× - ~	1			, ——.	PCT/E
1002 HIYEKEVDARELKHGVEEFTADIPDVKE EALAHLDESGIVKVGTYVSAGMILVGK TSPKGEIKSTPEERLLRAIFGDKAGHVV NKSLYCPPSLEGTVIDVKVFTKKGYEK DARVI SA	1004 YKPYTPSRRFMSVLDSKDITAKSSVKG LLTKLKATAGRNNNGRITSRHKERGAK LLTKLKATAGRNNNGRITSRHKERGAK KLYRIIDFKRNKYNIGGKVAAIEYDPYR NARIALVVYPDGDKRYILQPSGLKVGD SVIAAGGGLDIKVGFAMKLKNIPIGTVV HNIEMHPGAGGLARSAGMSAQIIMGR ENKYTIIRMPSSEMRYILSECMASVGV VGNEDFINVSIGKAGRNRHRGIRPQTR GSAMNPVDHPHGGG	1006 FVGHLERFKELLREEVNSLSNHFHNLE SWRDARRDKFSEVLDNLKSTFNEFDE AAQE	1008 DENTTKLFLWILTATIALV/LTLIYAKLRI VKRIDELVLKINAFSRGDKDLRAKIDVG DRNDEISQVGRGINLFVENARLIMEEIK GISTI NKTSMOK	1010 GKISPNEWPPPPPTEEHKVVHQLDDV TRDSEVKATQIFDQLDLIGASAEKIAKM VKKIQEPLQKH	1012 VPLAYYLEAMGQQTRVLMQMLCPDPS KRCLLYAGGYKNGSSNTNGDTGNNPP RGNVNATFDMOSI VN	1014 DKGLKKVFKDSKKDACGFIYEISEFMK AYTALLKKQDRYVYLLRYLPSRYWASI LTTALYVKYPDFDALKKLLVSYYYQTWI AGGTITRIKQTSINIIKNVKSNKSVETIKE LILNSIDSYNTFDQYLYNLWDSSSVYHS KWVRPVLALANYFMADEEKPHFIAMD AETQVEHILPQTPKRGSQWNADFDKE KREEWVNNIANLTLLKRKKNAHALNGD FDEKRKIYGGKDTSKVISCYDITKELYS N
1001 CCACATTTATGAAAAAGAGTGGATGCTAGGGAGCTTAAGCATGGTGGGAAGAATTTACCGCTGATATTCCTGATG TGAAAGAAGAGCGCTCGCTCATCTTGATGAAAGCGGGATCGTTAAAGTCGGTACTTATGTGAGCGCTGGATGATT TTGAGGCAAAACTTCTCCTAAAGGCGAGATTAAAAGCCGCCTGAAGAGCGGCTTTTAAGGGCTATTTTGGGGA TAAAGCCGGGCATGTGGTCAATAAGAGTTTGTATTGCCCTCCCAGTTTGGAAGGCGCTGATTGAT	1003 ITATAAGCCCTACACCCCAAGCAGCGCTTCATGTCGGTGTTGGACTCTAAAGACATTACCGCAAAAAGCCGGTGTCA AAGGCTTACTCACTAAAGCAACAGCAGGGAAACAATAATGGACTCACCACCACCACACAGGAGA AAGGCTTACTCACTAAAAAACAGCAACAGGGAAACAATAATACAATATTGAAGGGAAAGTGGCTGCGATTGA GGGGCTAAAAAACTCTATCGCATTATTCAATGCGCAATAAATA	1005 TTTGTAGGGCATTTAGAACGCTTTAAAGAGTTACTAAGAGGGAAGTGAACAGCTTGAGTAATCATTTCCATAATTTA GAATCATGGCGAGGGCTAGGAGGGGATAAATTTAGCGAGGTGCTGGATAATTTGAAAAGCACTTTCAATGAATTTGA TGAAGCTGCGCAAGAGCA	1007 TGATGAAAACACCACGAAATTATTCCTTTGGATACTGACGACGATAGCGCTAGTGGTTTTGACGCTCATATACG CTAAATTAAGGATCGTGAAACGCATTGATGATGAACTGGTCCTTAAAATCAACGCTTTTAGCCGTGGGGATAAGGATTTGA GAGCCAAAATTGATGTGGGTGATCGCAACGGATGAAATCTCGCAAGTGGGCCGTGGGGATCATTGTTTGT	1009 CGGCAAGATTAGCCCCAATGAATGGCCTCCCCCTCCCCCATGAAGAGCATAAAGTCGTGCATCAATTAGATGATG TTACAAGAGATTCTGAAGTGAAAGCCACGCAAATTTTTGATCAATTGATTG	1011 GGTGCCTTTAGCCTATTATTAGAAGCGATGGGCCAACAAGCGGGTTTTAATGCAAATGCTCTGCCCTGATCCTT CCAAACGCTGTTTGCTCTTATGGGGGGTTTTAAAAAAGGGGATACAAGGGGATACAGGCAACAACCCC CCAAACGGCATACAGGCAACAACCCC CCAAGGGGGAATGTCAATGCAATCTCTAGTCAATAA	1013 CCGATAAGGGATTAAAAAAGGTGTTCAAAGACAGCAAAAAAGACGCTTGCGGGTTCATCTATGAGATCAGGAGTTC ATGAAAGCCTATACCGCATTGCTAAAAAAAAAA
HP1032	HP1032	HP0062	HP0062	HP0062	HP0062	HP0062

2/066501	PCT/
1016 HAVMSKIGGDAFGVYQQʻ3EFEDLCKG PHLPNTRFLNHFKLTKLGKJYLGGDEN NEMLIRIYGIAFATKEGLKIYYLFQIEEAK KRDHRKLGVELGLSDCEIGAGLPLW LPKGARLRKRIEDLLSQAI.LLRGYEPVK GPEILKSDVWKISGHYDNYKENMYFTT IDEQEYGIKPMNCVGHIKVYQSALHSY ROLPLRFYEYGVVHRHEKSGVLHGLL RVREFTQDDAHIFCSFEQIQSEVSAILD FTHKIMQAFDFSYEMELSTRPAKSIGD DKVWEKATNALKEALKEHRIDYKIDEG GGAFYGPKIDIKITDALKR «WQCGTIQV DMNLPERFKLAFTNEYNHAEQPVMIHR ALLGSFERFIALLSEHFGGNFFFVAPT QIALIPINEEHHYFALKLKEALKKRDIFY EVLDKNDSLNKKVRLAEKGRIPPILOG NEEVETEILSIRDREKQDQYKMPLKEFL	1018 GNILMSFVVLASI WEKSGRLDKYGKEL LVFKDRKDNDFVLSPTLE =NITEIAANFI KSYKQLPVHLYQIHTKFRIJEIRPRFGLV RAREFIMKDGYSFHEDAE SLDKEFLNT OSAYKEILSDLGLDFRIVEADSGAIGGS KSREFVVLTECGEDTIVVCONCDYAAN IEIAKRSKRPEPLNVPKAQLAKFPTPNT TSAQSVAEFFKTEPYFVLTALVRKVIHK DKETLACFFVRGDDNLEEVKALNALNII GANALELREASOMDLDNVGLIAGANE KDFHAVGYDLKGFENLVADIVQVKES DRCPNCQGALKYHKSLEVGHIFKLGQ GYAKSLKASFLDKNGKEGFFEMGCYGII GISRLLSAILEQKSDDLGCVWTKNTAP FDVVIVVSNWKDEAQKKLAFEVYERLL QKGVDALLDDRDARFGAIGMRDFELIG ERLALIIGKQTLESKEFECIKRANLEKQT IKDIELEKILEMLESE
1015 AGCATGCGGTGATGAGTAAAATCGGTGGCGATGCCTTTGGCGTGTATCAACAAGGCGAGTTTGAAGATTTGTGTAAGGTGTGTATTGGCGCGCGAGGGCGCGAGGGCCGCATCTCCCAAACACCCCGATTTTAAACCATTTTGCCACTCACT	1017 GCAAATATITTAATGAGTTTTGTGGTTTTTGGGGGAAAATGGGCCGTTTGGATAAATACGGCAAGG AATTATTGGTTTTTAAAGGCTTAAAAGTTTGATTTGTTTTTAAGCCCCACTTTAGAAGAAATTCCGGAAATTGC CGCTAATTTCATTAAAAGTTACAAGCAATTGCCCGTCCATCTATCAAATCCGTGATGAATCCG CGCTAATTTCATTAAAAGGTTACAAGGGGGAATTTATCATGAAGGTTTCAAGCATTTCGTGAGAATCCG CCCAAGATTTTTAAACAGGGCAATTTATCAGGGGATTTTAAGCGATTTGGGTTTTTAAGCGGTTTGGATTTTTAAGCGGTTTGGATTTTTAAGCGGTTTTAAACGGATTTTTAAACAGGGGAATTTTAAAGGGATTTTAAACGGGTTTTAAACGGGTTTTAAACGGGGGGATTTTAAACGGGTTTTAAACGGGGAATTTTTAAACGGGTTTTAAACGGGGGGATTTTAAACGGGGGGATTTTAAACGGGGGGATTTTTAAACGGGGGAATTTTTAAAAGGGGGGGATTTTTAAAAGGGGGGG
HP0184	HP0184

_	_
0	ĸ,
_	-
-	-
	v

SFKPFVSI PIKLAIDR SSPCAF LGQSELL QLALKE NVAPYQ SEGNIL	DYSGAN WVSFGK IDITGTIR LNIANA GNLNVT WDKGS SGVTFN NNTFNS YSFNDT SSVSIEN SIKYNN RTRDSI	ACCUTE BOUNDED
TGLSKKSKSAILSPTEAYSNTLLELAKK DEKIVGVTAAMPSGTGLDKLIDAYPLRF FDVAIAEQHALTSSSAMAKEGFKPFVSI YSTFLQRAYDSIVHDACISSLPIKLAIDR AGIVGEDGETHQGLLDVSYLRSIPNIMVI FAPRDNETLKNAVRFANEHDSSPCAF RYPRGSFALKEGVFEPSGFVLGQSELL KKEGEILLIGYGNGVGRAHLVQLALKE KNIECALLDLRFLKPLDPNLSAIVAPYQ KLYVFSDNYKLGGVASAILEFLSEQNIL	1022 VFYLNGMTTWKIAGTGVFTQDYSGAN SVLVFNQTTPFLAGANPTSNSVVSFGK TSGAEWGLVGYIQGVFKANQIDITGTIR SGNGAKTGGGATLVFNAQKRLNIANA HLNNDKAGLQNSWMNFIVNNGNLNVT NAKFSNQTPHGGFNLKANNITWDKGS VNGGGNFGVDNADSNGATTISGVTFN NNGTLIYKGGENSAGNSLTLENNTFNS YNINAKAQNLIFNNNSFNGGSYSFNDT KNTTFKGTNTLINSDPFSRLKGSVSIEN NSVFNIERDLTDKTTYTLLSGNSIKYNN QALAGQCFFKKFMEFNPLWWRTRDSI KSG	EIVKIRVGDIVDSKKIDTAVLALFNQGYF KOVTATFEGGILEFHFDEKARIAGVEIK GYGTEKEKDGLKSQMGIKKGDTFDEQ KLEHAKTALFALEGGGYGSVVEVRT EKVSEGALLIVFDVNRGDSIYKGSIYE GSAKLKRMIESLSANKQRDFMGWW WGLNDGKLRLDOLEYDSMRIQDVYWR RGYLDAMISSPFLKTDFSTHDAKLHYK VKEGIQYRISDILIEIDNPVYPLKTLEKAL KVKRKDVFNIEHLRADAQILKTEIADKG YAFAVVKPDLDKDEKNGLVKVIYRIEVG DMVYINDVIISGNQRTSDRIIRRELLLGP KDKYNLTKLRNSENSLRRLGFFSKVKI EEKRVNSSLMDLLVSVEEGRTGQLOF GLGYGSYGGLMLNGSVSERNLFGTGO SMSLYANIATGGGGRSYPGMPK
TGLSKKSKSALSPTEXNTLELAKK DEKIVGVTAAMPSGTGLDKIJDAYPLR DEKIVGVTAAMPSGTGLDKIJDAYPLR FDVAIAECHALTSSAMAKEGFKPFVS YSTFLQRAYDSIVHDACISSLPIKLAIDR AGIVGEDGETHQGLLDVSYLRSIPNMV FAPRONETLKNAVRFANEHDSSPCAF RYPRGSFALKEGVFEPSGFVLGQSELI KKEGEILLIGYGNGVGRAHLVQLALKE KNIECALLDLRFLKPLDPNLSAIVAPYQ KLYYFSDNYKLGGVASAILEFLSEQNIL KPVKSFEIIDEFIMHGNTALVEKSLGLD	1022 VFYLNGMT SVLVFNGMT SSUVFNGT SGNGAKTG HLNNDKAG HLNNDKAG NNGTLIYKG YNINAKAGN KNTTFKGTN KNTTFKGTN KNTTFKGTN KNTTFKGTN KNTFKGTN KNTFKGTN KNTFKGTN	1024 EIVKIRVGDI KOYATFEG GYGTEKEKK KLEHAKTALI EKVSEGALLI GSAKLKRRN WGLNDGKIN WGLNDGKIN VKEGIQYRIS VKEGIQYRIS KVKRKÖVFN YAFAVVKPD DMVYINDVIIS KDKYNLTKLF EEKRVNSSLI GLGYGSYGG SMSLYANIAT
GGCCTTTAGAATT ACCCTTTAGAATT CAAACTCATTGAC STATGGCTAGAGGG GACGCTTGTATT AAAAAGGGCCTTT TAAAAAGGGGG ACTCATAGGGTAT TTTAGCGATATT	TTACAGCGGCGC GCGTGGTGAGTTT CAAATTGACATTA CTCAAAAGCGTTT TGTCAATAATGGT CAATAACATTACT SCAACCACTTACT SCAACCACTTACT SCACCACTTACT SCACCACTTACT SCACCACCATTA	
SCIENAGEGGGCTTTTGATTT SCIENAGEGGGGCCTTTTGATTT SCECAATCTTATCGCCCCTTTTGATTT AACCGCGGGCGATGCCCACTGAGGGATTAGACACCCTTTTGATTG AACCGCGGGCGATGCCCACTGAGGGATTAGACACCCTTTTGCAGGGCTAGGCTAGGCTAGGCTAGGCTAGGGGCTATTGCCGGGGCGTATTGTGCGTTGAGCGCTTGTAGGCTAGGGCTATTTTGCCGGGGCTTTTTGCCGGGGGCGTTTTTGCCGTTTGTGGCTTTTAGCGCTTTTTGCCCTTTTTGCGCTTTTGCGCTTTTGCGCTTTTGCGCTTTGTGGGTTGTGTGGGGGG	3GAAGATCGCTGGCACAGGCGTTTTCACGCAAGATTACAGCGGCGC CCCTTTTCTTGCTGGGCGCAATCCCACTTCTAATAGCGTGGTGAGTTT TAGTGGGCTGTGGGCGCATTTTTAAAGCCAATCAAATTGACATTA AAAACCGGTGGGGCGCGCTTTTAGTGTTTAACGCTCAAAAGCGTTT AAAGCCGGTTTGCAAAATTCATGGTGAATTTCATTGTCAATAATGGT ACCAAACCCCACATGGAGCTTTAACCTTAAGGCCAATAACATTACT SAATTTTGGCGTGGATAACGCCGATAGCAATCGTTTAACCCATA GATTTTGGCGTGGATAACGCCCGGAAATTCTTTAACCCTAG GCCAAAAGGGCGTGAAATTTTTAACAACACCGTTTAATGGCG ACCTTTAAAGGCCAAACACGCTCATTAACAGCGATCCTTTTAGCCG ACCTTTAAAGGCCAAACACGCTCATTAACAGCGATCTTTTAGCCG ACCAAGCCTTTAGCGGAATTTTTAGCAAAAATTTAGCAGGAACTTTAATGGCGGAACGCGTTTAAAAGGCGAAACCCTTTAAATGCCGAAACCGTTACAACGCGAAACCGTTTAAACGCGAAACCGTTACAACGCTTACAACGCGAAACCGTTACAACGCAAACCGAAACCGAAACCAAACCGAAACCAAACCAAAGCAACCAAAGCAACAA	TIGTGGATTCTAAAÁAAATAGACACCGCTGTTTTGGCCTTTGTTCAATG TGAAGGCGGCATATTAGAGTTCATTTTGATGAAAAAGCCAGGATTG TGAAGGCGGCCATATTAGAGTTTCATTTTGATGAAAAAGCCGGATTGAAAAGCGG SAAAAGGGAAATTAGAGTTTAGAGGGGCAGGGCTATTATG GCTAAAACGGCTTTAAAAACCGCTTTAGAGGGGCAGGGCTATTATGGGGGGG SGGAAGTGAGTTAAAAACCGCTTTAGATTGAATAGGGGGA SGGAAGCGCCGAAATTGATTGCGTTTTGATCATTGAGTGCGATGGGGTTACTTAGAGGCGTTAGAGGGTTACTTCGCCTTTTTTTAATAGAGGGGTTACTAGAGGGAAAAGGGGTTATTCTTCGCCTTTTTTTAATAGTGGGTTAGAGAGAAAAGGGGTTATTGGGGTTTTAATAGTGGGGTTAGGGGTTATGCGGTTTTAATATTGAGGCCGAAATCGCGGTTATGGGGTTATGCGGTGTTATTGAGGGCTAATGGGGTTATGCGGTTATGCGGTGATATCAATGAGCGGATAGGGGTTATGCGGTGTTATGGGGTTATGATGAGCCGATAGGGGTTATGGGGGTTATGGGGTTATGGGGTTATGATG
ANGATICACIGANGGCCGCIA CCAAAGCGCATCTTTCG GTATTCTACTTTTTGCAGAG GTATTCTACTTTTTTGCAGAG ATTGACAGGCTGGGATTGT TCCCTACGTTGTTTTTG CAAGCCCTTGCGAATTGTT ATTTAGGCCATGGTTTAGT AAATTTAAGCGCATTGTTGAGGCGATTGTTGAGGCGAACTGGAATTGTTGAGGCGAATTGTTGAGGCGAATTGTTGAGGCGATTGTTGAGGCGATTGTTGAGGCGATTTTGAGGGAACACGGCTTTAGAGCGCATTGTTGAGGGAACACGGCTTTAGAGCGCATTGTTGAGGGAACACGGCTTTAGA	ACGACTTGGAAGATCGCTGG WACGACCCTTTCTTGCTGG GGGGGTAGTGGCCTGTGCGGGGGTTGCCGTGGGGGGGGGG	GCGATATTGTGGATTCTAAAA CCACTITTGAAGGCGGCCATA GGGACTGAAAACGGCTT AGAAAAGGTCAGTGAGGGTG AGAAAGGTCAGTGAGGGTG TTATGAGGGAAGCGCGAAA1 TGGTAGGGGTTAATAGA ATGCGTAGGGGTTACTTAGA ATGCGTAGGGGTTACTTAGA ATGCGTAGGGGTTACTTAGA ATGCGTAGGGGTTACTTAGA AAAACCGAAAACGCCT CATGTGAAAACCCGA
GGATACCGGCTTGTCTAAAGATCGCTGAGGGGGCGTATGAAAATGGCATGGGGTGGGGCTTTTGATTT GGATACCGGCTTGTCTAAAAAATCCAAAGCGCAATCTTATCGCCCACTGAAGCGTATTCTAACACCCTTTTAGAATT AGCTAAAAAAGCTTTTGTGAGGCGTAACCGCGGCGGCGCTTTAACTTCTAGCACGCTTTTGAGG GCTTACCCTTTGCGCTTTTTTGAGCATTGTTTTTTTTTGCAGGGCTTTAACTTCTAGCAGCGCTATGGCTAAGAG GGGTTTAAACTTTTTTGGCATTTATCTACTTTTTTTTTT	1021 CCGTGTTCTATCTCAATGGCATGACGACTTGGAAGATCGCTGGCACGGCGTTTTTCACGCAAGATTACAGCGGCGCTTTAACAGCGCGCGC	1023 ATGAAATTGTAAAGATTCGTGTGGGCGATATTGTGGATTCTAAAAAATAGACACCGCTGTTTGGCTTTTGTGAAAAGGGGATTG AAGGGTATTTTAAAGACGTTTATGCGATATTGAGGCGCATATTAGAGTTTCATTTTGATGAAAAAGCCAGGATTG AAGGGTATTTTAAAGACGTTTATGGGACTGAAAAGGGGGCATATTAGAAATCCCAAATGGGGATCAAAAAGGG CCGGGGTAGAAAATCCAAGAAAATTATGGGGCTGCATAAAAACCGCTTTAGAGGGGCAGGGCTATTATG CGACACCTTTGATGAGCACAGAAAAGGTCAGTAGAGGGGCTTTAAAAACCGCTTTAGAGGGGCAGGGTTTTTAATAGGGGGGGAATTAGAGCGTTTATATACAAAAACAATCAAAAAGGGAAATTAAAAATTGCGTTTGAATAGGGGGGT ATAGCAACGAGATTTCATGGGCTGGAAGAGGGGAAATTGAGAGAATTCATGGAGTTTTTAAAAACGTAGAGGATTTTTAAAAACGTTAGAGGGGTTACTTAGAGGGGATTTCATGGGCTGATTTTAAAAACGTTAGAGGGGTTATTAAAAAGGGAAATTGAGAGGATTTCACCCATGACGTAGTGCTTAAAAAGGGAAAAGGGGATTTTAAAAAACCTTAGAAAAGGGAAATTGAGAGGAAATTGAGAGGATTTTAAAAAA
<u> </u>	25 2453945845846	1023 1000 1000 1000 1000 1000 1000 1000
10 80 90 80 90 90 90 90 90 90 90 90 90 90 90 90 90	HP0184	HP0184

TGCLILLS FRWKGG STAVKGG STAVKGG STAVKGG ADVLNMS MDVGLG LAKELSKK VNHLLQVL	MHETMIA LPOEDGV AMYREGC QNRFAEV IGVLFVDK KHE	LLKKGDRY YVKYPDFD TRIKGTSIN OSYNTFDQ VLALANY EHLPQTP VNNIANLT (IYGGKDT	KVEEPSK KYDESVFK ELLDEVG TLALKLKI KNKIFAQ NKPVGSF ILNLHFER GVVG	SODLSARI NAEKRLA WLDTAMN WEKLRSF OANYDLS SEN
INTERPRETATION OF THE STATE OF	1028 RTISKEVVSFDSKLHCOLDDMHETMIA SEGIGLAAIQVGLPLRMLIINLPOEDGV QHKEDCLEIINPKFIETGGSMMYREGC LSVPGFYEEVERFEKVKIEYQNRFAEV KVLEASELLAVAIQHEIDHLNGVLFVDK LSILKRKKFEKELKELJKKQKHE	1030 KKDACGFIYEISEFMKAYTALLKKQDRY VYLLRYLPSRYWASII.TTALYVKYPDFD ALKKLLVSYYYQTWIKGGTITRIKQTSIN IIKNVKSNKSVETIKELILNSIDSYNTFDQ YLYNLWDSSSVYHSKWVRPVLALANY FMADEERPHFIAMDAIETQVEHILPQTP KRGSQWNADFDKEKIREEWVNNIANLT LLKRKKNAHALNGDFIJEKRKIYGGKDT SKVISCYDITKELYSNYRKWN	1032 EEYRSVFEKDKAFNRRFSVIKVEEPSK EACYLILKKIAPLYEEF HQVRYDESVFK ACVDLTSDYMHDKFL PDKAIELLDEVG SRKKISPKKGKKIGVDDVKETLALKLKI PKMRLSSDKKALLRNLEKSLKNKIFAQ AEAISLVSNAIKIQHCGLSAKNKPVGSF LFVGPSGVGKTELAK ELALNLNLHFER FDMSEYKEAHSVAKLIGSPSGYVG	EQKDLMVGFENSESHILLVVSQDLSARI ALMKLFAQNFKTANKIELLFYNAEKRLA RELDELKKHHITPMQGPLGSVLDTAMN PNSVLVIDNLNEAKELHDKIGVEKLRSF LEKATDNEQYCIFAHIDLKQIQANYDLS KLKELLNNHFKQRLAFRCNGEN
NYLDOAF KVYLDOAF RILFAEOKE RCEKCOGI CKGAKYNF VEEAYEFF YITLGONA I DTGKTLYIL	B RTISKEVV SEGIGLAV QHKEDCL LSVPGFY KVLEASEI LSILKRKK	O KKDACGF VYLLRYLF ALKKLLVS IIKNVKSNI YLYNLWD FMADEEK KRGSQWI LLKRKKNI SKVISCYC	2 EEYRSVFI EACYLILK ACVDLTSI SRKKISPK PKMRLSS AEAISLVS LFVGPSG FDMSEYK	4 EGKDLMV ALMKLFAC RELDELKH PNSVLVID LEKATDNE KLKELLNN
				1034
1025 CACCGCTCAAACCCTTTAAACCATGCTAAAAAACTCAAAGCTTGAATGGGGTGGAGATTGTAGGGTTGGAGCATT TGGATAAAGTGATTTATTTAGATCAAGCCCCCATAGGCAAAACCCCACGAAGCAACCCTGCCACTTACAGGGAGTG ATGAAATCAGGATTTTATTTGCCGAGCAAAAAGGCAAAATTTTAGGCTATAGTGCGAGCGTTTTAGCTTT AATGTTAAAGGAGGGCGGTGCGAGAAATGCCAAGGCGATGGAGCATTAAAATAGAAATGCAATTTTTGCTGATGT GTTAGTCCAATGCGATAGCTGTAAGGGCGCTAAATACAACCCCCAAACTTTAGAAATCAAGTGAAAGGCAAATCCA TTGCCGATGTGTTGAACATGAGGGCGTAAATACAACTTTTGCTAAATTCCCTAAAATCGCGGGGGGAATTCA AAACGCTTATGGATGTGGGGTTAGGCGTAATACACTTTAGGGCAAAACGCTACGAAATTTAGGGGGGGG	1027 AAGAACGATITCTAAAGAGGITCGTITCTTITGATICAAAACTCCACCAACAGCTGGATGACATGAGACTATGAT CGCTAGTGAGGGGATAGGCGTTAGCCGCTATTCAAGTGGGTTTGCCTTTAAGAATGCTCATCATCAACCTCCCGCAAG AAGACGGCGTGCAACACAAGAAGACTGCTTGGAAATCATTAACCCTTTAAGAAACTGGGGGATCAATGATG TATAGAGAAGGGTGCTTGTCGTGCCGGGATTTTACGAAGAAGGGGGGCTTTTGAAAAAGGGTTAAGAAGGTTAAGATGATGA AAACCGCTTCGCTT	1029 GCAAAAAGACGCTTGCGGGTTCATCTATGAGATCAGCGAGTTCATGAAAAGCCTATACCGCATTGCTAAAAAAACAA GACCGATACGTCTATTTATTGAGGTATCTCCCCTCTAGGTATTGGGCCAGCATTTTAACCGACTGCCCTTTATGTCAAA TACCCTGATTTTGACGCTTTGAAAAAGCTTTTGGTGTTTATTACCAAACTTGGATTGCAGGGGCACGATCAAA TACCCTGATTTGACCAGTATCAACATTATCAAAAAGGTTAAAAAGCAATAAGGGTTGAAACTTGAATAGCATCAAAGGAGCATCAAAAGAAGCATTATAAAAAGGAACCATTATAAAAAGAAACTTTATAAAAAGAAAAGAAAAAAGAAAAAAAA	1031 TTGAAGAATACCGCAGCGTGTTTGAAAAAGACAAGGCTTTTAATAGGCGTTTTTCAGTCATAAAAGTTGAAAGGCCTTTAAAAGAGCCTTTTAATGAAGAGCCTTTTTAAAAAAGATCGCCCCTTTATGAAGACCCCCAGGTGCGTTATGATGAGGCCTTTAAGGCGTTTAAGGCATTGATTTAAAAAAGATGCGTTGATGAGAATTATTAGGCGTTGATGAGGATTGAATTATTAGGCGTTGATGAGGATTGAAAAATTATTAGATGGTGGGATGAAAAAA	1033 ATGAGCAAAAGGACTTGATGGTTTGAAAATAGCGAATCGCATTTGTTGGTGGTGAGTCAAGATTTAAGCGCT CGCATCGCCTGATGAAGCTTTTCGCTCAAAATTTCAAGACTGCCAACAAGAGTTGCTTCTTCTACAACGCGAAAA ACGCCTTGCAAGAGAACTTGATGAGTTGAAAAAACACCACATCACGCCATGCAAGGCCTCTAGGGAGCGTTTTG GACACCGCTATGAATCCTAATAGCGTGCTTGTGATAGACAATCTCAACGAAGAGCAAGAGGTGCACAAAAAATAGG GGTGGAAAAATTAAGATCGTTTTTAGAAAAAGCCACAGAACAGTTTGCCCACGACGACCTCA AACAGATTCAAGCTAATAAGATCTTAGCAAGATTAAAAAGAACAACGAGCACTTCAAACAGCCTGGCCTTTA AACAGATTCAAGCTAATAACGATCTTAGCAAGTTAAAAAGAACTTCAAACAACAACGCCTGGCCTTTA GGTGTAATGAGCTAATAACGATCTTAGCAAGTTAAAAAGAATTGTTAAAACAACCACTTCAAACAACAACAACAACAACAACAA
HP0184	HP0184	HP0184	HP0879	HP0879

HP0879	1035 AGACGA	1035 AGACGAGTTGGCCAGACAGGAATTGAAAAATCCAGGCTTCACCCAAGCGCAAGAATTAAGGCAGTTGATCAGAGAT	1036 TSLARGELKNPGFTQAQELRQLIRDGA
	TTGCGT	TIGGETGAAAAGCCTGAAAAAACAATGCAAAACAAAAAAAAAA	VRLQ I SAIPLSYYLDIL GNKTATLLRESL
	100011	COAGCCTTAGCCAATTTAGACCAAATTTTAAAAAAAAAAA	KNNACHSCHNACHFCCNGPSNCALA
	TOLOGO	CONTRACTOR TO CONTRACTOR TO A CONTRACTOR TO	NLEGSLGILGKLLDLSQQYASQGVIKPL
		CANANA MATERIAL MAGGETTA CONTRACTOR TO THE CONTRACTOR CANANA MAGGET CONTRACTOR CONTRACTO	VVDVGKEQIGITDSMLLVAQNIVLALGQ
	ATTATA	MOCTON TO THE MOCE OF THE MOCE	VDLSKIQQNNNEQLYENIMKVMLLGAG
	45 C C C C C	ALTRIBUTE CALLECT IN TABLE CEGEGE CEGEGE CALL AN I GEGEC GIATAN EGCET GAGT GEGEC GACATT GCCA	GTNGAYNGVSVGDIATGMQNFSSQTG
	A) 10 10 10 10 10 10 10 10 10 10 10 10 10	Cesecca i schada I I I I i i i i i i i i i i i i i i i	LIGANSTVSELNALIKSGISLDRETLGLG
_	AAGAGC	AAGAGCGGGATI ICTTTGGATCGTGAGACTTTGGGGTTAGGGGGTTTTATTGAAAAAATATCTGTAGCGGTGCATC	SFIEKNICSGASSCFSGNQLIYKKGLDR
	91019	GICLIGIIITAGIGGGAATCAGCTTATCTATAAGAAGGGCTAGACAGAACCATAA	F
HP0879	1037 TTTAAGC	103/TITTARGCGCCTTACAAGCTCAAGGCGCGAAGCACTTATAAAGAAAG	1038 LSALQAQGASTYKESELSRNHTEIMLK
	1 I AAAAG	AAAAG GGGAGCTGATATCACAATCAAGACGGCGTTTTAAAAATTTCACCCCTAGAAAACCCCTAGAAGCCCT	SLGADIHNQDGVLKISPLEKPLEAFDFT
	IIGAIII	I GATITIACGATAGCTAATGATCCGTCTAGCGCGTTTTTTTTCGCCCTCGCTTGCGCGATTACGCCAAAAAGCCGCC	IANDPSSAFFFALACAITPKSRLLLKNVL
	TICITI	ITCTTTTAAAAAATGTCTTGCTCAACCCCACTCGCATAGAAGCTTTTGAAGTTTTGAAAAAAAGGGTGCTTCCATAGA	LNPTRIEAFEVLKKMGASIEYAIQSKDL
	GTATGC	GIATECGATTCAGTCCAAAGATTTAGAAATGATTGGCGATATTTATGTAGAGCATGCCCCTTTAAAAGCGATCAATAT	EMIGDIYVEHAPLKAINIDQNIASLIDEIP
	TGATCAA	IGAICAAAAIATGGCCAGTCTTATTGATGAAATCCCCGCTTTAAGTATCGCTATGCTTTTTGCAAAAGGCAAAAGGAT	ALSIAMLFAKGKSMVKNAKDLRAKESD
	GGTTAAA	GGTTAAAAACGCTAAAGATTTACGAGCTAAAGAAAGCGACAGGATTAAAGCGTTGTTTCTAATTTCAAAGCTTTAGG	RIKAVVSNFKALGIECEEFEDGFYVEGL
	GATTGAG	GATTGAGTGCGAAGAGTTTGAAGATGGGTTTTATGTAGAGGGATTAGAAGA	EDISPLKQRFSRIKPPLIKSFNDHRIAMS
	TAGGATT	TAGGATTAGCCCCCCTTATCAAAAGCTTCAATGACCACAGGGATGCGATGAGTTTTGCTGTTTAACTTTAGCGT	FAVLTLA
HP0879	1039 TTTCACG	CAGAAGTATCCTAACAAAAATCCCCAATCGCGCTCGCTAGCGCTAATGTTTTGAAAGCTGTTGGTGTTTTG	1040 SRRSILTKIPIALASANVLKAVGVFEKVE
	MAMAMGI	AAAAAGI AGAA I CCALO I CCGCA I I CCGCA I I I I GGCCCCI I I AI CGCAAAGGI I CAAAAA I GGAGT GATTAAAGATA	SIPHATHFGPFIAKVQNGVIKDIVPQKS
	2221911	116 I CUCUCAAAAAAGGA I I A I AACCO I ACI A I GATGI I AAAAGGGA I GATGATAGAGATAGTAGGG	DYNPTMMLKAMVDRVYSDSRVKYPCV
	I GAAGIA	IGAAGIAICCIIGCGTGCGCAAGAGCTTCTTAGAAAAAAAAAA	RKSFLENKKNHKELRGREEFVRVSWD
	616061	GIGCGIGIGAGTIGGGATIGGGATITAGCGGCTAAAAAGCTTAAAGAAATCCCTAAAGAAAACATTTATAAT	VALDLAAKKLKEIPKENIYNASYGGWG
	SCCAGT	GCCAG ATGGT GGGGGGCATGC	
HP0879	1041 TATTGCT	1041 TATTECTCAAAGGCCAAAGGGCCTGATGAGAAAAAATCAAACTTTTAGCCCAAAAACTAGGCGTAAAAGCGGAGTTT	1042 LLKGKGPDEKKIKLLAQKLGVKAEFGF
	911999	GEG I I GI CAATI CCAATGAATTG ITAGAGATCTTAAAAACTTGCACCCTTTATGTGCATGCAGCCAATGTGGAAAGC	VNSNELLEILKTCTLYVHAANVESEAIA
	SAAGCG	GANGCIGA I IGCIG I GC I AGAGGCCA I AGCG I GGGGATI GIGCCTG I TATCGCTA	CLEAISVGIVPVIA
HP0879	1043 1GGC1CA	1043 GEGULAAAAACA CCAAGTGGTTTTAGAGGCTTTTAGAAGAAAATGGTTTGAAAATAGCGATGGGG	1044 AHKNIQVVLELLKALEENRLKNSDGES
	AGICICI	AGICICI I I AI CECTI GETGATCI TETATGAAGATAAGCCTTGCGAGAGCGTGGAGAGCGCGTATATGAAACTTTTA	LYRLVILYEDKPCESVESAYMKLLALSL
	111000	SCOULD IN THE STATE OF THE STAT	GKAPLRSLNLEGIFNQLSNAAWSGNKP
	400000 100000	ASCERTITADA ANTICO TAGA I GEOLI AGA I GA COMO TO TO TO TO TO TO TO TO TO TO TO TO TO	YELEWLRMNEVALKMRDHFPSIDFIDK
	CALIGAL	CALI SALLI CALAGALAGA I CCCACCO ALLI GALGCALI AALCCCI GAGTI I GALATAT CCGCTTATT GGATAGC	FPRYLMQLIPEFDNIRLLDSSKTRFGAY
	ICAAAAA	ICAAAAACGCGCCTTTGGGGCGTATTTAGGGACTGGAGGTTATACCCAAATGCCTGGGGCTAGTTATGTGAATTTTAA	LGTGGYTQMPGASYVNFNAGAMGVC
	CGCAGG		MNEGRISSSVVVGAGTDIGGGASVLG
)999 (99	GE GEGEGEGEGEGE EL LAGECCE I LI LAGET GEGEGEA TA ACCACCCATTA GCAT CEGEGA A A ATTETTEC	VLSGGNNNPISIGKNCLLGANSVTGISL
-	I AGGGG		GDGCIVDAGVAILAGSVIEIEENEFKKLL
	GAGCGI	GAGCOS ISA I ASAAA I GAAGAAAA I GAAGAAAA I GAAGAAAA I GAAGAAAAAAAA	EVNSALEKHANNLYKGKELSGKNGVH
	CCLLIAC	<u>CULLIACAAAGGAACILICCGGAAAAAAIGGCGTGCATTTCGTTCCAATAGT</u>	FRSNS

02/066501			PCT/EP01/15428
1046 ALKIAIYERLSNLVAPMKALRDAFAQKA KEFAHVIKMGRTQLQDAVFMTLGQEF ETYALMVDRDIEQVLDARNWVRELNL GGTAIGTGINSHPDYRSLIEKKIQEVTG RPFVMANNLIEATQSTGAYVQVSGVLK RIAVKLSKVCNDLRLLSSGFRAGLNEIN LPKMQPGSSIMPGKVNPVIPEVVNQVC FAVIGNDLSVALAAEGGQLQLNVFEPVI AYKLFHSFVILGRAIFTI TTKCVF	1048 FKNPKDALAKLDESFDLVITDINMPHM DGLEFLRLLEGKYESIVITGINATLINKAID SIRLGVKDFFQKPELLLESIYRTKK VLEFQKKHPLEKPLKKPHKISFLAASK ALESSKROALKVASTDANVMLLGESG VGKEVFAHFIHQHSQRSKHPFAINMS AIPEHLLESELFGYQKGAFTDATAPKM	GLFESANKGTIFLDE 1050 KRPIAFFKAALLNADHTMIAYLAKKNNO IVAIPFKEPFKRPVSLKHSOKSLELPN HCVVKIDTKKREISEILGALEDPLIDENL SLSLFDRVKDFSKDCLNLACHYAQLKA SDFKDRINYSHIPFTTIDPKD4KDFDDAI FYDQEKRVLFVAVADVSEFVPKHSSLD KEARVRGFSVYFPNSVYPMI_PLSLSQ GACSLKAFEKRLALVYEIPLCINLKNARL SQGVIEVRANCTYEEINHFLSIANQSSL DKDLQOSLLGFLEMALKLKKERLKKGF NFNSFENKLYLNKEGRIEKIETEKESDA HTLIEEAMLLANQSSARLLDEHFHNKGI YRTHKEPSLEQQKRLYDYEIVRF	
0			1054
1045 GTGCGTTAAAAATCGCTATTTATGAGCGCTTGAGCAATCTAGTCGCCCCCATGAAAGCCTTAAGGGGATGCTTTCGCT CAAAAGGCTAAGGAATTCGCTCATGTGATTAAAATGGGGCCCCCCGCCCTGCAAGAGCGCTGTGCCTTTGGC CAAAAGGCTAAGGAATTCGCTTGATGGTTGATAGGGGGCCCCCAGGTTTAGGACTTTAGG CCAAGAGTTTGAAACTTATGCCTTGATGGTTGATAGGGATATTGAGCGTAGGAATTGGAAAAAAAA	1047 GTTTTAAAAACCCTAAAGACGCTTTAGCGAAACTTGATGAAAGCTTTGATTTAGTCATCACGGATATTAACATGCCCC ATATGGACGCCTTAGCGAAACTTGATGAAGCCTTTGAATACGAATCCATTGTGATTAGCGGATATTAACATGCCCTTGA ATATGGACGCCTTGGATTTTAGGCGTGAAAGGCAAATACGAAAGCCTTTTAAACCGGAATTGCTTTTAGAATC CATCTATCGCACCAAAAAAGTTTTAGAATTTCAAAAAAACCCCTTTAGAAAAACCTTTTAAAAAAAA	1049 AAAACGCCCATAGCCTTTTTTAAAGCCGCTCTTTTAAATGCAGTCGATGATGAAAAAAAA	1051 AAGCTAAAGACCAAGCGCTTTATGATTTAGGAGCGTTGTATGCAAGGATCAAGGACTTTAAAAACGCCCAACCTTTAC AATCTGCAATATTTGCAGGACCATGCGGATAAAGCTTCTGTCGTTAGGGCGCGCGATGAAAAAGGCCTTTT AATCTGCAAGAATTTGCAAGAAAAATTGTTGAAAAACAAGAAAAATTGATGAAATTTCCCAAAAAAAA
	10	90	1053
HP0879	HP0879	HP0879	HP0879

c	٠
_	_
c	٧

wo

VGKTSLANS	1056 DTLNLNTTFSMKGNLSVNEPKTYAK WQEQQAFKRMQARKDNHGDFTLHDG PPYANGHLHLGHALNKILKDIVVKREYF KGKKIYYTPGWDCHGLPIEQQILERLE KEKTSLENPTLFREKCRDHAKKFLEIQ KNEFLQLGVLGDFEDPYKTMDFKFEAS IYRALVEVAKGLIKERH CONTAINANTEREN BBRADES		1060 I YMK I DSLNIJAREALEZANNILLAD TON DYLPPKAKVYSKNKNAGEAHEAIRPT SIILEPNALKDYLKPEELRLYTLIYKRFL ASÖMODALFESOSVVVACEKGEFKAS GRKLLFDGYYKILGNDDKDKLLPNIKE NOPIKLEKLESNAHVTEPPARYSEASII KVLESLGIGRPSTYAPTISLLÜNRDYIK VEKKÖISALESAFKVIEILEKHFEEIVDS KFSASLEELDNIAQNIKADYOQVLKDF YYPFMDKIEAGKKNIISOKVHEKTGÖS CPKCGGELVKKNSRYGEFIACNNYPK CKYVKÖTESANDEADÖELCEKCGGEM VÜKFSRNGAFLACNNYPECKNTKSL NÜRFSRNGAFLACNNYPECKNTKSL KGSFYGCNNYPKCNFLSNHKPINKRE EKCHYLMSERIYRKKKAHECIKCKEFÖ FLEEDNG	8
GCTTTTATGGGCCTCCTGGCGTGGGTAAAACAAGCTTAGCTAATTCCA	1055 AGACACCCTAAAACTTAAACACCACCTTTTCTATGAAGGGGAATTTGAGCGTTAATGAGGCTTAAAGCTTACGCCCAAAACTTACGCCCAAAAGCTTACGCCCAAAAGCGTTAAAACGCATTGCAAAGGCATTGCAAGGGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	1057 GCCAGATTGAAACCTTAAAAATTGGCTATCGCACCCCATGGCTTTTATTGAGTTTTTAAGAGCGCTTTTCCTTGCTTTTCCTTGCTTTTTAGAGAAACTTTTCCTTGCTCTTTAGAGAAAAGATAAGGCTCTTAAGGGCTTTTTAGAGAAAACTTTTCCTTGCTCTTTTAGAGAGATTAGAGAGTTAGGGGGTTTTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTAGAGAGTTTGCCCAAAACAGAAAAAAAA	1059 TCACITACATGAGGACCGATAGCTTGAATATCGCTAAAGAGCTTTAGAAGAGGGCGAGGAATAAGATTTTAAAAGACTAACGAAGAAGCAGCAAGAAGCCCAAAGAGCCAAAGAGCGAAAGAGCGCAAAGAGCCGAAAGAGCGAAAGAGCGCCAAGAAG	
	HP0879	HP0879	нР0879	

2/066501				PCT/EP0
1062 IILSSGIATHTELQDAISLCRRVNNFDITL LKCVSAYPSKIEDANLLSMVKLGEIFGV KFGLSDHTIGSLCPILATTI.GASMIEKH FILNKSLQTPDSAFSMDFNIGFKSMVEA IKQSVLALGEEEPRINPKTLEKRRFFAR SLFVIKDIQKGEALTENNIKALRPNLGL HPKFYKEILGQKASKFLKANTPLSADDI ERSL	1064 TFARLYEKNPIVONAGFYIGVLILKEFD KAOKIAELFPFDRRLLLDLYTAOKKFDO ASKQASLIYOEKKDPKFL(3LEAIYHYES LSANKKKLTKEEMLPIIOKI.EQATKERO	1066 KNAPYKLUN I PIEENCACYACKRTSKA YLHHLFRAKELTYARLASLHNLHFYLEL VKNARNAILEKRFLSFKKEFLEKYNSRS H	RKPREGEVOGLHVRVSKEEFKOGIEK RKPREGEVOGLHVRVSKEEFKOGIEK GRIVIFOIDVOGHEILKKHYPNACSVFIS TKNOEILKERLLLRGTDSKETIEKRLINA YKEMOCLESFDYLIINEDLEKSKEIILSIA KTLVHRLKAFNFEKICKAWKNETL	1070 III KNFS I PSSSKUIPKUSKALSIKEG ARLQSFDDNYKFCGSGSAKRLQIGNA VPPLLSVALAQAVFDFLKG
1061 CATTATCCTTTCTAGCGGTATCGCTACACACCGGAATTGCAAGACGCTATCTCATTGTGCAGAAGAGTGAATTATTGACATCACCTTTTAAAATGCGTGAGAGAGA	1063 CGACTTTTGCTCGTTTGTATGAAAAAACCCTATTGTTCAAAATGCTCAGTTTTACATAGGGGTATTAATCTTGTTAAA AGAGTTTTGATAAGGCCCAGAAAATCGCAGAATTATTCCCTTTTGACAGGCGTTTGTTGTTGTTAGACTTATACACCGCACA AAAAAAAATTCGATCAAGCTTCCAAACAAGCTTCTTTGATCTATCAAGAAAAAAAA	1065 CAAAAACGCGCCCTATAAATTGGATAATACCCCTATTGAAGAAATTGCGCATGTTATGCTTGCAAACGCTATTCTAA AGCCTATTTGCACCATTTATTTAGGGCTAAAGAACTCACTTACGTTGGTTTGGCCAGCTTGCACATTTTTAT AGCCTATTTGCACGCTGAAGAACGCCATTTTAGAAAAGGGTTTTTGGGTTTTTAAAAAAAGAATTTTGGGGAAA TAGAGCTGCTGCTCATTGAATGAATGGAATG	1067 CCCTAGCGGAAAAAAGCACCCTTACAAAGTATTTGCAAGAAAAATCCCAAAAACCCA I I I I I I I I CCU I I I I CCU I I CACACAGGGAAAAAAGAAAAACCAA I I I I I I I CCU I I I CACACAGGGAAAAAGAGAAGAAGAAGAAGAAGAAGAAGAA	1069 CCACCATTACAAGAATTITTCTACCCCAAGCGTTCTAGGTGTATCCATCCAGAGAGACTGTAGAGGGTTAAAGATTATAAATTCTACCATCCAT
HP0879	HP0879	HP0879	HP0879	HP0879

HP0879	1071	1071 CAGTCAGGTCGCATTTAGACATCGCCCTACGATTATTGAATTAGTCGCCCTAAAAGGCTTTCAATTCGTGA	1072/SOVGSHI DIAPTIIEI VAPKGEDEVSEG
:	<u> </u>	GTTTTGGGAAGCCTTTATTTCTAACAATACAACCCCCCCAAGCCACCCCCAATTACGCCGCTAGGCCTATGAAGCG ATCGCTACCAAAGATTATTTTTATAACCCAAGTTTGGGGTTAAGGTATTTGAACGAAAGCCCTAAAGAGCCCAAAGGAT	KPLFSNNTTNPPSHPNYALGYEAIATK DYFYNPSLGLRYLNESPKEPKDKOND
	τ∢⊢	ATCATGGGGCTAATCTTAAAGATTGACAAGTTTTTATTCCATTAAACGCATGATTTTGCTACATAATAGGAT TTTAATTATATAAAGGACAAATGGGCATGCCAAATAGGGCGTTGTTTTTTTT	KIEASKFYQQLESIKALSYYLLYHGANL KD
	<u>- F</u>	TAGAAAAAGATTTGAAACATAAAATCCCAAATAATAACCGCACAAAGGCATAAAGGCCCCAAACTAGCGTGGGTTTTAG TGGGGAAAGATCCCGCTAGTATCACTTATGTCAATATGAAGATCAAAGCATGCGAAAGGGTGGGCATGGATTTTGAC	
	<u> </u>	TAAAAACCCTCCAAGAAATATTACTGAAGCCAATTGCTATCCTTCGTTAAAGATTACAATACCGATCAAAACATTT	
	<u> </u>	ATGTGGATGGTTTCCACCCCTTAATATCGGTAAGCTCTGCACTCAAAAAGAATCGTTTCTGCCAGCCA	
	<u> </u>	GGCGTGATGCGGCTTTTAGAGCATTACCATATTGAAATCAAGGGTAAGGATGTGGCGATTATTGGAGCGAGAATAT CATTGGCAAACCTTTAAGCA	
HP0879	1073 G	TATCACC	1074 PNRNAIFITLLHSYAOKLGASNIALGVS
	∢ <	AGTTTCGCAAGCGGATTTTAGCGGCTATCCGGATTGTAAAGAAGATTTTATTAAAAGCATCGAGCATGCCTTAAATTT	QADFSGYPDCKEDFIKSIEHALNLGSN
	₹	AGGATOMACACGOGATTIAGAAATOCTAACGOCTTIAATGITITIGAATAAAGGOGOGAAGATTIGAAATGGOTAAAGA TTTGGGOGTCTTGGATTIAGTCATCAAAGAAACGCACACACGCTATCAAGGAAAGAATTITGGATTITGATAAAAAAAAAA	I AIKIL I PLMFLNKAGEFGMAKDLGVLD II VIKFTHTCYOGEBKII HAVAYGOODKO
	<u></u>	GTTATGGTTGCGATAAATGCCCGGCATGCCAATTGAGAAAAAAGGCTTTGAAGAGTTTCAAGCTAATAAAAATAAG	PACQLRKKGFEEFQANKK
	<u>o</u>	GTTTTTTAAAAAACCAACTAAAGAGCGGTAAAAAGCGTGTTTTAATGTTTTTAAAGTTATATGTATAGTTAAGATA	*
	₹`	AACGCTCACCACTCTTTATAATCCAATTTATCCCCATAATCATC	
	<u> </u>	ACCCCI AATTICAACACTAGAACCTCCAAGATAGATTICATCGCCATAGCGATCAATATCGTATTCATCATTATTCCAAC	
	<u>৩ ই</u>	GAACGCCAAATTTCCTAGTTCCAAGAATTGCGAACTGGGGGGCTCTTGACTAAAATACTAAAATACCAATGCATTGTTACTTGCAA	
	<u> </u>	TOURNEY OF THE TOUR OF THE TOU	
	<u> </u>	TGGGACGCTCGCTTATCGTTAGTCCAATTAATGAGCAAATCCGTATTGAAACCATAGGGTAAAAAAAA	
	C	CTACCAGGAACAACCACCAAGT	
HP0879	1075 T	1075 TTACCGGCGATAAAGACACCACGCTTTTTTAGTGAAAAAAAA	1076 TGDKDTTLFLVKKNIEWFESYLDKVDA
	A	SCGATCATTGTGCCTGAAGCCACATGCGCTAGCATGCTCATCAACGATTATTACAAGGTGTTTTTGGGCGAAAAA	IVPEATCASMLINDYYKVFLGEKDKDLY
	<u>ა</u>	GATAAGGATTIGTATGTGAAGCGCTTGGAAAAAATCACGCCTAAAATCTATCT	VKRLEKITPKIYLASVFLEKHTPLKSLLE
	<u> </u>	ACCCCTTTAAAAAGTCTTTTAGAAAAAATCCCTAAGGGAAAAAAGAGAGACTATCACCTATCAAATTAACCCTTGTCATGCC	KIPKGKKETITYHNPCHAKKTLNAHKEV
	(F	TGTTGCGGTTTTGGGGGGGATTACGATGCAAAAAAGGCGGGATTTTCTTTAAAAGTGGGGCTTCTTAGGGCTAA	CARAGESI KVGLI RAKEIIDTKAAII SAEC
	<u>₹</u>	AGAAATCATAGACACCAAAGCTGCAATTTTGAGCGCTGAATGCGGGGCATGCCATATGCAATTAAACAACGCTTTAA	GACHMOLINIALKSLDDPNTPPFLHPL
	Ž.	AGTCTTTAGACGACCCTAACACTCCGCCATTTTTGCACCCTTTAGAACTCATCGCTAAAAGCCTTAAAAAGCGCTGAAT	ELIAKALKSAE
	₹;	AAAAAGCCTTTTTAACCCCCATCTCCCAACATCTTTTATAATACAGAGCTTTA	And the state of t
HP0879	1077 G	1077 GCCAAATCCCCCTAAAAGACTTGAATGCCTTATTAGAAAAATGAAACCCACGCGCCTTGAATTGCTCTTTAACATTCA	1078 OIPLKDLNALLEKMKPTRLNCSLTFNAL
	<u>₹</u> [ACCCICIAGAIGAAAAACCIIAAACGACAACIIAAAAAAAA	DEKTLNDNLKCDLTNAENILAYTFFQE
	70		GLMEAGENCSLKNIFK I LSSKUAKAIEE
	2.2	TANGOOD TOO TOO TOO TOO TOO TOO TOO TOO TOO	LUUNEN SAFALGVSUUAHIENIKEEAF IVHÜNIKESI ÕEESDVESI DSÕTDSVSVE
	<u> </u>	CAAACCCCTAGCGTCTTTATGAAAGCGCGTTAGCTTCTTTAGAAAACTATTTTATGGCTTTGTTCAAT	SALASI FIVEMALEO
			ション・コート コート・コート・コート・コート・コート・コート・コート・コート・コート・コート・

2/066501		PC
1080 YDTTKQQNALKIENIPTI:¢ERLKTILVVD EIVDSGNSLEAVLKVLEIEKHPDKKFYS ASLFQKTSAKYKADAFLKDAPEWIDFF WEVDLKNLKSH		1084
1079 TTATGACACCACCAAGCAAAAACGCCCTAAAAATTGAAAATATCCCCACGATCAAAGGGCGTCTAAAAACCATTTT GGTGGTAGAAATCGTAGATAGCGGTAATTCTTTAGAAGCGGTGCTTAAAGTGTTAGAAGAAAACACCCCGATA AAAAATTTTATAGCGCGAGTTTGTTCCAAAAAACAAGCGCGAAATACAAAGCCGTTTATAAAAGAAAAACCCGTG AATGGATTGATTCTTTGGGAAGTGGATTTGAAAAACTTAAAAAGCCATTAACATGCAAGTTAAAGAAAACCAACC	1081 TTGGCCCTTTTACGAGCGGGGCTAAGGATT GCATCAAGGATAAAAAGGCATGCATTTTTT AAGAGTATTTAAAAATCGCTAAAGAATGTTTTT AATGGAGCGCCTTTCTAATAACTTGCGTTT CGCCCCTTTCACTTGCATGGATTTAGCCAA GGTGTTAGTGAAAATGTTCATGCGTGGGG TGACOTGATGAAAAGGCCAA ATGAACCTCCTAAAAAAGGCGATCTAAAAAGGTTAA AAACCTCTAAATGAAGACAAGCTCGCT AAAACCTCTAATGAAAAGGCAAAGCGTTAAAAAGGAAAAGGCAATCTTAGAAAGGAAAAGGAAATGAAGAAAGGAAATTTAGAAGGAAAAGGAAATTTAGAAGGAAAAGGAAATTTAAAAAGGAAAATTTTAAAAAA	1083 AAGAGCCTAAGCAAGATGGAACGGCAGTCGTCGTCATAAAGATGGGGTCCATTTAGAATGGGTGGCCTTGG GTATAAAGTGCCTGCTTTCAAGCCTAAAGATCAAGTCGACTTAGACGCACTAAGTGGGTGCCTTGG GTATAAAGTGCCTGCTTTCAAGCATAAGACATAAAAAAAA
HP0879	HP0879	HP0879

Š	3
_	
_	

2/066501			101/12	P01/15428
1086 EINKDLRGCDYATDVLSFPLEAIPHTPL GSVVINAPLAQTNALKLGHSLENEIALL FIHGVLHLLGYDHEKDKGEQRQKESEL IKAFNLPLSLIERTQD	1088 TLPIGAISPQDEKLLACSKESLMHAINSI RVGMHFKELSQILESTITERGFVPLKGF CGHGIGKKPHEEPEIPNYLEKGVKPNS GPKIKEGMVFCLEPMVCQKQGEPKIL	1090 PPKĞĞRKHPEGNFIQIDTSDILFICAĞA FDGLAEIIKKRTTĞNVLGFTQEKMSKK EQEAILHLVQTHOLVTYGLIPELIGRLPV LSTLDSISLEAMVÖILĞKPKNALIKÖYQ QLFKMDEVDLIFEEEAIKEIAQLALERKT GARGLRAIIEDFCLDIMFDLPKLKĞSEV RITKDCVLKQAEPLIIAKTHSKILP	1092 IKIQGFVTREMENAMQEGLKLENATKG AHQKTPIKSMEFAPFIGYEIIKNHAKYS KLRVIINEGKNRELRRFFAFFNAGVLDL RRVRYGFVNLNALPVGKMRFLNRQEY NELHAFMANAANVKGD	1094 LEEILÄLKPSLLSFSADKFFNSADAGIIM GOKERVEALKNHPLYRVLRVGKITLTLL FCSLKAWINHÖEDITIHALLNÖTKDALL OKALKLYALLKPLELNVSIASSFSKIGNL FGRELESFCVKIÖPKNTRALNSEKLYL KLFÖKGVIARISCEFVCFEVFSLNEKDF EKIALVLEEILNKA
1085 AGAATCAACAAGGATTTAAGGGGTTGCGATTACGCTACCGATGTTTTGAGCTTCCCTTTAGAAGCCATTCCTCACACACA	1087 CACGCTTCCTATAGGTGCGATAAGCCCGCAAGATGAAAAATTGCTCGCTTGCTGAAGAGAGGTTGATGCCTGCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCATTTAAAAGAGTTTTAAGAGAGCTGTATTAGAAAAGCGCGTTTTGAAAGGGGGCTTTGAAAAAAAA	1089 CCCCCCAAAGGCGCAGAAAGCACCCTGAGGGCAATTTCATTCA	1091 CATTAAAATTCAAGGCTTTGTTACAAGAGATGGAAAACGCGATGCAAGAGGGCTTGAAATTAGAAAAACGTACTA AGGGAGCGCACCAAAAAACTTAAAAAGCATGGAAATTGCCCCTTTATTGGTTATGAAATCATCAAAAACCATG CCAAATACTCCAAACTGAGAGTCATTATCAATGAGGGAAAAACAGAGAATTGAGGCGTTTTTTTGCAATGCATG CCAAATACTCCAAACTGAGAGTCATTATCAATGAGGGAAAAACAGAGAATTGAGGCGTTTTTTTT	1093 CTTTGGAAGAAATITTAGCCCTAAAACCATCGCTTTTAGCGCGGGATAAATTCTTTAACAGTGCCGGCAGGCGGGGGGGG
	HP0879	HP0879	HP0879	HP0879

	000 000 000 000 000 000 000 000 000 00	1095 CTCGTTTATTAATACCTTGTTAGGGAAAAATCTCGCTAAAAGGCCAACCTTTAATGTGAAAAACCGTTTAGCGAATTT TTTTCCACCACTTGGGAAGATAAAGAAAACCCTTAAGGGCAACCTTTAATGTGATTGAT	1096 SFINTLLGKNIAKSSATPGKTRLANFFS TTWEDKENALRATFNVIDLFGFGYAKV SKSLKKEWEGFLWELLSVRVSIKLFIHL VDARHLDLEIDKNAKENIGALLRPDGA YLSLFTKFDKLNKNEGHRLFLNAPKFF LINTAHFNALSSKYPTLEIVFGTLLKHLL TNPL
HP1238	7601	1097 GGGAAGTATCGGTAGTATGGGCAAACCTATTGAAGGGTTTTTAGTGGCAGCCATTCAGTTCCTGTGCCAATTGTCA ATAGCCGTAAGGATATTCATCACAATATTGAAAGCGTTATTAGAACCTTGCATGCGACTAAAGCGGGTATCCGGGA ATAGCCGTAAGGATATTCCCTGAGTATTGAAGGCGTATTGAATACCGCTAAGTGCGTTAGCGAAGGTTTTTATTA GTGGAGCTTATCATTTTCCCTGAGTATAGCAGCGCAAGGTTAAAGAGGCGAAAGTTTATGGTGTTTTTTTT	1098 GSIGSMGKPIEGFLVAAIQFPVPIVNSR KDIDHNIESIIRTLHATKAGYPGVELIIFP EYSTQGLNTAKWLSEEFLLIDVPGKETE LYAKACKEAKYYGVFSIMERNPDSNKN PYNTAIIDPQGEIILKYRKLFPWNPIEP WYPGDLGMPVCEGPGGSKLAVCICHD GMIPELAREAAYKGCNVYIEISGYSTQ VNDQWILTNRSNAWHNLMYTVSVNLA GYDNVFYYFGEGQICNFDGTLLVQGH RNPWEIVTGEIYPKMADNAIŁSWGLE NNIYNLGHRGYVAKPGGEHDAGLTYIK DLAAGKYKLPWEDHMKIKDGSIYGYPT TGGRFGK
HP1238	1080	1099 TGAAGCTCAAAAAGAAACCCCCCAATCAAACGCCTAAAGAATTGTGAAGTCAATTCTTATGTGGGCCTTTTGAAGAAAATTGTAAAAAAATTGTAAAGAAATTGTAAAGAAATTGTAAGAATTGTAAGAAAATTGTAAAAAA	1100 EAUKE I POSNOJ I PREMKVKSISYVGES YMSDMLANEIVKIRVGDIVDSKKIDTAV LALFNOGVEKOYGTEKEKDGLEFHFDE KARIAGVEKOYGTEKEKDGLEFHFDE KKGDTFDEOKLEHAKTALKTALEGOG YYGSVVEVRTEKVSEGALL VFDVNRG DSIYIKQSIYEGSAKLKRRMIESLSANK QRDFMGWMWGLNDGKLR.DQLEYDS MRIQDVYMRRGYLDAHISSIPLKTDFS THDAKLHYKVKEGIQYRISDILIEIDNPV VPLKTLEKALKVKRKDVFNIEHLRADA QILKTEIADKGYAFAVVKPD.DKDEKN GLVKVIYRIEVGDWAYINDV.ISQURT SDRIIRRELLLGPKDKYNLTKLRNSENS LRRLGFFSKVKIEEKRNNSSLMOLLVS VEGRTGQLQFGLGYGSYSGLMLNG SVSERNLFGTGQSMSLYANIATGGGR SYPGMPKGAGRMFAGNLSLTNPRIFD SWYSSTINLYADYRISYQYIQQGGFG

2/066501		PCT/EP01/15428
- /O - III	RRAQKGEAKPKOEVTPTKETPKAPK TETKAKAKADTEENKAPSIGVEGTVRV DVRRLDHLMNLIGELVLGKNRLIRIYSD VEERYDGEKFLEELNQV/SSISAVTTD LQLAVMKTRMQPVGKVFNKFPRMVRD LSRELGKSIELIIEGEETEI.DKSIVEEIGD PLIHIIRNSCDHGIEPLEERRKLNKPETG KVQLSAYNEGNHIVIKISDDGKGLDPV MLKEKAIEKGVISERDAEGMSDREAFN LIFKPGFSTAKVVSNVSGRGVGMDVVK TNIEKLNGIIEIDSEVGVGTTQKL	QAKALDAMLNYMAYTKDEIKSMILEUL QAKALDAMLNYMAYTKDEIKSMILEUL EEELEAQKSALIRRYEKEAKEEGKKKS YAILAEATARFAGNYAAENLTTRIALPC SDYIGKUGKDGKNIEAFIKVSGVDIEF SEDSSELCLSSFNLYRRE:VSETLKILI EDGRIQPNRIEEVYHRVARNLEKELLS EGESVVLELELGAMEDE'-KILIGKMRY RSSFGQNALQHSKEVALLAGLIAEQLG GDKKLARRAGILHDIGKALTQELGRDH VNLGVEVCKRHKEDPVV:INAIYAHHGH EEILSVECASVCAADALSAGRPGARRK SDEEYAKRMQALEEIALI:FDGVEKAYA MESGRELRVIVKSNQVRDNQVPIIARKI
FGGTTTCAGATGTGAAAGCAGGGAATTTTGCGGTGCGCATCACGGCT 3AGGGACGCCTAAATGGGATCATGGATTATTGCAAGAAAGCGTAG 5AGGGACGCCTAAATGGGATCATGGATTATTTGCAAGAAAGCGTAG TTAGGGCAAGAAATCCAAAAAAGCTTCAAATTTTGCC AAAGGCCAAGAAATTTAGAAAAAGCTTCAAATTTTGCC AAAGGGCAAGAAATTTAGAAAAAGCTTCAAACTTTTGCC AAAGGGCAAGAATTTAGAAAAAGCTTCAAAGTGAATTTTGCC AAAGGGCAACACTTCCATTCAAGGCGTGAGCAACTTTTAGCCTT TTGTAGAAATCATTAGAGATATTGCTGATCAACCAATCTTTTAGCCTT TTGTAGAAATCAAGCCTTTGCGGTGGTGGCTGATGAGGAAAAAAGCCTT TTTAGAAATCAAGCCAATATCAATATTTTAGTGCAAAGCATTTCAGACA GCGAGATTGAAGCCCAATATCAATATTTTAGTGCAAAGCATTTTAGAA ATTAGAAATCAGTCAATGATTTTAAAAAGGCTTACT TTTAGAAATCAGTCAATATTTAAGCGCTAATTTTAAAAAAGGCTAA TTTAGAAATCAGTCAATATCAATATTTTAAAAAAGGCTAA TTTAGAAATCAGTCAATATTTAAAAAAGGCTAAA TTTAGAAATCAGTCAATATCAACCCCTAATATTTTAAAAAAGGCTAA TTTAGAAATCAGCCCAATATCCACCCTTATAGCGAATATTTTACAAA GGTTTTTTTATAAACCCCAATATCCACCCTTATAGCGAATACTTGTTGCG	TGAAGAAGTGGAAGCAGAGATTGAACGGCTGCTGAACAAACGCCAAAGAGCAAAGAAGCCCCAAAGGCCAAAGAGCCCCAAAGAGCCCCAAAGAGCCCCAAAGAGCCCCAAAGAGCCCCCAAAGAGCCCCAAAGAGCCCCCAAAGAGCCCCCAAAGAGCCCCCAAAGAGCCCCCAAAGCCCCCAAAGCCCCCTTTGGGGAAGATTGATGGGAAATTGATGGGAAAATTAAACCAGGTGGTTAAACCAGGTGGTTCAATAACCAGCTTGAATTGATGGGAAAAAGCTTTTAAACCCAGGTGGTAAGGTGTTCAATAAAAAAGCATTAGAGCAATTGAACGTTGAATTGATGGGGAAGAAACCATTGAAATTGATGAGCGGTAAATTGAGGGGTAAATTGAGGGGTAAATTGAGGGGTAAATTGAGGGGTAAATTGAGGGGTAAATTGAAAAAA	1111 AAAGACTTGAAAAAGACGCCAAAI II I AGAACTACATTACTATACTAAAAGAATTAAAAGCATGATTTTAGAG TCTCAAGCCAAAGACGCCAAAAAAGCGCCTTATCGAGGGTAATTATGAAAAGAAGAGGGCAA TCTCAAGCCAAAGAATTTAGCGGAAGCGCCTTATCGGGGTAATTATGCGGCAGAAATTAACAACTC CAATTAGAAGAATTTAGCGGAAGCGCCGTTTTGCGGGGAAAAATATTAGCGGAGAAATTAACAACGTTTAAAAAGG GAAAAATCGTATGCCTTGCTCAGATTATAGCGGAAGCGGCGAAATTGTTGTCCAGTTTCAATCTTTATCGGCGTGAA TCAGCGGGGTGGATATAGAATTTAATAGAAGAAGGAGCGCGTATCCAGCTTAGAGTTTGAACGGTTTAACAGGATTAAAAAGGAATTTAATAGAAGAAATGGTATCGGCGGCGCGCAACATGAAATTTTAATAGAAAAAGAATTTCAAAGAAGAAATGCGTTATCGCTCGAGTTTTGGCCTTAAAGAAGAATTTTAATAGAAAAATTTAATAGAAAAATTTAATAGAAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAATTGGAAGAGCTTAAAGAAGGAAAAGGAATTTAAAAAGAAATTTAATAGAAAAATTTAATAGAGCAAAAAGGAATTTAGAAGAAATTTAATAGAAAAATTTAATAGAAAAAA
HP1444	HP1444	HP1444

1119 CGGTGATGGAATTAAACGCAGAAGATAAGGGTAATAGGGAATTTATTT	1121 CGCAAGCGATGCTGAAGCGCTAGAAGCTTTCAAGTTGTTGTGCCAAAAAGAAGGAGGCATTATCCCAGCGCTAGAAGCGCTAGAAGCGCTAGAAGCGCTAGAAGCGCTAGAAGCGCTAGAAGCGCTTAAAAGCTCGTAGAAATTTAAAGCGGGTATCAAAAAATTTAAGCGTATTAAAGCGTTTGAAAAAAAA	1123 CTACACCCCAAGCAGCCTTCATGTCGGTGTTTGGACTCTAAAGACATTACCGCAAAAAGCAGTGTCAAAGGCTTAC TCACTAAGCCTTAAAGCAACAGCAGGAAACAATAACGGCGCATCACCAGCCCCCACAAGGGGGGCTAA TCACTAAGCTTAATGATTTCAAGCGCAATAAATACAATATTGAAGGGAAAGTGGCTGCGATTGATGTGA AAAACTCTATCGCATTGATTTCAAGCGCAATAAAAAACTGGGAAAGTGGCTGCGATTGATT
AATTGATGAAGAGATAAAAGAAG TAGCGACATTACCATAGAAAGGG GATTTAAAGTTATACCTTACA GATTTAACGCCTTTGACAAATG AACAAAGACAAACTCTACAAATG AACAAAAGCAAACTCTACAAATG AAAAGCAAAACTCTACAAATG AAAAGCAAAACGAAATGATTTAAAGCGTTTAAGTTATATT TTTAAAGACCATTTTGAGTATAAT CCGCTATTTGATAGCGTTTAAA 3AGCTTATTTTATAGCCCAC CCCGATTTTGAAAGATTCGCCTT TTTGGTGGTGGTTTTGTTTT	CATTATCCCAGCGCTAGAAAGC ITCATCGTAGTGAATTTAAGCGG IGAGGTATCAAAACATTTGAA STAATTATGAATTGAGTTTTGAA TTGATCCTGTGGCGGATGGCA ITTCCAGCTTTAAAAAAGATTA ATAGAAAAGAATTAGTCATCAA AGTAAAGATTTAGACAAGTCG GGGCCGTATTTAGAGAATGAT AGTAAAGATTTAGAAAAAGAA ITTGGCCGTTTTAGAGAAAGAA ITTGGCCATTTCCAAAAAAGAA ITTGGCCATTTCCAAAAAAGAA	
1120 VMELNAEDKGNREFILVGIDEEIKEDES AYDFCKKELKSAKPVISDITIERVKRAA GKISQLSKDSGLDLGFKVYTLQDKVQII NDKEEITLFNRSDLTPFDKALNLALQC GKTLNQALEIIIKDKLYKCE JAYFCIVCD EEAQEYLAKSKNEMIFLDGYEEIDLEAF LINLNASFKERLSVVY	1122 ASDAEALEAFKI.COKEGIIPALESSHA LAYALKI.AOKCEEESIIVVNSGRGDKD LSTVYNALKGGLK	1124 YTPSRRFMSVLDSKDITAKSSVKGLLT KLKATAGRNINNGRITSRHKIERGAKKLY RIIDFKRNKYNIEGKVAAIEYJPYRNARI ALVYYPDGDKRYILQPSGLKVGDSVIA AEGGLDIKVGFAMKLKNIPIGITVVHNIE MHPGAGGQLARSAGMSAQIMGRENK YTIIRMPSSEMRYILSECMASVGVVGN EDFINVSIGKAGRNRHRGIRPQTRGSA MNPVDHPHGGGEGKTGTSJHPVSPW GTPAKGYKTRKKASDKI IISBKKHK

c	•
c	
Ċ	u

1				
PC			CATTGACAGCCTAAAATACGCCGATAAAATGCCCGATTCTGCGAACATGATCATTITATTTTCACCTATGATATTTA TTCGCTCTCAATTACACCTTGCCCATTTCCTTGCGCGATGGTTTTATTTTATATCGCATTCATT	
			GGAATGGAGGGCATAATGCTTAAAATCCATTGATTGTTGTTCTAATTCTTATATCGCTTGAGGGTGGGGATTT CTAAAGGAATAGGCGTAATTGAGCATGTGCTTTCAAAAATCCACAAAAACGAAGAGCCTTTAAAAAAACGCTGCGTTTG AACATGCCAAAAACGCCTTAAAATTTTTTAAGAATTTTTAACGCTATGCAAAATCGTTTCACAAAAAAAA	
			TATAAGGATTTTATAAAAATCCAAGAATTTATGCGTTTATTAAGGGGGGTTTTTATGCGTTTTTATGCGTTTTTTATGCGTTTTTTAAAAATTTTATGCGTTTTTTAAAAATTGTCCAAGAGCGTTTAAAAAATTGTCCATGAGAATTTAACCTTTGGGGGGGG	
	1130 DFRL	113	1129 GATTTCAGGTTATGACGCTTTAGGCAACCCTACTTTGCGTTACGCTCACACCAGACACAACACACGCTGGTT TTGATATTTTAGACACAACACA	(HP1074
			GCGAGCTTGATGTATTCCTTGCTTTGATTTGAATAAAAAGACCGCTCTTTTAGGCACAAGAGGGTTTTTATCAAC	
			AAGAAAAICUIIIIIGICAAAACGCCTTTAAATGAAAAATACTCTCACTTAATTGCAGAAAAAAACCTGGCTATTTTAGA TTTCAACGAGGTTAAAAACTACTTTGATTTTAAGATTAAAATTGTAGGGGATTACAGGGCACTAATGGCAAAACGAAAACCAA	
			CTTAAAAAAACCCTGACTTATCAAAACCACACCTATTTTTGAGCGATAAACGCTTTAGAAAACTTTAGAAAACCCTA	
			GATTITATGAATTITTGAAAGAATTGAACATTATGGCTATTACGAATTAGCAATTTAGCATTAGCATTAGCAATTAGCAATTGAAAACATGCATG	
			TGGCTGAAAAGATTGATGTGCAAATTTCTCAAAAAGCGAAGAATTGAATGGCATTTTGTATGCGGATTTCAAACGCT	
			IATTAAGGGACATCGCTAAGGATTTCCCTAAAGAAGCCCCATAGCTTTTATGAATTGTATCAAAAGGTTGATCGCTATGC	
	28	1128	1127 TAGGCATGCAAAAGTTTGATTATGAATTTAAAAAGCGCGCGTTGATTAAAGAGCGTTTTAGCGTTCAAACAAGCGTCAAAAAGCGTTACGCCTTACGCCTTACGCCTTTTTTCTGAAAAAAAA	HP1074
			ACAAGAGGTGCTAAGAAAGAATGAATAGCTTTTGATCAAGAATTTTAAGACTAATTGTAATATACACAAA CATAAAAAAGTAATAATCTAGGGCAAGCGCTTTTGAGATCATTTAAAGCTTAGGCCTAGATTAT	
	LDLIINSCKIKDKKHSFARSY		ACAATAGGAAGAAGAAAGCAGGTTTTAGAATCTTAGATCTTAGATCATCATCATAAAAATTAAAAATTAAGAAGGAGTAAAAAATTAAAGAAG	
	GVRENNGLSFDELKOLLGLLLESFKDR KAVFVTFYNPTVSIKHNNEFEKOVI EI		GTTTGCTTTTAGAAAGTTTTAAAGACCGATTAAAAGCGGTTGAGGTAACCGAATACAACCCCACGGTGAGTATAAAAC	
_	KTKESLKAVDIIYLSLDLDIMDGKLFTST		TGCAAGAAGCTTTTCACTTTTAAAAGCGGTGGATATTATTTAT	
	CSLGLEKGGLEIDPKCLVYFGVRSTEQ		CACCGAACAGAGGAAAGAGATGTGATTAGGGAATTGCAAATTCCTTAATTAA	
.,	IZO IGIL TLDAHADIM AYDSDSKHIHGMPL GMVLNRVRSGFNRMSFSFFKAWOK!		ATGCCTTTAGGCATGGTTTTAAATCGTGTCCGTAGTGGGTTTAATCGCATGAGCGAGAGCGAAAAGGCATGGCA	
٠.			1125/AAATAGGGATTTTGTATTTAGACGCGCATGCGGATATTCACACGCCTTATCACACACA	IHP1074

r	ኅ
r	V
r	V

-		- INCOME.	1132	1132 GL KKVFKDSKKDACGFIVEISIFFMKAYT
HP0515	1131	AGGGATTAAAAAAGGTGTCAAAAAAAAAAAAAAAAAAAA		ALLKKODRYVYLLRYLPSRYWASILTTA
		ATTITAACGACTECCETTATGICAAATACCCTGATTTTGACGCTTTGAAAAAGCTTTTGGTGTGTTATTATTACCAAA		LYVKYPDFDALKKLLVSYYYCTWIAGG
		CTTGGATTGCAGGAGGCACGATCACGCGCATCAAGCAAACCAGTATCAAAAACGTTAAAAAGCAATAAAAAGCAATAAAAAAAA		TITRIKOTSINIIKNVKSNKSVETIKELILN
		AGCGTTGAAACCATCAAAGAGCTTATATTGAATAGCATCGACTCTATAAACACCTTTGATCAATACCTCTATAAACTTAT		SIDSYNTFOQYLYNLWDSSSVYHSKW
		GGGATAGCTCTTCTGTTTATCATAGCAAATGGGTGCGTCCTGTCTTAGCCCTAGCTAATTATTTCATGGCAGATGAAG		VRPVLALANYFMADEEKPHFIAMDAET
		AGAAACCCCATTTTATCGCTATGGATGCCGAAACCCAAGTGGAGCATATTTTGCCACAAACGCCCAAAAGGGCGCAGT		QVEHILPQTPKKGSQWNADFDKEKKE
		CAATGGAACGCGGATTTGACAAAAAAAAAAAGAGAAGAATGGGTAAATAATATCGCGAATTTAACCTTTTAAAGCGT		EWWNNIANLTLLKRKKNAHALNGDFDE
		JAAAAGAACGCGCATGCTTTAAACGGGGATTTTGATGAAAAAAGAAAAATTTATGGGGGGCAAAGACACGAGCAAAGT		KRKIYGGKDTSKVISCYDITKELYSNYR
		GATTAGCTGTTATGACATCACTAAAGAATTGTATAGCAATTATAGGAAGTGGAATGAGAAGTCCCTCCAAGAGGGGTAT		KWNEKSLOERYKSLYNIIIPVLHIEGO
		CAAATCTTTGTATAACACTATCACGCCTGTTTTACACATAGAGGGGCAAGAAGATGATTTTGAAGATGATTTTGATCTA		EDDFEDOFOLE
		GAATGATTAAAGATTGCCAAGCATCAAAACAACAAGA		
UD0515	1133	1133 GCCCCATGTGGAATTCAAACCTGCCTAAACCCAATGCGATTTATGTGTATGGAGTCGCTAATGCAAACATCACTTTT	1134	1134 PMWNSNLPKPNAIYVYGVANANITFFK
CICOLLI		<u> TTAPAGGCTCAGATATTTTGAGTTATGAAACCAGAGAGGGTCTTGCTCAAGTATTTTGATATTTTAGATAAAGGTGAAAG</u>		GSDILSYETREVLLKYFDILDKDERSLK
	_	AAGTTTGAAAAACGCCTTAAAGGATTTAGAAAACCCTTTGGGTTTGCCCCCTACATCAGAAAAGCTTATGAGCATAA		NALKDLENPFGFAPYIRKAYEHKRNFL
	_	A A GGA ATTITICT A GCA CACCA CAGA TTG A A A GCAT CCA A CCACCA CTTTT A A GGA A TGTCTT GGA A	-	TTRLKASFRPTTF
	_	TTTTGAAAACGCTCATTAGCGTATTTATTGCCCATTTATCTTTCTT		
	_	AAGAAATTGATGATGAGTCTCATAGAAAAAGCCCCTTACATGCCCTCCCCTTTTTCAATTCAATTGACTTCGCTCC		
	-	AAACTTTTCTTTTCCACGCATAAGCCAAGAACGACAGCACCGCAAAGAAAATCATGATTTTTATCCCTAAGGTATTCC		
	-	TTTCATGTTTTTTCCTATCGCCTGCTTTTTCCAAATATGCGATGACTTGTTTTGAGCTTGTTGTCAGCTCAATCCCACTCT		
	_	GGGCATAGCCGTGCCAGGCAAAAGCTTTTGCGGATCGTTGATGAAAATATTCAAACCATGTTCGCCT		
1100615	1135	1135 Transacratia secondica de la compana de la compana de la compana de la compana de la compana de la compana	1136	1136 DISVEKIVKENPEIIFIWWISPLIPEDVLN
C1 C0 JH	2	AGATGTT AAACAACCCCCAAATTT GCTACCATCAAAGCCATTAAAAACAAGCAGGTTTATAAACTCCCCACAATGGA		NPKFATIKAIKNKQVYKLPTMIJIGGPKA
	•	TATTGGCGGGCCTAGAGCCCCACTCATAAGTCTTTTTATCGCTCTAAAAGCCCACCCTGAAGCCTTTAAGGGGCGTGG		PLISI, FIALKAHPEAFKGVUIN/IMVKUY
		ATATTAATGCGATGGTTAAAGACTACTATAAAGTGGTTTTTGATTTGAATGATGCAGAGGTTGAGCCTTTTTATGGCA		YKVVFULNDAEVEPFLWM
		TTAATTTTTAAAAAAGGGGTTGATGTTTTTAGCCTTTCGTGTATCGCGCTAGGXTTAGAACAAGCCCTATAGCGATACA		
		ATTCGCTAGAAGCGAACTCCCTCCCATAGCTCAAAACGGCACCGCTAGACCTTTAACCGGAAGAATCCCGCCCACC		
		CCAAAGGCGTTGATCACCAAAGAAAACTAATAAGCAGCACCACGCCCACGCAAAATAGCGAATATTTGGCTTTTT		
		CAAGCGGTTAGCGATCCTAAAAATCAAAACAATCAAAACAGGAAAAAAAA		
		CCATTCTTCGGCGATCCCAGCTAAGACCATGTCCGTATGCACTTCGCTCAAAAACCCAAGCTTGATTTGCTCAAAAACCC		
		CAAGCCCTTGCCCAAACAACCCCCCCATTATGCATGCCATTGCCTGCATGAAAGACCTGATAGGATTCGGGATGCAAGTC		
		GCTTATTCTAAGAGCGTTCGCTAATCTATCCGGCAAGAGCGTGAAAAGCGAATTTGCAAATTAGAACACACAC		
		CAGGCGCAAAATCCTATGCTGCTTGTAACAATCGCTAAAACGCTGATCGCAAACGCCCCTGAAATAATAATAATAAAAAAAA		
		ACAAATGCACGCTCCCCCAGAAAAAACCAACAACAACGCTAAAACCGCCCCCAAAAGAAAG		
		TTTTGCAAAACCCCCACC		

HP1444	1137 AAAAGAGCTAAAACAGAAGCCAAAGCACACACAAGAAAATAAAACTAAAGAAATAAAAGCCCAAAGAAAG	1138 KRAKTEAKAEATGENKTKENNKAKES KIKESKIKEAKAKEPIPVKKLSFNEALEE LFANSLSDCVSYESIIOISAKVPTLAQIK KIKELCOKYOKKLVSSSEYAKKLNAIDK IKKTEEKQKVLDEELEDGYDFLKEKDFL EWSRSDSPVRMYLREMGDIKLLSKDE EIELSKQIRLGEDIICDAICSVPYLIDFIYA YKDALINRERRYKELFRSFDDDDENSV SDSKKDEDNEEDEENEERKKVVSEKD KKYEKVQESFKALDKAKKEWLKALEA PIDEREDELVRSLTLAYKRQTLKDRLY DLEPTSKLINELVKTMETTLKSGDGFEK ELKRLEYKLPLFNDTLIANHKKILANITN
HP1444	1139 ATTAAAGGCTCTAGCTCGTTTTTGAATCTTAACATTCTCACGCACCTCACGCACCACGACATGGAAGATGTCTTGAATCGC GCCAGAAAGGCCCTTGAATTTTTTTTTT	1140 KGSSSFLNLNILTHLTHINMEDVLNRAR KGEIKITPOIMDVVLRSIDLMKTLLVTIR DTGSDTNNGKENEIEEAVKOLQAITSO NLESAKERTTEAPQKENKEETKEEAKE ENKENKAKAPTAENTSSONPLADEPDL DYANMSAEEVEAEIERLLNKROEADKE RRAQKKQEAKPKQEVTPTKETPKAPK TETKAKAKADTEENKAPSIGVEGTVRV DVRRLDHLMNLIGELVLGKNRLIRIYSD VEERYDGEKFLEELNOVVSSISAVTTD LOLAVMKTRMQPVGKVFNKFPRMVRD LSRELGKSIELIIEGEETELDKSIVEEIGD PLIHIIRNSCDHGIEPLEERRKLNKPETG KVOLSAYNEGNHIVIKISDDGKGLDPV MLKEKAIEKGVISERDAEGMSDREAFN
HP1444	1141 AGAAATGATTGAGCTTGGCTAAAAGCATGCAGGCATGAGATCACTTTAACGATTGAGGGTTTGAAGTTTAGGAGATTGAAATTGAGGGTTTGAGGGTTTGCACAATTGGAATTGGCATCCGCATCCGGTTTGCACAATTGGAAATTGGCATCCGCATCCGTTTGCACAATTGGAAATTGGCAGCGCATCCGGTTTTTTTT	1142 EMIELGFIAKSMÖHEITLTIEGLNELKTII AVAKÖNEFLACPKIGIRIRLHSTGTGVV AKSGGINSKFGLSSTEVLEAMRLLEEN DLLEHFHMIHFHIGSGISDISPLKKALRE AGNI YAELRKMGAKNLNSVNIGGGLA VEYTOHKHHÖDKNYTLEEFSADVVFLL REIVKNKQEIEPDIFIESGRYISANHAVL VAPVLELFSHEYNEKSLKIKENNNPPLI DEMLDLLANINEKNAIEYLHÖSFDHTES LFTLFDLGYIDLIDRSNTEVLAHLIVKKA VQLLYVKDHNDILRIQEQVQERYLLNC SFFQSLPDYWGLRQNFP

† † † † † † † † † † † † † † † † † † †	1143 ISCTAAAGECGGCTAAAATGCGCTTAGCGTGTTTTTTGACTTTGGTTTTTTAAAGCCTTTAAAACCCCCAACTAGAGGGGAG TTTTTCTATAACGCTCCTGTTACGACAATTTTAAAGATTTGGCGTTATAGGGGCTGGGTTTGAAAGAGCGCAC TTGGAGGGCTTCCACAGGCTTGCAGATTGAATGGATTTCGCCCATGGGGCTTTGGTGTTTTCCCTATAGCGT TTTCAACCAATGGGGCAATGGCAAAATGTAAAGGGCTATGCTTCAACCCTAACAGGGTTTAAAAGGGCTTTAAAAGGGCTTTGAATTTTGAATTTTTAAAATGGGCTTCAACCGTTAAAAAGGGTTTAAAAAGGGCTTTAAAAAAAA	1144 LKAAKMRLAWFFDFGFLTFKTPTRGSF FYNAPVTTANFKDYGVIGAGFERATW RASTGLQIEWISPMGPLVLIFPIAFFNO WGDGNGKKCKGLCFNPNMDDYTQHF EFSMGTRF
HP1444	1145) AAAGGCTTAAACCAAGCCGCCAAGGCCAATTTTTCTGATTTTTTTT	1146 KGLNQAGASQGDFSDFFEDLGSFFED AFGFGARGSKRQKSSIAPDYLQTLELS FKEAVFGCKKTIKVQYQSVCESCDGT GAKDKALETCKQCNGQGIAVFMRQGF MSFAQTCGACQGKGKIVKTPCQACKG KTYILKDEEIDAIIPEGIDDCNRMVLKNK GNEYEKGKRGDLYLEAQVKEDEHFKR EGGLFIKAPVFFTTIALGHTIKVPSLKG
HP1444	1147 ATTIAAAAGGCGCGGTTGATTAAAGATGGCTTTTTAGCGTTCAAACAGGCCCATTACGCTGAAGCGTTACGCTTTTTTTT	1148 FKKRALIKDGFLAFKQAHYAEALRLFSE VLFLDKDNQKAKVGALLSIJAKDFPKE AHSFYELYQSLIAMQKRSI KNQAEEQII NLLASFDEGLNQMAEKIDVQISQKSEEL NGILYADFKRLSLERGFKEAFEDLMFS SRVIFDNKEDFYEFLKELNI+YGYYELAI NYIENMHEDSFIYDEFLRSI.LEDALKSN KA

	2000		
HP1238	1149 GC AT	1149 GGGAAGIAICGGIAGIAIGGGCAAACCTATTGAAGGGTTTTTAGTGGCAGCCATTCAGTTTCCTGTGCCAATTGTCA	1150 GSIGSMGKPIEGFLVAAIGFPVPIVNSR
-	5	GTGGAGCTTATCATTTTCCCTGAGTATAGCACGCAAGGTTTGAATACCGCTAAGTGGCTTAGCGAAGAGTTTTTATTA	EYSTQGLNTAKWLSEEFLLDVPGKETE
•	8 G	GATGTCCCGGGTAAAGAGAGAGACAGAGCTATACGCTAAGGCGTGTAAAGAGGCGGAAAGTTTATGGTGTTTTTTCAATCAT	LYAKACKEAKVYGVFSIMERNPDSNKN
	AŢ	ATACCGCAAGCTATTCCCATGGGATCCCATTGAGCCATGGTATCCTGGGGATTTAGGAATGCCTGTGTGGGT	MYDEDI CMBVCECBCCKI AVOICIO
	ပ္ပ	CCGGGCGGATCAAAATTAGCCGTGTGCATTTGCCATGACGGCATGATTCCAGAGCTCGCCAGAGAAGCGGCCTATA	GMIPELAREAYKGCNVYIRISGYSTO
-	¥ S	AAGGGIGCAATGTGTATATCCGCATTTCAGGCTATAGCACTCAAGTCAATGATGATTTTGACCAACCGCTCCA	VNDOWILTNRSNAWHNI MYTVSVNI A
) <u> </u>	ACCCA (GCCACAATTIGATE ATTICATE CONTRACT TAGCCGC TATGATATITACTACT TO THE CONTRACT CONTRACT TO THE CONTRACT CONTR	GYDNVFYYFGEGGICNFDGTTLVQGH
	3 5	GGCAACCTTGGGAGATTGTAACCGGGGGAACGGGGTAAACGGGGAAAT	RNPWEIVTGEIYPKMADNARLSWGLE
	ATC	ATGTGGCTAAACCGGGGGGGAGAACATGACGCAGGCTTAACCTATATCAAACATTAACCTAACGTAAAAAAAA	INNIYNLGHRGYVAKPGGEHDAGLTYIK
	8	CCTTGGGAAGATCACATGAAAATCAAAGACGGCTCTATTTATGGCTACCCTACCACGGTGGCGTTTTGGGAAAAA	ULAAGKYKLPWEUHMKIKUGSIYGYPT (1700BCC)
	AT	ATCCCTAACCTTGCATTTTTGC	VO. VO.
HP1048	1151 AA	1151 AAGGGCTATTTTGGGGATAAAGCCGGGCATGTGGTCAATAAGAGTTTGTATTGCCCTCCCAGTTTGGAAGGCACG	1152 RAIFGDKAGHVVNKSLYCPPSLEGTVI
	5 0	STORI I GAI EL GARAGO CO CACARAGAGO CONTROL CO	DVKVFTKKGYEKDARVLSAYEEEKAKL
	₹£	ASCULABLE AND THE SEASON THE SEASON THE SEASON TO THE SEASON THE S	DMEHFDRLTMLNREELLRVSSLLSQAI
	100	ANTICOME CARGO CONTROLL I CAGO CONTROLL I CAGO CAGO CAGO CAGO CAGO CAGO CAGO CAGO	LEEPFSHNGKDYKEGDQIPKEEIASINR
	12	TOWN CONTINUES OF THE STATE OF	FTLASLVKKYSKEVONHYEITKNNFLE
	Y A	4.000 FOR THE CONTRACT OF THE	OKKVLGEEHEEKLSILEKDDILPNGVIK
_	Y	AAATGGCAGGCACCATGGCAATAAAAGGGCATTGTGTTTAATATGCCCGTTTCCCCATATATAT	KVKLYIATKRKLKVGDKMAGRHGNKGI
	9	GGCGAAGCCTGTAGATTTTAAACCCTTTAGGCGTGCAAACAAA	VSNIVPVADMPYTADGEPVDIVLNPLG
	<u>SE</u>	TT AGGCTTAGTGGGGAAAGAATTTGGGAAATTGGCTAAATTGGCTAAAAGAAATTGGCTAAAAAAAGAAATTGGAAAATTGGAAAATTGGAAATTGAAATTGGAAATTGGAAATTGGAAATTGGAAATTGGAAATTGGAAATTGGAAATTGGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTAAATTAAATTAAAATTAAAA	VPSKMNIGOILEMHLGLVGKEFGKQIA
	¥	AATTGGGTGGTAAATTGGTAATTGGTAATTGGTATTAATGAAAAAGAACCCCTTTGAAAATTCAATTAATT	COLUMN TROCOSTI IN TRACE IN TR
	GT	GTTCTGATGAGGGCTTTTGGGAATACGCAAAAGATT	UPLIHALENCSDEELLEYAKD
HP0990	1153 TTT	TTTGATGATGATAAACCTTTACATGCTCATCAATCAACGCGAGCGCTCAAATGAGCCACCAAATCAAAAGAT	1154 LMMINLYMLINDINASADMSHOIKKIEE
	Y Y		RLNDEOK
_	2 2		
	₹ 6	AAAA AACCATAAAAAACTTATTTAAAAAAAAAAAAA	
	STS STS	GTGCTTTATTATAAAGGATTCTTATGACAAAAGACAACAAAAATAAAAAAAA	
	<u>GA</u>	GACGCCAAAGACAAGGTTTTTGGCCGCTTGATCACTGAAATCGCTGTGCTTTTAAGAGAGAAAAAAAA	
	<u>8</u>	CACCCCTAATGTGGGATTGTGGGGGATTTTGTGGGTGTTATCAACGCTAATAAGGTTAAATTTTCAGGCATGAAATTAGA	
	99	GGATAAAGAGTATTTTACCCATTCAGGCTATTTTGGCAGCACTAAGAGCAAGACTCTCCAAGAAATGCTAGAAAAAGC	
	<u> </u>	CCCTGAAAAGCTCTACCACTTAGCCGTTAGGGGCCATGCTCCCTAAAAAGGAAATTAGGGAAAGGGATGATTAAAAAAC	
_	TAC	TACCAST AND AND AND AND AND AND AND AND AND AND	-
	ည်	GCTTGAATCAATGGTTGGGCGGACATGAAGCCATTAAAATGAAAGTCATGCAGCCCTTGCTTTTAACCAACAAGAA	
	CA	CAATCTGTGG	

r	•
ř	
_	j
•	•

	TITAL ALECTION CONTRACT AND CON	1156 TYMRTDS	1156 TYMRTDSLNIAKEALEEARNKILKDYGK
HP0990	155 ICACI I ACAI GAGGACTATTTACCCCCTAAAGCCCAAGAGTTCCAGCAAGAATAAAAACGCCCAAGAAGCGCCCATGAAGGCG	DYLPPKA	DYLPPKAKVYSSKNKNAQEAI1EAIRPT
	ATCAGGCCCACTTCTATTATAGAGCCAAACGCTTTAAAAAGACTACCTTAAGCCTGAAGAATTAAGGCTCTATACCAA	SIILEPNA	SIILEPNALKDYLKPEELRLYTI.JYKRFL ASOMODAI FESOSVVVACEKGEEKAS
	TTAATTTACAAACGCTTTTTAGCTTCTCAAATGCAAGACGCTCTTTTGATGGCTATTATAAAATTTTAGGCAATGACGATAAGGA	GRKLLFD	GRKLLFDGYYKILGNDDKDKILPNLKE
	CAAATTGCTCCCCAATTTGAAAGAAAATGACCCCATTAAATTAGAAAACTAGAGAACGCCCATGTTACAAACC	NDPIKLER	NDPIKLEKLESNAHVTEPPARYSEASLI
	TCCAGCACCTATTCTGAAGCGAGCTTGATTAAGTTTTAGAAAGTTTAGGCATAGGCAGGC	KVLESLG	KVLESLGIGRPSTYAPTISLLONRDYIK
	CAACGATTCCCTTTACAAAACAGAGACTACATCAAGGTAGAAAAAAAA	VEKKOIS	VEKKOISALESAFKVIEILEKHI-EEIVUS
	AGGTGATAGAAATTTTAGAAAAGCA1TTTGAAGAAATCGTGGATTCCAAATTCAGCGCTTCTTTAGAAGAATTGG	Krsasle	KFSASLEEELDNIAUNKADT COVLKDT
	ACAATATCGCTCAAAATAAAGCCGACTACCAGCAAGTCTTAAAGGACTTTTACTACCCCTTTATGGATAAAATTGAAG	YTYPHMUX	Y Y P F MUKIEAGKKNIIS UKVHEN I GUS
	CTGGGAAAAAGAATATCATCTCTCAAAAAGTGCATGAAAAAACGGGTCAATCATGCCCTAAATGCGGTGGGGGAATTA	CPRCGG	CPKCGGELVKKNSKYGEFIAUNNYPK
	GTCAAAAAAAAATAGCCGTTATGGGGAGTTTATCGCTTGCAATTACCCTAAATGCAAATATGTCAAACAAA	CKYVKO	CKYVKOTESANDEADUELCERCGGEM
	AGCGCTAATGATGAAGCCGATCAAGAATTGTGCGAAAAATGCGGAGGGGAAATGGGTGCAAAAATTCAGCAGAAACG	VOKFSR	VOKFSRNGAFLACINIYPECKNIKSLK
	GGGCGITITIAGCITG	NTPNAKE	NTPNAKETIEGVKCPECGGDIALKRSK
		KGSFYGC	KGSFYGCNNYPKCNFLSNHKPINKRC
		EKCHYLM	EKCHYLMSERIYRKKKAHECIKCKERV
	A PARTICIAN A CANANA A CONTRACTA A CANANA A CONTRACTA A CANANA A CONTRACTA A CANANA A CONTRACTA A CANANA A CONTRACTA A CANANA A CONTRACTA A CANANA A CONTRACTA A CANANA A CONTRACTA A CANANA A C	1158 II KFRI I I	1158 II KERI I I RGTDSKETIEKRLINAYKEM
HP0990	115/ [GAT TARARGAGUET TO THE ACTION TO THE ACTION TO ACTION TO THE A	OCLESED	OCI ESEDYLINEDLEKSKEIIL SIAKTLV
	AGAAA GCAG GCAG GCAG GCAGCATTICAA CATTITICAAAAAATCTTGTAAGGCTTTGGAAAAACGAAACCTA	HRLKAFN	HRLKAFNFEKICKAWKNETL
	CALL COCCUMENTATION OF THE CONTRACT OF THE CON		
	IAAAACCIAI CAAI IAII III IAAAAAGATCOTTATTATTATTAGTGATTGTGTTGTTTGGGGCTAAAAAGATCCCAGA		
	ATTECTION OF THE SECT		
	A COLORADA COCOLORA DE CONTRA DE COMO		
	TAAAGCATGCACATTTCATTAAGGGCATTTTAGAAGAGATTTTAGAAGAAGAAGAAGAAGTCATTGTTGAATACCCTAAAGACA		
	GAAGAGITAGCCCTTAAAATCAGCACGCATGAAAAAACTCAAGGGCTTTTTGACAGCGTAGTGGCTTGTAAGGGCTA		
	TATCAATTTCACGCTTTCTTTAGATTTTTGGAGCGTTTCACCCAAAAAGCTTTGGAATTGAAAGAAA		
	CAAGTTAAAAGCGAACGTTCTCAAAAATCTTTTAGAATTTGTGAGCGCTAACCCCACAGGGCCTTTACACATAGGG		
	CATGCTAGAGGGGGGGTGTTTGGCGATAGTTTGGCTAAAATCGCTCGC	4 460 270 ECT	4150 VOESTI ALVI ADMILI NI TSK EVIKTIV
HP0990	1159 TGGTGTGCGAGATTTGTTAGCGTTGGTGTTGGCTGATATGGTATTACTAAAA	NEW WENT	יייייייייייייייייייייייייייייייייייייי
	AAACGATTTATAATGAGAATTAAACGAAATTAGAATAAAAAAAA	<u>.</u>	
	AACGAGIII ICIAAAAACII CACAAAAACII AACAACAAAAAAAA		
	CAGCGCUAL ISAN I LOCAL THOUSAN THOUSAND THOUSAND THE CAGCAGAGAAAAGGCCAGAGAGGCTTTTGACAAGGCTTTTGACAGAGAAAAGGCCAGGAAAAGGCCAGGAAAAGGCCAGGAAAAAGGCCAGGAAAAAGGCCAGGAAAAAGGCCAGGAAAAAGGCCAGGAAAAAGGCCAGGAAAAAGGCCAGGAAAAAGGCCAGGAAAAAGGCTAGAAGAAAAAAAGGCCAGGAAAAAAAA		
	CATTACA A A RECEARTATTAL CONTROL OF THE CONTROL OF THE CATTACA A RECEARATION OF THE CATTACA CONTROL OF THE CATTA		
	ACTATT GAAAAATT ACGCCAAAAAGAT GGGAATTT GCCTAATAT CAACACCCTT AAACTTT GTCAAACAACAACAAAAAAAAAA		
	CAACACCCTAATTTATTCTTTAATTTTGACAACATGTTCAAACAACCCCCTTTTAATGAGAATAATTTTGAAAATTTTGA		
	CAATAGGGATGAGGAAAATTTTTAATGCAAACCATTGATTTTGAAAAATTTTCACAATATTCCAAGCCGGCCCACGA		
	TACACCAGCTACCCCCCCGCGCGTGGAGTTTAACGAAAATTTTAATGAAGAGGCTTAAAAACGGCGTTTTTTAACCAT		
	GACAACCTCAAAAACCCCATGCCTTTATCGCTTTATACGCATTTGCCCTTTTGCAGGAGTGCGTGTTATTTTTTTT	_	
	TGTTCAGTCATTTACACCAGCTTAGAAGAGAAAAAAAAAA		
	AAAACGCGATGGATACCAACAGAGAGAGGCGCGAATTCCACTATGGAGGCGGGCACCCGACCTTTTTCGCCCC		
	TCAATT		

HP0990	1161 648 848 864 864 864 867 867 867 878	1161 GAAAAAAGCCTGGTTTTAGAACATTTTGATAAAATGGTGGAGTTTTATGGGGGATATGGGGGTAATCGTGTTTAGGAA AAATTTGCATGCTACGCTAAGGCCGAAATGCAAGCGAGCG	1162 KKDLVLEHFDKMVEFYGDMGVIMFRK NLHAYAKGEMQASAFRNCVNTLTEIKS MRESIEEFFNQEMLQSEVPLWVELNQ KSV
HP0990	1163 GAG AAG ATT TAA CTT AAAA	1163 GAGACITTGATGGGAGTAAAAACTCTATCTTAAGCGCTTTAGCTAAAAGCGTTGCGAGTTTATTTA	1164 DFDGSKNSILSALAKSVELRVYLAFKEV FGEFFE
НР 0990	1165 TAG 1766 1777 1777 1771 1771 1771 1671 1685 1685 1685 1685 1685 1685 1685 168	1165 TAGCGGCTTAGAAGACGCAAGAGGCGATATTAAGATTGCTGGGAATTTAGAAGGCATTACGGCCATGCAAA TGGATACCAAAATGAGCGGTATCAAGCTAGAAATTTTATACCAAGCCTTACTCCAAGGCGAAAGATTTTAAAAATGATTTTAAAAATGATCCAAGCCGAAAGATTTTAAAAATCATGCAGCGAAACATTTTAAAAGGCGAAACATTTTAAAAATTGCAGCGAAAATTGATGGAAAATTGATGGGCGGTGAATTGAATTAAAAGAGCGTTAAAAGAGCGTTTAAAAGAGCGTTTTAAAAGATTTGAACAAACCGTTTTAAAAGAGCGGTTTTTAAAGAGCGGTTTTTAAAGAGCGTTTTTAAAGTTGAAGTGAAGTGAATTGGAGGCGTTTTTAAAGAGCGTTTTTAAAGAGCGTTTTTAAAGAGCGTTTTAAAGAGCGTTTTTAAAGAATTTTAAAAGAGCGTTTTTAAAGATTTTAAAAAGCGTTTTTAAAAGCGTTATTAAGAAGCGTTTTAAGAAATGGAAAATTGTTTAAAAATGGTTTAAAAATGGTTTAAAAAGCGTTTTTAAAAAGCGTTTTTAAAAAGCGTTAAAATGAAATTGTTTAAAAATGAAATTGTTTTAAAAATGGTTTAAAAAA	1166 SGLEĎAEGDMĎFKIAGNILEGITAMÓM DTKMSGIKLEILYĎALLĎAKEARKHILKI MMEAKEKIVINFSHLPTTEIFNVAPĎKIV EIIGŎGGRVIKEIVEKKEVKIĎLNKPSGE VKIMGNKERVLKTKEFILNYLHSLĎČEL EQYAIĎEVLEAČNKRIVĎFGAFLSLPKG GEGLLRKÓNMĎKCQVVLKEGĎSIRCR VISFNKGKIALĎLA
HP0990	1167 CGC AAC. 17AK 17AK 17AK 6AA 17CC	1167 CGCACCACCTAGAAACTCCTTAAAAATTAGAAACCTTGCAAAAAACCTAGAATCGATCAATAAAATCATCA AACAGAATGAAAAACCCTAGAAACTCATATGCGCTTGCAAAAACCTAGAATCGATCAATAAAAATCATCA AACAGAATGAAAAAACCATTCAGATCACCCAGCTTGATTTGAAATCTTAATGCCGTTATTTGTTTTACAAACCCTTT TAACGACAAAATCACCATTCAGATCACCCAGCTTGATTTGATTTTTTTT	1168 HHLALKLLKKLETLÖKNLESINKIIKÖNE KIAĞIYALDLKSNĞDYNAYYNAFNDKITI QITĞLETLSALNSTYLSLQNLKGLE

HP0990	1189 TAAGCGAATTAAATAAGCAAATGGCGTTTTTGAATGAAACCATGGCGTTAAACGCCCGAGTTTTTAGCCCTTTTTAGCCCTTTTAGCCCTTTTAGCCCTTTTAGCCCTTTTTAGCCCTTTTTAGCCGTGGGTGG	1170 SELNKOMAFLNETMALI HAKTPKPFNLSGGLSGI RLDPHGFPSFKNFKQE	1170 SELNKQMAFLNETMALNARVLALLAKÖ HAKTPKPFNLSGGLSGDLSGGKALIKNI RLDPHGFPSFKNFKQE
HP0990	1171 ATTGITGATGTAGGGGGGGGCTAAGGTCAAACTCACCCTATTAAAAAACATTTTAGATCTCATTGACAAGCT CATCATTGTGTAGGGGGGGGGG	1172 LLIVGGAKVSSI AMSNTFLKALG LELLQSAKEKK PKHIKISPVODI SEVIESAPTILW TTFLAHKIADTY GEKDNMSFIST FEVLDKRH	1172 LLIVGGAKVSSKLTLKNILDLIDKLIIAG AMSNTFLKALGYDVQDSSVEDALINDA LELLQSAKEKKVKVYLPIDAVTTDDILN PKHIKISPVQDIEPKHKIADIGPASLKLF SEVIESAPTILWNGPLGVIEKQEFARG TTFLAHKIADTYAFSLIGGGDTIDAINRA GEKDNMSFISTGGGASLEILLEGKILPC FEVLDKRH
HP1046 11	1173 TTTGAATACAGAAGAGCGGCTAAAGAAAACGATGGGATAAGATGAGTTAAGGTTTTCCCAAAGCTCGCTAAAGCGAT CACTCTAGCGGCAAAAGATGGCGGAGCGAACCGGACCGAACTACGAACTACGAACGGCGATTTTAAACGCTAAA GCGCAAAACATGCCTAAAGACAATATTGACGCGGCGATTAAAAGACGCGAGCAGTAAAGGAAGG	1174 FEYRRAAKEKR LAAKDGGSEPC MPKDNIDAAIKR ANFGVLIIMECN KTQGASIVPNG NEVENLKLSLEI EDKI	1174 FEYRRAAKEKRWDKMSKVFPKLAKAIT LAAKDGGSEPDTNAKLRTAILNAKAQN MPKDNIDAAIKRASSKEGNLSEITYEGK ANFGVLIIMECMTDNPTRTIANLKSYFN KTQGASIVPNGSLEFMFNRKSVFECLK NEVENLKLSLEDLEFALIDYGLEELEEV EDKI
HP1046	1175 AGAGCCTAAAGACAAAGAAAAATGCGAGAGTATTGTAGGGAGGG	1176 EPKDKEKCESN KVEDESTILQVV HLEVGDIVLVKC FHILSKTIVPLPE LDLIVNPSVKDV MEG	1176 EPKDKEKCESIVGRVKLLIÄLMGKACFI KVEDESTILQVYVSQNELNDEFKSLKK HLEVGDIVLVKGFPFATKTGELSIHALE FHILSKTIVPLPEKFHGLSIJIELRYRQRY LDLIVNPSVKDVFKKRSLIVSSVRKFFE MEG

I IKSGMRIGKGYVLGRIDORLGFEVTM REKHINPLE	AACGCTTGGGCTTTGAAGTTACCATGAGAGAAAACACATCAACCCTTAGAAC	
1186 KIFSESITLVSKTPNALVRNVLDGKIVFA KEINMLKKVVIIEHKNGIRTIYSQLDKIAP	1185 AAAAATTTTTAGGGGGGAAAATCGGTGTGGGGGAAAAAGGCCTTTGGTGCGTAATGTTTAGACGGGAAAATTCGGTGGTGCGGGGAAAATTCGGTGGAAAATCGCACGATTTATTGGTGGGAAAATCGCACGATTTATTCGTTAAAAAAAGGGGGAAAATCGCACGATTTATTCATTC	MP1046
FVEFFDKDLEDGKKYRYQVIAENFMGD KSRPSVIVEGKTKDLPKEITNVRVS	CTTGTTTGTGGAGTTTTTGATAAAGATTTAGAGGATGGGAAAAAA	
	1183]TCCCAGCGTTTCTAAATACATCATTCAAAGGCAAAATAAAGAAAAAAAA	HP1046
	GTAGAGGAGAAAAAGGAGAGAAAAATCGTAGAGCAGAAAGGAGAAAAAGGTAGAGCAGAAAAAGGAGAAAAAAGAAGAGAGAAGAGAGAG	
	ACAAACCTGAACCAAAACCAAAACCAAAAACCTATAGAAAAGCTTAAGAAAAGCTGAAGCCTAAAACCAAAAACCAAAAACCAAAAAACCAAAAAAACCAAAA	
	GCAAGATCCCAGTAAAAACACCCAGGGCGCTCCTAAACCCACGCTGGCCCCCAAAAACCTCCAACGCCTCCC	
	ATCATICTAACAGGAATTTTTCTTTCTCATTCTGTCTGTATTGTTACACTGGTTGATTATTTTTTTT	
DKISPKTSKEELIKEAENNIKNSKLGNL	ATTCAAAATTAGGAAATTTATATGCCGGAAAATTCTAAACTACAACCTGCTAGGTAGG	
VDANHKIISIETNKERYLVLLSDKYGLLL	GICGIGITGATGCGAACCATAAAATCATTTCAATAGAAACCAATAAGGAGCGTTACTTGGTCTTACTAAGCGATAAT	
1182 YVIKKIVPTOGSESAKDEKI EISVI GR	1181 TATGTCATCAAAAAAAATTGTTCCCACACAAGGGTCTTTTCTGCAAAAGATTTTAAGTTAGAAATTAGCGTTTTGG	HP1046
KTMSSGVTPVAMEFLDNLSIKAVEERF	MONTO MONT	
KLLAKPPLKQSAMGVFNHIEDAMNAVY	GATTTCTGAAATCACTTTAAAGCTTTTAGCCAAACCGCCCTAAAACAAAGCGCGATGGGGGGTTTTTAACCATATTGA	
AKYGITKDYVMALRVVLANGEIIRAGKK TIKDVAGENVAGI MIASEGCI GVISEITI	GCAAAAAACGTGAAAGGCGCGGTTTTAATGTTGCAGGGCTGATGGTGAGGGGGTGTTAAGGGCAG	
1180 PPDPASENQSTLGGNVAENAGGMRA	1179 CCCCCCAGATCCAGCGAGTGAAATCAAAGCACTTTAGGGGGGGAATGTCGCTGAAAATGCCGGTGGCATGCGTGC	HP1046
	TATCCGCCCGATGCTTATGATGGAT	1
	TATTACTI GGTGGATATTCTTAAGAGTGCGGAGAATGGAAGCTGAAAAACTTAAAGCGGCGTAATAAAATGGAAGCTGAAAAAACTTAAAGCGGCCTAATAAAATGGAAATGGAAGCTGAAAAAACTTAAAGCGGACCGCTAATAAATGGAAATGGAAGCTGAAAAACTTAAAGCGGACCGCTAATAAATCC	
	CATCGTGTGCGGAGTGCGCTGAGTTAGGTACGATTAAAGAGTGATTAAGCTCAATGATTAAAAGCGTTG	
	GAACAGCGATCGCAAGCTCAGACATGATGGTTGTGCTTGAATAAAAGAGTCCAAGATGCGGTAAAAATCACG	
	IVAILABERGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEG	
	TTTAGTGGGTTCGGTTCTCTGGGACGCATATTCTAAAGAAGTTCAAAGGCGCATGGACAACCCCACGCATTTAGGGG	
	CONTROL OF THE CARROLL CALL CARROLL LANCACGGAAGC GAAATT GACAAACGATTGAAGTTTTCTC	
1178 TGSACASEDLEANPVMVAIGASKELAH	1177/CACAGGGAGCGCGTGCGCGAGTGAGGATTTAGAGGCTAATCCGGTGATGGTAGCGATTGGAGCGAGTAAGGAATT	HP1046

HP1046	1187	1187 GAAGCGTTTAAAAAAGGTCAGCGGGGTGGATATAGAATTTAGCGAAGATAGCAGCGAATTGTGTTTTGTCCAGTTTCAAAAAAGGTTTCAAAAATTTAATAGAAGATAGCGGCGAATTGTGTTTGTCCAGCTTTAAAAATTTAATAGAAGAGGCCGTATCCAGCCTAACAGGATTAAAAAATTAATAGAAGAGGCCGTATCCAGCCTGACAGGATTAAAAAAAA	(0.00	1188 EAFKKVSGVDIEFSEDSSELCLSSFNLY RREVASETLKILIEDGRIQPN RIEEVYH RVARNLEKELLSEGESVVLE:LELGAME DELKILIGKMRYRSSFGONALQHSKEV ALLAGLIAEQLGGDKKLARRAGILHDIG KALTQELGRDHVNLGVEVCKRHKEDP VVINAIYAHHGHEEILSVECASVCAADA LSAGRPGARRKSDEEYAKRMQALEEI ALEFDGVEKAYAMESGRELRVIVKSNQ VRDNQVPIIARKIAEKIEESAQYVGEVG VQVVRESRFKTTATLKQ
HP1046	1189	189 AGTGGGCATCAATAATGAGACTTTTAGGCTTAAAATCCCTATTGGCGTGGAAGGGGGCGAAAAGATTAGGGTTCGCA ACAGGGGCAAAAGATGAGACTGGGGCGAATTTGCTCTTAGAGATCCATATTGAAGAGATGAATTAG GCGGGAAAAGATGATTACCCAAATGTTTGCTTTTGCTCTTAAAAACGGCTCTTTTTGGAGGGAAAATTGAAATTGC TACTTGGCATAAAACCTTAACCCTAACCATTCCCCCTAACAAAGCGGTGCAAAAATTCCGCATTAAAGAAAAGGGGTTCAAAAAGGGGTTCCGCATTAAAGAAAAAGGGGTTAAAAGAGGGGTTTGGAAAAAGGGGTTGGAAAAAGGGGTTGGAAAAAGGGGTTGGAAAAAGGGGGTTTATTGCCATGAAAAAGGGGTTGAAAAAGGGGTTGAAAAAAGGGGTTGGAAAAAGGGGGTTTATTGCAGAAAAGGGGTTGAAAAGGGGAATTGTAATTGTAATGAAGGGGTTGAAAAGGGGATTTTTT		1190 VSINNETFSLKIPIGVEEGEKIRVRNKG KTGRTTRGDLLLEIHIEEDEMYRREKD DITQIFDLPLKTALFGGKIEIATWHKTLT LTIPPNTKAMQKFRIKEKGIKINRKTSHV GDLYLQARLILPKTETLSNELKALLEKE L
HP1046	1101	1191 CCTGCATTAGTGGGAATGCCCTCAAAGGAGGGGGTTTGTACTAGGGTTTATACGACTACCCCTAAAAAAGGCCTAACTC GGCTTTAAGAAAGGTTGCCAAAGTTGGACCAGTAAATTTGAAGTGATTATTATCCCTGGTGAAGGGCATAA GGCTTTAAGAAAGGTTGCCAAAGTTGGCGTGGGGGTTAAGGATTTACCCGGTGTGAAATACCACATCGTTC GTGCCGCTTTAGACACTGCAGGGGTCAATAAAAGAACGGTTTCACGCTCTAAGTATGGGACTAAAAAGCG ACCGACAAGAAAGCACCGACAACAACAAAAAATAAGAACGGAAAAACAAGAAAAACATGAGAAAAAAGCGACAACAACAAAAAAAA		1192 PALVECPGRRGVCTRVYTTTPKKPNS ALRKVAKVRLTSKFEVISYIPGEGHNLQ EHSIVLVRGGRVKDLPGVKYHIVRGAL DTAGVNKRTVSRSKYGTKKAKATDKK ATDNKKK
HP1046	1193	1193 TTATGCCAAAAAGAACAAAATACAGAAATGCAAATGAAAGGCCGCAATCGTGGGGAAAGCCCATCGGGGTAACTCCATTAATGCCAAAAAGCAAATTGAATCCCCAATTGATTCACGCCAAATTGAATCCGCAAGGGTGTGGCGTTTGGGGGATATTGCGATTAAAAGGCCATAGAGCTTAGAATTGATTCACGCCAAATTGAATCCGCAAGGGTGCCATTGAAAAGGCACATTAAAAGGTAAAGGTAAGGTTAGGAAAATTGAAAAAGCCTTTGAAAAGCCTTTGAAAAGCTTAGAAAAATTGAAAAAAAA	1194	1194 LMPKRTKYRKOMKGRNRGKAHRGNSI AFGDIAIKAIEHGRIDSRQIESARVAMT RHIKRAGKVWIRVFPDKPLTAKPLETR MGKGKGSVEKWVMNIKPGRIVYEMLG IEEGLAREALALAQSKLPFKTIKIVTCES ENEIY
HP1046	1195	1195 ACGGACAAGACTTGGGAGGCATTGCGACCAACTCGCCCATTAATTA	1196	1196 TDKDLGGIATNSPINYKGIQVISNVIKVG FAKDKVGVVRLDLMIKSSVKIIRKDSK

HP1046	1197 AAG	1197 AAGGGTTTTCCTGTGTTTTAATGATAGATTTAAAGGATAGTTGGTTAAAAATCAGCGTGCCTGAAAAGTTTTGAAC	1198 KGFP\	1198 KGFPVVLMIDLKDSWLKISVPEKYLNEF
	GAG	GAGCGTGATGGGGGGAT	KVGK	KVGKEFEGYIPALKKSTKFRVKYLSVM
HP1045	1199 TGT GGC GTT TGC	1199 TGTTGAGCGCTCGAATCATTAAGGTGCTAGAAAACGGGGAATTATTTCATCTATGGGAATAAGGAAGTGCTAGTGGATGGGTTGGGATGGGAAAAGGGAAGTGCTAGTGGGTTGTGGGATTGAAAAGGAATAGAAGGGAATTGAGGAATTGAAGGAATTGAGAATTGAATAGAAATTGGCTGCTGATTTAGGGCGATTCCAATAGAAATTGGCTGCTGCTGATGAGAATTGGCTGCTGAAAAAGAGGCGATGAGAAGGCGATGAGAATTGAAAAAAGAGCGAAAGGAGCGATGAGAAGGCGATGAGAATGCCTAATTAAAAAAGAGCGAAAGGCGATGAGAGGCGATGAGAATGCCTAATTGAAAAAGAGCGAAAGGCGATGAGAAGAGGCGATGAGAATGCCTAATTGAAAAAGAGAGCGAAAGGAGCGATGAGAAAGAA	1200 LSARII OILKV: IEYTNI	1200 LSARIIKVLENGNYFIYGNKEVLVDGEK OILKVSGVIRPYDIERNNTIQSKFLADAK IEYTNLGHLSDSNKKKFAADAMETQMP
HP1045	1201 CGC 17AA 17AA 17AA 17CC 17TC 17TC 17TC 17TC	CGCAAGCTTTAAAAGTCAAAAAACAGCATTCAAAAAATCTCCATCATAGATGAGCAAAAAAACTCGTGAAGTAACCT TAAAATCCTTGAAAAACCGAACAAGATAAGCTCTTTTTGAGCAAAAAGATTATGCGATCTACAACCAAC	1202 OALKVKNSIG KTEQDKLILS RONLNALLK SSQALEVKO IAPLNDYEVY SITLVSKTPN MLKKVVIIEH GMRIQKGYV	1202 OALKVKNSIOKISSIIDEOKTREVTLKSL KTEODKLILSMOKDYAIYNORLTLLEKE RONLNALLKRLNIIKONRENEEKVSLKK SSOALEVKQVASSYONINTTSYNGPKT IAPLNDYEVVOKFGPYIDPVYNLKIFSE SITLVSKTPNALVRNVLDGKIVFAKEIN MLKKVVIIEHKNGIRTIYSQLDKIAPTIKS GMRIOKGYV
HP1045	1203 GCG 6GG 6TG 174 GAA 176 GAA 176 GAA 176 GCD	1203 GCGATGACACTCCTATCGTAGCGGGTTCAGCTTTAAGAGGCTTTAGAAGCAAAGGCTGGTAATGTGGGTGAATG GGGTGAAAAAGTTCGTAACGTTATGGCTTTAAGAGGCTTTAGAGAGGAAAGGCTGGTAATGTGGGTGAAAAAGTTT GGGTGAAAAAGTGAAAGTGGAAATGGTTTTGCGGGTAGGGGACTGTGCTTACAGGTAGGATTGAAAGAAGCGTT CTTGAAAGTAGGCGATGAAAGTGGAAATCGTTGGTACAGAGAAAAAAAA	1204 DDTPIN EKVLKI PVEDV DEVEN KGEAG CKPGS TPFFTN VEMVIN VEMVIN	1204 DDTPIVAGSALRALEEAKAGNVGEWG EKVLKLMAEVDAYIPTPERDTEKTFLM PVEDVFSIAGRGTVVTGRIERGVVKVG DEVEVORIPTQKTTVTGVEMFRKELE KGEAGDWULRGTKKEEVERGMVL CKPGSITPHKKFEGEIYVLSKEEGGRH TPFTINYRDGFYVRTTOVTGSITLPEG VEMVMPGDNVKITVELISPVALELGTKF AIREGGRTVGAGVVS
НР 0870	1205 AACI TCA(GTT(1205 AACCGCGACAACCACGCAAGACGCCGTAACGATCACCACTACCTATAATAATAAAGCAAAGCCACCGTCAAATTTGACA TCACCAATAACGAACAGCTGTTAAATCAAGCGGCAAACATCATGCAAGCATTAATACGCAATGCCTTTAGTGC GTTCCACGAATAACGAAAACACTCCAGGGGGTGGTCAACCATGGGGTTTAAGCGTCCGGGAATGCGTGCAGCAT CTTCCAACAAGAATTTAGCCAGGTTACTAGCATGATCAAAAACGCCCAAGAAATAATCAC	1206 TATTTC NAEQLI NENTP	1206 TATTT GDGVTITT YNNNKATVKFDITN NAEGLLNGAANINGVLNTGCPLVRSTN NENTRAGOOWGLSTSGNACSIFQGE
нР 0 870	1207 TAMA AAGI CAAV CGAY CGAY GATI AAAG GCAY TTCC TTCC CGAY	TAAAACAAGCGAAAATTTAAACGAAAGCCTACCAACTTAAGCCCCGCTAGAACAAGCCTAAAAACCTGAAACAACAAGCCAACGCTGAAAACAAGCCAACACTTAAAAAAAA	1208 KTSENI AKLESEN LKKKLE LKKKLE TOTOAC ABNLKP ABNLKP ASNOC BLOCK ELDOK ELDOK ELDOK ELDOK SPHNLIN NEWKKG SPHNLIN	IZOR ITSENINGSTREED AND SERVICE SERVER SERVE

12	1219 TTGGCCTAGCTGACACGACTGGCGTTATCAAAAATCGCATGGATTTATTT	1220 GLADTTGVIKNRMDLFDYFFPNKRKG
	GTITTAGCCATATTGTGAAATGGTTTTTGCAAGAAATTATGGATTGATAGCTTGTTTAAAGATGAAGACGCTAAAGG GTTTTAGCCATATTGTGAAATGGTTTTTGCAAGAACAAT ACGGCGTCAAAGATTTAGGCATTACCCCTAACGCTTACC TCAAAACCCGCTATAAAAGCATGCAAGAAACAGGTTTGGAAGCCGAATTGTATTTCTTAAACCACTATAAAAACATCA AAATATTCTCTTGTGGGCATTTAAAAGACATGCGTCTTTTTGGCGATGGGTATGACTTCTATATTCAAACCAACAAGA AGGCGTTTTAGTGGAAGTTAAAGGGGATTAGAGAAAAGCAAGGACATTGAGATTGACCCAAAAAGAATACGAACAA	WWOKGDAYIHRKLWIDSLFKDEDAKG FSHIVKWFLQEQYGVKDLGITPNAYLK TRYKSMQETGLEAELYFLNHYKNIKIFS CGHLKDMRLFGDGYDFYIQTNKQAFL VEVKGIRFKOGTI RI TOKFYFOAOTYS
	GCGCAAACTTATAGCCATGATTATGTGCTTGTAGTGGTATTGAATTTGAGTGAAAAACCCCATCTTTATCTATC	HDYVLVVVLNLSEKPHLLSIANPLKHLE FKACERKQKSILEYHLIGQIK
1	1221 CAAACTTAAACGCACCCAAACCCTTATTTGAATGTTTTGTAGGAGTTAATCTGGCCAAAGCCAAATATTATTCTAAAAA AGAAGAAAAAAAAAA	1222 NLNAPKPLFECFVGVNLAKAKÝÝSKKE EREKEKMILNFCKIFEIILFEAIOKOPKP OFKNKDELLGDYPNIKNI OSL
	CCAGCATCAATTATGTGGGCAACACCTGGTGGGATTAAACATGGGAAGACTCGTGAAAATTGGGCAAGACATCGTGAAAACTCGTGAAAACTCGTGAAAACTCGGGAAGACTCGTGAAAACTCGGGAAGACTCGTGAAAACTCGGGAAGACTCGTGAAAACTCGGGAAGACTCGTGAAAACTCGGCAAGAAAATTGCCCAAAAATTTAAAACTCGAAAAAAAA	1224 ISTVIESVUGVI FKYPIPVGNILTFLASI NYVGNTSCEVGIKVLSEDIKTREITHTN SCYFTMVAVENGKPTPMPKYEPKTEV EIRRYEGALKRKEMRTRGYLKSGKHE GV TASKVRRFRMGHIELATPVAHIWYVNS LPSRIGTLLGVKMKDLERVLYYEAYIVK EPGEAAYDNEGTKLVMKYDILNEGY QNISRRYEDRGFYAAOMGGEAIKDLLE IDLITLQSLKEEVKDTNSDAKKKKLIKR LKVVESFLNSGNRPEWMMLTVLPVLP POLRPLVALDGGKFAVSDVNELYRVI NDANGDLYGNEGAROUNELYRVI NDANGDLYGNEGAROUNELYRVI NDANGDLYGNEGAROUNELYRVI NDANGDLYGNEGAROUNELYRVI NDANGDLYGNEGAROUNELYRVI NDANGDLYGNEGAROUNELYRVI NDANGDLYGNEGAROUNELYRVI NDANGDLYGNEGAROUNELYRVI NDANGDLYGNEGAROUNELYRVI NDANGDLYGNEGAROUNELYRVI NDANGDLYGNEGAROUNELYRRVI NDANGDLYGNEGAROUNELYRRVI NDANGDLYGNEGAROUNELYRRVI NDANGDLYGNEGAROUNELYRRVI NDANGDLYGNEGAROUNELYRRVI NDANGDLYGNEGAROUNELYRRVI NDANGDLYGNEGAROUNELYRRVI NDANGDLYGNEGAROUNELYRRVI NDANGDLYGNEGAROUNELYRRVI NDANGDLYGNEGAROUNELYRRYVI NDANGDLYGNEGAROUN
1	AAATCATTGTGCGCAATGAAAAGGATGTTGCAAGAAGCCGTGGATGTGCTTTTTGATAACGGCGCGCGC	1228 LIKKEVSINIKEVKHPQADAQLAAENVA TQLEKRVAFRRAMKKVMQAALKSGAK GIKVČVSGRLAGAEIATEWYMEGRV PLHTLRAKIDYGFAEAMTVYGIIGVKVW
	GAAGGCGCGTGAAAGTTTACACACCTTAAGGGCTAAGATTGATT	

]{
GATGGTTCCCTAGTGCGCGCCCCCCCCCTCCAGGCGTTGAGGCGATAAAATTAGGAAGTTCCTTAAAAAAGGGGCTCGTTATTATGAAAAAGGCGTCAAAAAAGGCGTCCTTATTAGTGCCTGGCGCTCGCGCTCCAGGCGTTGTGATTGAAGAAGGCGTCCCTTATTATTAGCGGGGTGTTGTGAAAAAAGGCGTGGATTGTGAAAAAAGGCGTGGATGTTGAAAAAAGGCGTGGATGTTGAAAAAAGGCGTGGATATTAAAAGAAGGCGTGGATGTTGAACAAAAAGGCGTGACCCCAATTAGCCGCAGAAAATGTAAAAAAAGGCGTGAAAAAAAA
CCIAGAAGAAGCAGAAGCCATGGGGGAAGCTCCATGGCGTTGGGGGATATTGCGATTAAAGCCATAGAGCATGGGA CGCAATCGTGGGGAAAGCCCAATGGGGTAGCTCCATGGCGATGGGGATAAAAGGGGGGGTAAGGTGTGGAT GGATTGATT
1231 GGCAGAAGAAGTAAAGGGAGTGTTGOAAAATAAAATAGAAGCTCAATACAGCATIGATITIGATITIGATICTGCAGAACAACAACAAGCAAGAAGAAGAAGAACAAGAAGAA
CGATGOGGCGTGGCTAACATTGCCAACCAGCTTAAGGGAACAACCCCTAAAGAAAG
CGTTTGATTTTCAAAATAATCACAAGGAAGTTTTTATCCCGTTGAATCGTCATAAAGACATGCAGTTATGAAAAATTTTGAAAAATTTTGAAAAATTTTGAAAAAA
<u>GTTTTTGAAACGAAAGATTTTGGCGTGTTTGACAAACCCCATCAAGTCTATACCCACCC</u>
AGCTTATTTGCACTAGCGCATGGGTTGGTTGAAAAAGCCATGAAAATAGACAACGAAGCCATTCTAACGCCACAAACAT TCAAAAAGATTTGCACATTCGATCTAAAATTTCTCCTTTAGGCAAGCAA
CAGCGTGGATCATAGGATCGTGGGTGAGGGGCTTTATGGGGTGGCAGATGAAAACGCTAGGGAGTAICH I CAAHHA AAGCGTGAAAATAACGCCCCATTACTCATGCTCCATGCCGCTAGTTTAGAGTTTGAATTTAAAGGAGCGATCTATAAAA ATCGCTTCCCCCATGCCTGAACGCTTCATGCCTTTTTTAAAAGATCTATCCTTTTTTTATTGATTG

110011	12261	COTTAN ATTITUTE CONTINUE CONTI	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		CACGGCTTTTGCATGCGCCAACATGCGGTTTTGATGCAACAACGCTAGAAAAATGCAACAATTAGCCTTAAAAG CACGGCTTTTGCATGCGCCCAACATGCTATGGGGATTATGATGCTCAACAACAGTTGCCTTGAAATT CACGGCTTTTGCATGCAACATGAAACGCGCACACTCCAAAAAGATTTGCGAGGGGATTGCTTTGAAATT TGAAACTTGCGGTAGGGCTAGGGGGGTATGAAAAAATCCCAAACAACACGAGGGGTTTTATTAGAGG GAAACTTGGCATAGGCGCGTTAAGGGGGGGGTATGTGCCCTAATCACCGATCAGGGTTTTTTTT	1236 PKILVSGTTGLEKETLEKMQQLALKAPL LHAHNMSIGIMMLNQLAFLTSLKLKDA DIEIIETHHNLKKDIPSGTALSLYETCAK ARGYDEKNALITHREGLRSKESIGIAAL RGGDVAGKHTIGFYLEGEYIELSHTAT NRSIFAKGALEVALWLKDKAAKKYEINE MFG
HP1464	1237 T C C C C C C C C C C C C C C C C C C	1237 TGAAAAGAATTAGACAACTTGTCTGAAGAGGATGGAAAGGATTTGCCTATGATTTTTCAAGCGCTAAGGAGTTT GCTAGAATTGTGCCAAAAACACCCAAAAAAGCATCGCTGAAATCGTGCGTTTGAGAGAAACGCCCTGAAAAACCACC CTGATGCAACGATGGTTAAAATTTATCATGCGATGCTTGAGTGTTATGATAATGGGGCTAATTCTAAAGAAAG	1238 EKELDNLSEEDGNESIAYDFSSAKELL ELCOKHOKSIAEIVRLRENALKNHPDA TMVKIYHAMLECYDNGANSKERYLPG SLKVTRLAPSIKTRLEKHPTSGKDPLAL IDYISLYARAIA
MP.1464	1239 A	1239 AAAAAGCCTTTAATAGACTATTCTAGCCCTATGCCCCTAAAGATAGCCCTTTAATAGATATTCTAGCC TGGTTAAAAACATCCAATCCA	1240 KAFCYSVEKIKPYAPKÖSPLIDYSSLVK NIQSTLKGTSFEMLIGSVW
HP1464		1241 ITATGCGGACACTTTGATTGATGAAGAGGGTGCTAAAAAGGTGGTTGAAGCCGGGGATTAAATCCATTACGATCCGCA CCCCAGTAACTTGTAAGGGCCAAGGGCTGTGCGCGAATTGAATTTGGGCAAGGCAAGATGA CCCCAGTAACTTGTAAGGGCGTGGTAGCCGCGCAATTGGGGAAGCTTGAATTTGGGCGAAGGCTTTAAGGAC TTATCCGGGTGGAAGGGGGGAGCGCGCGCAATCTTTTAGGACGCTCAAGAAGAGGTTTTGTGC TTTTCATGGGCGGACAGCGAGCAGCAGGATGAAAGGGTTATGCGCAAAGAGGTTTTTAGT TGAAAAGCGCTAAGATAAAGAGGGTAAAAAAAGGGTAAAAGGGTTTATGAAGAA	1242 YADTLIDEEGAKKVVEAGIKSITIRTPŲT CKAPKGVCAKCYGLNLGEGKMSYPGE AVGVVAAQSIGEPGTQLTLRTFHVGGT ASRSQDEREIVASKEGFVRFYNLRTYT NKEGKNIIANRRNASILVVEPKIKAPFD GELRIETVYEVVVSVKNGDQEAKFVL RRSDIVKPSELAGVGGKIEGKVYLPYA SGHKVHKGGSIADIIQEGWNVPNRIPY ASELLVKDNDPIA
HP1464	22. 64. 0000000000000000000000000000000000	1243 CTTTAAGGCGATGTTTACTCCCTTGATCATGCAGGCGCAGTTGAGCTTTAGGAACATTGATAATTTTGTGGGAAAAGG CTCTGCTTTGATAATTTGACGCTAACCCCTATAAAACGATTTTTGGAGAAATAATCATGAGGGCTACG CTCTGCTTTGAAAATTTGACGCTAACCCCTATAAAACGATTTTTGGAGAAATAATCATGAGGGCTACG GCGATAAAAATCTTTTCACTCTCAGCATTTGACCCCTATTGCTTCCTTGGTTCCTTGGCAATGCGCTTGAATTTAAAAGCTTTGACTGAAGTGA GGCTCATTAGTATTTTGAGCGCGGATTTATTCAAGACTAAAGAGACGCAAAGACCTTTAAAGCCAAAAAGCGGCAGATCACG CATGGGAAGCACCAAAAATGGATTAATTCAACACTAAAGAGACGTTTTAAAGCCCAAAAGAGAGAG	1244 FKAMIFTPLIMQAQLSLRNIDNFVEKĞS ALIDKFDANPYKTIFGERK
HP1464	1245 T GG T T A A A	TTCAAAAGATGCAAGAAAACCAATACCTTCTCATTGAAGACGCCCTGAAAGATTTGAGCCATGCTTTAAAAAAGGC GCTACAAGGAGATCACTGAACTTTAATTAAAAATCAGCAAGTTAGAGATTTCTCCCAATTCTCAAGTGGGAGCG TGAAAATCCGCTATGAAAGCAATCTTTAGCCTCTTTTTCCTTCTTATTGTTTTAAAAGCAAACCCCATAAACCCTTTATT AGAGCCGTTATATTTCCCCAGTTACGCGCAATTTTTAAACTTAGCACCTCACTTTGTTAAAAAAAA	1246 GKMMGENGYLLIEDALKDLSHALKTRY KEITELYLKISKLEISPNSGVGASVKIRY ESNL

HP0070	1247 AAAAATTGGAGTTTGTGGTCCTGTAGGAAGCGGTAAAACCGCCTTGATTGA	1248 KIGVCGPVGSGKTALIEALTRIHMSKDY
	ATTATGACATGGCGGTCATCACTAATGATATTTACACGAAGGAGGCGGAGAGTTTATGGGGTTATTAGAGAAGAGGCTTCTATGAATTT	UMAVII NUIT I REDAEF MCKNSVMPRE
	CACAGAGAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAA	MHGRFPNLELLLIESGGDNLSATFNPE
	CAGGACATTCAACCCAGAGCTAGCGGACTTTACGATCTTGTGATGATGGTGAGGGCGATAAAATCCCCCGA	LADFTIFVIDVAEGDKIPRKGGPGITRS
	AAAGGCGGCCCAGGAATCACGCGCTCAGACTTGCTTGTCATAAAATTGATTTAGCCCCCTATGTGGGAGCGG	DLLVINKIDLAPYVGADLKVMERDSKK
	ACTTGAAAGTCATGGAAAGGGATTCTAAAAAAAT	
HP0070	1249 TTTTAAAACCAGGCAAGGCAAAGACATAGCCATACGCCTTAAAGACGCTCCCAAGTTGGGGCTCTCTCAAGGGGATA	1250 FKTRQGKDIAIRLKDAPKLGLSQGDILF
2	TTTTATTTAAAGAAGAAGAAGAAATTATCGCCGTTAATATCTTGGATTCTGAAGTCATTCACATCCAAGCCAAGAGCG	KEEKEIIAVNILDSEVIHIQAKSVAEVAKI
	TGGCAGAAGTAGCGAAAATATGCTATGAAATAGGAAACCGCCATGCGGCTTTATACTATGGCGAGTCTCAATTTGAA	CYEIGNRHAALYYGESOFEFKTPFEKP
	TTTAAAAACACCATTTGAAAAGCCCACGCTAGCGTTATTAGAAAAGCTAGGGGTTCAAAATCGTGTTTTAAAA	I LALLERLGVUNKVLSSKLUSKERLIV I
	TTGGATTCCAAAGAACGCTTAACCGTGAGCCATGCCCCATAGTGAGCCTAATTTAAGGCCTCACTAGCGAGCCAATTT	SMPHOEFINITAVOLAGOTAVAA
	TAAAGTGGTCGTAAAATAGAAAAGAAATAGAAAAATAACAAA GAATAAAAAAGCACTGAAAAAAAAAA	
	GCGTGGGTATGCCCCCCAAAAACTCCAAAGACAGACAACAACAACGCTCATGTGGGATAACGAATTCTGGAAATTCTGCAAAGACAAAAAAAA	•
100077	ASSITEMENTAL ASSIGNATION OF THE ASSISTANCE A	1252 NOALNLALDLNHALCTTEHVLLVILEHE
T COLLE	1221 ILVACATE CONTROLL OF THE THEORY OF THE THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THE THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE TH	SGEKIIGTLERDDYDKLKOILKDYLLQY
	ATTION OF THE TOTAL OF THE TOTA	VPI KSDPAKMPARSFVI LRMI KRMYA
	TECT TO THE TECT T	SCHESVOVEELLI MI DHPDCYASKI M
	Addada Historia Control and Co	DSEGIARI YSNPALL DI DNHGIPNDIND
	ACCOL	NEEADKNIDI KKYAKNI SALAODNALD
	All ICCIAAl GARAN AND TAN GARANGO COCCUMANANANAN CAN INTERNATIONAL CONTRACTOR CONTRACTOR CAN AND TATA AND CONTRACTOR CAN AND TATA AND CONTRACTOR CAN AND TATA AND CONTRACTOR CAN AND TATA AND CONTRACTOR CAN AND TATA AND CONTRACTOR CAN AND CAN AND CONTRACTOR CAN AND CONTRACTOR CAN AND CONTRACTOR CAN AND CAN AN	
	AGCCCAAGACACCCI AGAI CCAGI GGCAGAGAGAAGAGAI AGAGI GAI AGAGAGAAI AGAGAGAGAAI AGAGAGAGAAI AGAGAGAGAAGAAI AGAGAGAGAAI AGAGAGAAGAAI AGAGAGAAI	F VIGINEELINVIEW ON THE OF THE
-	CAGAAAAAAGGATTITAATTGGCGAAGCGGGGCGTAGGGAAAACCTCCATGGCTGAAGCTTTTAATTGCCTTTAA	AGVGN OMERIALNIAGNEVETE
	AAATGGCTCAAAAAGAAGTGCCGGAG	Tagi Managadi Managada Ta wasan saas
HP0377	1253 CTTATACGGTTTTAGAGACAGCGGGGAGGCAATTTATCCAAGAAGG I GCTATCATGCCATGCTTCCAAGAGTTTATTCCAAGAAGGTTTATTCAAGAGAGAG	CONTINUE CON
	GCCCTTTCCAAGCTGAGGTGGATCGATATGGCGCGTATAGTTTGAGTGGGGGAATACGCGTATGACAGGCCATTTT	- CAEVURYGAYSLSGETATURPFLWGS
	GTGGGGTTCTAAAAGGATTGGCCCTGATTTGCACAGGGTAGGGGATTATCGCACAAACGATTGGCATGGCATGGCATGAAAAGCAC	KRIGPULHKVGUYK! IUWHEKHMPUP
	ATGTTTGATCCTAAAAGCGTTGTGCCCCACAGCATCATGCCCCCCTATAAGCATTATTTACAAAAAGAGCGTTTT	KOVVPHOIMPATRALFINANDINIA TO THE TOTAL TOT
	GACACCGCTTATGCAGAAGCTTTGACGCAAAAAAAGGTTTTTGGCGTGCCTTATGACACAGAAAACGGCGTGAAATT	EALTOKKVFGVPYDIENGVKI.GSVEE
	AGGGAGCGTAGAAGAAGCGAAAAAAGCCTATTTAGAAGAAGCTAAAAAAATCACAGCGGATATGAAGAGAGAG	AKKAYLEEAKKI ADMKUKKVLEAIEKG
	GTGCTAGAAGCGATTGAGAGGTGAAGTGTTAGAAATTGTGGCTTTGATTTGAATAGCTTGGGTAATTC	EVLEIVALIATLNOLGNORINAIVAINAN
	CAGGATCAACGCCAATCAAAAACGCTAAATAAGGGGTGAATGATGATTTAGAAAGTTTGAGAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAATTTAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAGAAGGTTTTGAATGATG	
	TITITIACCATTCTTTTACGCTCTTTTGTATGCCTATATTTTTACCATGTACAAAAAAAA	
	TTATGAGCGATACGGATACTTAGCGTTAAATGATGCTTTAGAGGACGAGGTGATTGAGCGAGGCCAGGCCATACATGAGCATTCTT	
	TGATAATGGCATAAAGGAAAGTTGAAATGGATTTTTTTTT	
	GATTTTAGTTTTAACCATCTA1GAA1CCAG11CGC1CA11AAAGAAA1GCGGACAGCAAA1G1GGAAA1G1GAAATGGCAAAGGTTAATGT	
	AGAAAA GGGCA GA GA GGA AGGGGAG GCCAA AA	

1256 AIERAKKLFNCGFANVQAHSGSQANN AVYHALLKPYDKI GMDLSCGGHLTHG AVYHALLKPYDKI GMDLSCGGHLTHG AVYHALLKPYDKI GMDLSCGGHLTHG AVYHALLKPYDKI GMDLSCGGHLTHG ALKIAQSVKPEINCGFSAYPREIDFKKF REIADEVGALLIGDIAHVAGLVYTGEHA HPFPHCHVVSSTTHKTLRGPRGGILT NDEEIAAKIDKAIFPGTQGGPLMHVIAA KAVGFKENLKPEFKAYAQLVKSNMQV LAKALKEKNHKLVSGGTSNHLLLMDFL DKPYSGKDADIALGNAGITVNKNTIPGE TRSPFVTSGIRIGSAAL	1258 YEPIWAIGTKKSASLEDIYLTHGFLKÖIL NÖKTPLLYGGSVNTÖNAKEILGIDSVD GLLIGSASWELENFKTIISFL	1260 LFSSADKYDSGCGWPSFSKPINKOVV KYEDDESLNRKRIEVLSRIGKAHLGHV FNDGPKELGGLRYCINSAALRFIPLKD MEKEGYGEFIPVIKKGELKKYINDKKSH	1262 SLMTDSVSLEDSKKRLNAIKDLIFHKNK AFROLQLKLNTPLKAL 1264 QLEVSKELLEATEPVLGVVROITPFGIF VEAKGIEGLVHYSEISHKGPVNPEKYY KEGDEVVVKAIAYDAEKRRISISI
1255 TAGCCATAGAAAGGCTTATAATTGCCAGTTCGCTAACGTGCAAGCGCATTCAGGCTCACAAGGCCAAT AACGCTGTCTATCACGCTCTTTAAAGCCTTATGACATTTTAGGCATTGAAGCTGTGGAGGGCATTTAACG CATGGCGCTAAAGTGACTTTAAACCGGCAAGCATTTTAGGCATTTTAAGCTGTGGAGGGCATTTTAACG CATGGCGCTAAAGTGAGTTTAAACCGGCAAGCATTATCAGAGTTTTCAGCGTGAATTTGATTATTTTAAGAAATTTTCAAGCGTTATTGAT TATGAAGAGGCGCTAAAAATTGAGCAAGCGTTAAGCCAGAAATCATTAGGCGGTTTTTCAGCCTTATTTCAAGAAATTTTAAGAAAATTTTAAGAAAATTTTAAGAAAATTTTAAGAAAATTTTAAGAAAATTTTAAGAAAAGAAAGAAAGAAAGAAAGAAATTTAAGGGGGG	1257 CGTATGAGCCTATITGGGCGGTTGGCACCAAAAAAGGGCGTTCTTTAGAGATATTTATCTCAGGCATGGTTTTTAA AGCAAATCTTAAATCAAAAAACGCCCTTGTTGTAGGGGGGGG	1259 CGTTATTTTCTTCAGCGGATAAATACGACTCCGGTTGCGGGTGGCCCAAGCTTTTCTAAGCCTATCAATAAGATGTG GTGAAATACGAAGAGGCGTAATAGGAAACGCATTGCGGCGTTTCTAAGGCCGTATTGGTAAGGCCGTTTAGG GCATGTGAACAGAGGCCTTAATAGGAACGCATTAAGGCCGTTTGAACGCCGTTTAGG GCATGTAAAAGGACGTGGAAAAAGAATTAGGCGGGTTTATCCATTACAAAAAGGGTGAATTGAAAAAATCATCA CCTTAAAAAGGCTTAAAAAAGGGGTTATGGCGAGTTTATCCCTTAATCAAAAAGGGTGAATTGAAAAAAAA	1281 CTAĞCTIGATGAÇIGATAĞCĞIĞAĞTITĞĞAAĞATICTAAAAAĞCĞITTĞAATĞCĞATTAAAĞĞTTTĞATTITÇATAA AAATAAĞĞTTTĞATTITÇATAA AAATAAĞĞĞTTTĞAĞĞATTĞCAĞAĞÇIÇAAĞÇÇÇÇTTTĞ AAATAĞĞĞĞTTĞAĞĞATÇAĞĞATÇĞAĞĞĞĞĞĞĞĞĞĞ
HP0377	HP0377	HP0377	нР0377 НР0377

066501			
	1268 VKKEECLFVEELAKUGLAFUTIIDIAH GHSNSVIEMIGRIKTHLPETFVIAGNVG TPEAVRELENAGADATKVGIGPGKVCI TKIKTGFGTGGWQLAALRVGAKARK PIIADGGIRTHGDIVKSIRFGATMVMIGS LFAGHEESSGETKIENGIAYKEYFGSA SEFQKGEKKNIEGKKIWIQHKGSLKDT LVEMHQDLQSSISYAGGRÜLEAIRKVD YVIVKNSIFNGDAI	1270 VEKDSKKDACGFIYEISEFMKAYTALLK KQDRYVYLLRYLPSRYWASILTTALYV KYPDFDALKKLLVSYYYQTWIAGGTITR IKQTSINIIKNVKSNKSVETIKELILNSIDS YNTFDQYLYNLWDSSSVYHSKWWRPV LALANYFMADEEKPHFIAMDAETQVEH ILPQTPKRGSQWNADFDKEKREEWYN NIANLTLKRKKNAHALNGIJFDEKRKIY GGKDTSKVISCYDITKELYSINYRKWNE KSLQERYKSLYNTITPVLHIEG	
		127	<u> </u>
1265 CTATATTCTTTTATGCTACAATTATTTTTACAAGGGTAATTTATCTATTCTCAGGTAAGGGAAGGGAAGGAA	1267 GAGGAAAAGGAAAAGGAAGTITITIGIAGAAGAGTTGGCCAAGCAAGGATTAGCGCCAGACTATATCACGATCGAT	116aC 1269 AGGTGTTCAAAGACAGCAAAAAAGACGCTTGCGGGTTCATGAGATCAGCGAGTTCATGAAAAGCCTATACCGCA TTGCTAAAAAAACAAGACCGATATCTGACGCTTTGAAGCTTTTGGTGTGTTTATTATTACCAAACTTGGATTGCAACT TTGCTAAAAAACAAACCGATTGACGCTTTGAAACACTTATCAAAAAGCTTAAAAGCAATAAGGCTTGAAGCGTTGAAGCGTTGAAACCGCGTTGAAGCGTTGAAACCGTTGAAACCGTTGAAACCGTTGAAACCGTTGAAACCGTTGAAACCGTTTGAAAAGCGAATAAGCGTTGAAACCGTTTAACTTATCATAGCAAATGCGTCGTTTAACCTTTGACAAAAGCAAAGCGCAATTAGCAAAGCGAAACCCAATTAGCGCAAAAGCGCGAATTAGCGCAAAAGCGCGAATTAGCGCAAAGAGAAACCAAGTGGGCTCTTTAGCCCAAAAGAAGAAAGA	1271 TATTITATAACGATGAAAATTITT GGGACTGATGCGTGAGGGGTAAAGCAGGGGTGAAACLCACCCATGTTTTTTTTTT
нР0377	HP0377	HP0377	HP0075

HP0073	1273 TAAAGACGATTTAGCGGAAATCATTTAGCGGTAAGCCCTGGCATGAGGGGCGATGCGCAAGATGTGCAA TTAAACATCGGTCCAAATTGTTGTTGTTGTTGCCCAATCCTTTTTAGAAAAAATCCATAACATGAAGATTTGAA TTAAACATCGGTCCAAATTGTTGTTGTGGGGAAAACGCTTTTTTAGATTTTGCGCCTTTTCCGTTAATCCCCTTTGAA AACGCGCATTTTAAGGGCAACACCACGATTTTTTGCGCTCTCAATTGCTCTATTTTTAGTGAAATCGCTTTGAA AACGCGCATTTTAAGGGCAACACCACGATTTTTGCGCTTTTGCAATTGCTCTATTTTTAGAAATCGCTATTGTGCCAAACCCCTTTGAACATGCTCTATTTTTAGAAAACCGCATTGCCCATTAGCGCAAAACCCATTAGCAAAACCGCTTATTGAATTAGCGAAAGCGATGCATTAGCGCATTAGCGCATTAGCGCAAAGCGTTATTGCTTTTTTAGAAAACCGCTTATTGCTTTTTTAGAAAGCGTTATTGCTTATTGCTTATTGCTTATTGCTTTTTAGAAAGCGTTATTGCTTATTAGCGAAAGCGTTAATGCCCCTTATTGCTTATTGCTTTTAAGAAAACCGCTTATTTTAGAAAGCGTTAATAGAAACCGCTATAATAAGCGCAAAAGCTTAAGCGCTTCAAAAAGCTTAAAAGCCTTATTAGAAAAGCTTTAAGAAAACCGCTTTTTAAGAAAAGCTTTTAAGAAAGCTTTTAAGAAAAGCTTTTAAAAAGCCTCAAAAAGCTTTAAAAAGCCTCAAAAAGCTTTTAAAAAGCCCTTATTAAAAAGCCCAAAAACCGCTTTTTTTT	1274 KDDLAEIMLLAVSPGMMRGDAGDVGL NIGPNCKLRITSQSFEKIHNTEDGFASR DMHIVVGENAFLDFAPFPLIPFENAHFK GNTTISLRSSSQLLYSEIIVAGRVARNE LFKFNRLHTKISILQDEKPIYYDNTILDP KTTDLNNMCMFDGYTHYLNLVLVNCPI ELSGVRECIEESEGVDGAVSETASSHL CVKALAKGSEPLLHLREKIARLVTQTTT QKV
HP0073	1275 AGCAAAAGGATAAATCTTACAAGGTTGTTGAAGAATACCCCAGCTCAAGAACCCACTTATAGTGCGCGATTTGCAAGAAGGATAAAGGGTTGTTGCAAAATTGCAAAGAATACCCCAGCTCAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	1276 OKDKSYKVVEEYPSSRTHIIVRDLQGN ERVLSNEEIQKLIKEEEAKIDNGTSKLV OPNINGGSNEGSGFGLGSAILGSAAGAI LGSYIGNKLFNNPNYQQNAQRTYKSP QAYQRSQNSFSKSAPSASSMGGASK GQSGFFGSSRPTSSPAVSSGTRGFNS
HP0073	1277 CACCECTCAAACCCTTTTAAACCATGCTAAAAACTCCAAAGCTTGAATGGGGTGGAGATTGTAGGGTTGGAGGTTTTTAAACCATGCTAAAAACTCAAAGCTTGAATGGGGTGGGGGTTGGAGGTTTTTAAGGTTTAAAGTGAAAACTCAAAAACTCCACGAAGCCACGAAGCCTGCCACTTTACAGGGGGGGG	1278 TAÓTLLNHAKKTÓSLNGVEÍVGLEHLĎ KVIYLDÓAPIGKTPRSNPÁTYTGVMĎEI RILFAEGKEAKILGYSASRFSFNVKGG RCEKCGGDGDÍKIEMHFLPĎVLVÖCĎS CKGAKYNPÓŢLEIKVKGKSIADVLVMS VEEAYEFAKFPKIAVKLKTLMDVGLG YITLGQNATTLSGGEAGRIKLAKELSKK DTGKTLYILĎEPTTGLHFEDVNHLLÖVL HSLVALGN
нР0762	1279 GCATTGAAATAGACCAGCAAAGCGTGGTTGTTAGCGGTAAAACCCCTTCTAAAGAAGCCTTTTATTTTTGTTTCAAA ACAAACTAAACCCCATGTTTGATTATTCTAGGGCGGAATTTTCCCCTTAAGCGATGGGTGGTTTAATTTTGTCTCCA CCAACTTTCTAATTCCTTACTGATAAAAATCCGGAGTCTATTAAATGAAGCCATTGCATTTTCACACCTGGACAGA GAGCAATCAGGCGATGTGGGGTTTATCATTAAAAAACCTCGTTTTTTAGGGGTTTTTTCCTTATTGGGTTGGTT	1280 IEIDQQSVVVSGKTPSKEAFYFLFONKL NPMFDYSRAEFFPLSDGWFNFVSTNF SNSLLIKNPESIK
HP0762	1281 TCACGCTGTTAGGGTTTTTAGAAAAAACCATATCCCTCAAAAACTCTACTACAACCTGAGCTCTCAAGATAAAGAATT GAGCGCTGAAATTCAAAGCAATGTAACCTACACCTTAAGAGACCGCTAACAACACCGCTCATTCAAGCCTTATCC CTATAAGCCAGGATTTACAAATCCATATTACAAAAAGGGGAGGATTATTTTTAGACTTTATCCCCATTATCTTCAC TCGTAAAGCAAAAAAACCCCTTCTTTCTTTACAAAACTTCGCCCTATCAAGATATTATCAAAGCCACCAATGACCCCTT	1282 TLLGFLEKNHIPÖKLYYNLSSGÖKELSA EIQSNYTYYTLRÖANNTLIQALIPISODL QIHIYKKGEÖYFLDFIPIIFTRKEKTLLLS LQTSPYGÖIIKATNÖPLLANGLMNAYKK

	TTAGCCAACCAATTGATGAACGCGTATAAAAAAGCGTGCCTTTTAAACGCCTAGTGAAAAATGATAAAA	SVPFKRLVKNDK
HP0762	1283 TGTTTGAATGGGGGGGATAGCATTTATCAAACAATCCATTTATGAGGGGAAGCGCGGAAATTAAAAACGCCGC	1284 FDVNRGDSIYIKQSIYEGSAKLKRRMIE
		SLSANKQRDFMGWMWGLNDGKLRLD
	CTTCGCCTTTTTTGAAAACGGATTTTTCTACCCATGACGCTAAGCTTCATTATAAAGTCAAAGAGGGGGATCAATACAAAACA	L KTDESTUDAKI LIXIXI KATIONALI
	GGATTTCAGACATTTTAATAGAGATTGACAACCCGGTAGTCCCCTTAAAAACCTTAGAAAAAGCGCTTAAAGTGAAAA	
	GGAAAGATCTCTTTAATATTGAGCATTTAAGAGCGGATGCGCAAATTTTAAAAACCGAAATCGCCGATAAGGGTTATG	
	GGCGATTATGGTGTATATCAATTGATGATGAAGATGAAAAAAAA	
	COCCATAGGATAGGATAGAGGGAGGT	NORTSDRIIRRELLLGPKDKYNLTKLRN
-	CTCTAAAGTCAAAATTGAAGAAAAAAGGGTTAATAGCTCACTCA	SENSLRRLGFFSKVKIEEKIVNSSLMD
	CTGGGCAGTTGCAATTTGGGTTAGGCTATGGCTCTTATGGAGGGCTTATGCTTAATGGGAGCGTGAGGGAAAA	LLVSVEEGK GOLOFGLG*GSYGGLM INGSVEEDN EGTGOSMS VANIATO
		GGRSYPGMPKGAGRMFAGNI SLINP
	CCAMMAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	RIFDSWYSSTINLYADYRISYQYIQQGG
	49909 W. I. I. DOWN TO TO TO TO TO TO TO TO TO TO TO TO TO	GFGVNVGRMLGNRTHVSLGYNLNVTK
		LLGFSSPLYNRYYSSVNEVVSPRQCST
		PASVIINKLSGGKTPLQPESCSSPGAIT
		NTODOVEDBNOVIESSYATIAS INDUSTRI
		TI NSWNGI GGNVRNTKVVSKEAAVHH
		LOKYLLIDLIARFKTOGGYIFRYNTDDY
		LPLNSTFYMGGVTTVRGFRNGSVTPK
		DEFGLWLGGDGIFTASTELSYGVLKAA
		KMRLAWFFDFGFLTFKTPTRGSFFYNA
		PV I JANFKDYGVIGAGFERATWRAST
		GLUIEWISPMGPLVLIFPIAFI-NQWGDG
		GTRF
79/041	1283)CCGA1AAGGGA11AAAAAAGGTGTTCAAAGACAGCAAAAAAGACGCTTGCGGGTTCATCTATGAGATCAGCGAGTTC	1286 DKGLKKVFKDSKKDACGFIYEISEFMK
		AYTALLKKODRYVYLLRYLPSRYWASI
	ACCAAACTTGGATTGCAGGAGGCACGATCACGCGCATCAAGCAAACCAGTATCAAACATTATCAAAAAAGGTTAAAAAA	LITELYNKTPOPDALKKLLVSYYQIW AGGTTD!KOTSINIIWNVSNIVSYGTIKE
	AATAAGAGCGTTGAAACCATCAAAGAGCTTATATTGAATAGCATCGACTCTTATAACACCCTTTGATCAATACCTCTATA	CILNSIDSYNTFDOYLYNING CONTROL OF THE
	ACLIAIGEBALAGCIONTITATCENATAGEAAATGEGTGCGTCCTGTCTTAGCCCTAGCTAATTTCATGGCG	KWVRPVLALANYFMADEEKPHFIAMD
	GGCAGTCAATGGAACGCGGATTTTGACAAAGAAAAAAGAGAAAAATGGGTAAATAATAATTATAAATTAATTAAATTAAATTAATTAATTAAATTAATTAATTAAATTAATTAATTAATTAATTAAATTAAT	AETQVEHILPQTPKRGSQW/NADFDKE
	AAGCGTAAAAAGAACGCGCATGCTTTAAACGGGGATTTTGATGAAAAAAATTTATGGAGGCAAAGAACACGAG	FDEKRKIYGGKDTSKVISCYITKELYS
	COATACAATATATATATATATATATATATATATATATATA	NYRKWNEKSLQERYKSLYNTITPVLHI
	TGATCTAGAATGATTAAAGATTGCCAAGCATCAAAACAA	EGGEODFEDDFDLE
HP0156	1287 TGGATTTGCCCACGAGGGCTAGGATCTTAAAATCACGCTCACTTACCAAGATATTGATGGCTCTATCCATTCTA	1288 DLPTSARILKOITLTYQDIDGSIHSKVVG
		IDKGIDWHYPLKLSQHTLDPAAFEKR

		•
HP0452	1289/1GAAGCAAAGATTATTGCGAATAAAGAGGGTAAAAACACCACTCCTTCTATTGTGGCTTTTACAGATAAGGGCGAGAT TTTAGTGGGCGAGAGCGCAAAAGACAAGCGGTAACCAACC	1290 EAKIIANKEGKNTTPSIVAFTDKGEILVG
	GTTTGATGTTAATGAAGATAAGGCTAAAGAAGCGCTTGCCTTATAAGATTGTGGATAGGAATGGGGCT	DKAKEAEKRLPYKIVDRNGACAIEISGK
	IGCGCGATTGAGATTTCGGGTAAAGTTTATACCCCTCAAGAGATTTCAGCCAAAATTTTAATGAAGCTCAAAGAGAC GCTGAAAGTTATTTGGGCGAGGGGTAACGCAAGGGGTCATGAGCGTTAGAGGTTATTAAAGGAGAAGAAGAAGAAGAAGAAGAA	VYTPQEISAKILMKLKEDAESYLGESVT
	AAGCGACTAAAGAAGCCGGCATTGCAGGGCTTAATGTTTTAAGGATCATCATTAAAAAAAA	MINISTER AL ACCI DICECTION
	GCTTATGGCTTGGATAAAAAGAGAGCGAAAAATCATGGTTTATGATTTGGGTGGG	DLGGGTFDVTVLETGDNVVEVI ATGG
	TTTAGAAACAGGCGATAATGTCGTGGAAGTTTTAGCCACAGGGGGCGATGCGTTTTTAGGGGGGGG	DAFLGGDDFDNRVIDFLASEFKSETGIE
	AlceleleleatieAltrapercontrape	IKNDVMALORLKEAAENAKKELSSAME
	TATCACCECCECCT AND AND AND AND AND AND AND AND AND AND	TEINLPFITADATGPKHLVKKLTRAKFE
		SLTEDLMKETISKIESVIKDAGLTKNEIS
	TGGTGATGGTGATGTCTCGTATCCCTAAAGTCCAAGAAGGGTGAAAGCGTTTTATTAATAAAGATTTGATT	KSVNPDEVVAVGASIQGGVLKGDVKD
1100452	AAAAAQUSI QAAI IGAI IGAI IGAI IGAI IGAI IGAI IGA	WLLLDVT
11r0432	SOFT SOFT	1292 EVYLDLRDKHERLQQEITELQSKNVRL
	GATGATAGGTTTGGTGGTGTTTTAAGCGTTTTATTGGCTAGAGACAACCCTTTTGAGCCTGAAATCAATTCCAAGAA	
	TTTGCAAGGGGGCTTTAATGGGATCTATGATAGTTATTTTAAAGAAATCCATGTGGATTTGCCCACGAGGGCTAGGAT	
	CTTAAAACAAATCACGCTCACTTACCAAGATATTGATGGCTCTATCCATTCTAAAGTCGTGGGCATTGATAAAGGCCAT	
	1941166CATTAAAACTCTCCCAACACACCTTGATCCAGCCCTTTGAAAAACGCTACCAGATCCAAGA	
	CCTTATAGAATCGTGTGTGACACCACGAGGACCAATTTTGCATAAAATTTATCGCTCCTTTTATAAAAATTTTTAAAAAAAA	
	CTCACATTAAAGTCGGCACCCAAAAGATTATTACCGCATCACTTTTAGACGGGAATACTATTAGACGGAAATACCAGTATCTTTAGACGGAAATACCAGTATCTTTAGACGGAAATACCAGTATCTTTAGACGGAAATACCAGTATCTTTAGACGGAAATACCAGTATCTTTTAGACGGAAATACCAGTATCTTTTAGACGGAAATACCAGTATCTTTTAGACGGAAATACCAGTATCTTTTAGACGAGAATACCAGTATCTTTTAGACGAGAATACCAGTATCTTTTAGACGAGAATACCAGTATCTTTTAGACGAGAAATACCAGTATCTTTTAGACGAGAATACCAGAAATACCAGGAAAAAACAAAAAAAA	
_	AAGAAAAAGGGGGGGTATGAATTAAAATTGAAATAAAAGCATGCAGCATTTAGTCTTAATCGGTTTTATGGGGGAGC	
	GGTAAAAGCTCTTTAGCCCAAGAATTGGCGCTACCTTTGAAATTAGAAGTGTTGGATACGGATATGATCATTAGCGA	
•	GAGGGTGGGCTTGAGCGTGAGGGATTTTTGAAGAGCTTGGCGAAGACAATTTCAGGATGTTTGAAAAAATTTGA	
HP0452	1293 TCATTGATGGGCAAAAAGAAGCGCTCTATGGCGGGATTGCGTGCG	1294 IDGOKEALYGGIACANLLHKNSGITIDIG
•	ATAGATATTGGAGGGGGTAGCACCGAGTGCGCGTTGATTGA	GGSTECALIEKGKIKDLISLDVGTIRIKE
	GOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	MPLUKULEVKLAKAFIUKEVSKLPFKHK NAEČVĆĆTIGAI SKA PROGOVDIOSI
	ATGAAACGCTTTTGTTACCCTATTGATTCTTTGCCATGGCTATGAATAGATGCACATAAAAATTTAGCGTTCATTGAAA	HGYFIDAHKNI AFIFKIVMI KFDOIL RI
	AAATCGTCATGCTCAAGAAGATCAATTACGGCTTTTAGGGGTGAATGAA	GVNEERLDSIRSGALILSVVLEHLKTSL
	GCGTTGATTTATCAGTCGTTTTGGAGCATTTAAAAACTTCTTTAATGATCACTAGTGGGGTGGGGGTGAGAAAGG	MITSGVGVREGVFLSDLLRHHYHKFPP
	GATCGCTTTTTGCCCCATGAAAGCACAGCCAAAAGGTCAAAAAGAATGCGTGAAATTGCGTGAAATTGTTTGAAATTGCCTTAAAA	NINPSCISCEDEFLEMERHSOKVEKECV
,	TTTGCATAAAATAGATGAAA	

·	_				
1296 ILINHAKKTQSLNGVEIVGLEHLDKVIYL DQAPIGKTPRSNPATYTGVMDEIRILFA EQKEAKILGYSASRFSFNVKGGRCEKC QGDGDIKIEMHFLPDVLVQCDSCKGAK YNPQTLEIKVKGKSIADVLNIMSVEEAY EFFAKFPKIAVKLKTLMDVGLGYITLGQ NATTLSGGEAQRIKLAKELSKKDTGKT LYILDEPTTGLHFEDVNHLLQVLHSLVA LGNSMLVIEHNLDIIKNADYIIDMGPDG GDKGGKVIASGTPLEVAQNCEKTQSY TGKFLALELK	1298 CSDSEFEKRVLSLQEEIKKGEII-QAVLS RSFYMECLEGLSAYYHLKLTNPSPYMF YKDSDFILFGASPESALKYNALTNTAEI YPIAGTRLRGKDKQGNIDYDLCSKMEF DLQHDYKERAEHIMLVDLARNI)MARV SKKRYC	1300 KKDACGFYEISEFMKAYTALLKKUDRY VYLLRYLPSRYWASILTTALYVIKYPDFD ALKKLLVSYYYOTWIAGGTTRIKOTSIN IIKNVKSNKSVETIKELILNSIDSYNTFDQ YLYNLWDSSSVYHSKWVRPVLALANY FMADEEKPHFIAMDAETQVEH LPQTP KRGSQWNADFDKEKREEWVNNIANLT LLKRKKNAHALNGDFDEKRKIYGGKDT SKVISCYDITKELYSNYRKWNEKSL	1302 DIKSAKALGIEVKNVSAYSTES/AQHTL ACALSLLGRINDYDRYCKSGEYSQSDL FTHISDIKMGLIKGSOWGVIGLGTIGKR VAKLAQAFGAKVYYSPKDKKIEFYERL SLKDLLATSDIISIHAPLNES	1304 INYKDI PSHSW I SKEMHELVLLAFKUQ KLRK	1306 FQAYAPLMAKICSYQSKFVSAFYLYTQ LKKELKTSKOTLYKLLHALEKQRILFLV PNFENNKTKLYLCDFALPYSLTPSPSLL NVFENMVFLELYKQFPKYELYSHDNGI FILRENSTNKLALIAHAFPTPHFLEKQLL WCHKHGFLNIVVSINAPISATNTPYKH LNFIDFSLDIQSILV
		0		13(<u>.</u>
	1297 TTGTAGCGATAGCGAGTTTGAAAAAGAGTGCTATCCTTACAAGAAGAAATCAAAAAAGGCGAGATTTTTCAAGCGGT GTTGTCGCGCCGCAGCTTTTATATGGAGTGCTTGGAGGGTTTGAGCGCGTATTACCATTTAAAGCTAACTAA	1299 GCAAAAAGACGTTGCGGGTTCATCTATGAGATCAGCGAGTTCATGAAAAAGCCTATACCGCATTGCTAAAAAAACAA GACCGATACGTCTATTTATTGAGGTATCTCCCCTCTAGGTATTGGGCCAGCATTTTAACGCATTGCTAAAAACAA TACCCTGATTTTGACGCTTTGAAAAAGCTTTTGGTGTCTTATTATTACCAAACTTGGATTGCAGCGCTGCCCTTTATGTCAAA TACCCTGATTGCAACCAAACCA	1301 TGGATATAAAAAGCGCGAAAGCTTTAGGCATAGAAGTCAAAAACGTGAGCGCTTATTCTACAGAATCCGTAGCCCAG CACACTTTAGCGTGCGCGTTGTCTTTGTTGGGGGAGGATCAATGATTACGATCGTTATTGCAAAAGCGGGGAATACAG TCAAAGCGATCTTTTACGCACATTAGCGATATTAAAATGGGGCTTATTAAAGGGAGTCAATGGGGGGGTTATTGGTTT AGGGACTATCGGTAAAAGAGTCGCCAAGCTCGCTCAAGCTTCGGGGGCAAAGGTGGTGTATTATTCCCCTAAAGATA AAAAAGAAGAAGATTGAGTTTAAAAGGTTTAAAAGGTTTCGCGAAAGGTGGTGTATTATTCCCCTAAAGATA AAAAAGAAGAAGGTTTGAGTTTAAAAGGTTTGCTCGCTCG	1303 GAATTATAAAGACGCCGTCGCATTCTTGGACTTCAAAAGAGATGCATGAATTGGTGTTATTAGCTTTCAAGCAGCA	1305 TCTTTCAAGCCTTACGCCCCTTAATGCCTAAAATCTGCTCGTATCAAGTTTGTGGTTTTGTAGGCTTTTTTTT
HP0452	HP0452	HP0452	HP1072	HP1072	HP1072

1104070	1207 1 100		
7/01/41	11G	1307 ABB 16 AAAA GACGCCAAAAA GACGCTTGCGGGTTCATCTATGAGATCAGGGAGTTCATGAAAGCCTATACCGCAT	1308 VFKDSKKDACGFIYEISEFMKAYTALLK
	၁၁၅	GCCCTTTATGTCAAATACCCTGATTTTGACGCTTTGAAAAGCTTTTGGTGTGTTATTATTATTACAAACTTGGAGTTGCAG	KQDRYVYLLRYLPSRYWASILTTALYV (KYPDFDA) KKI I VSVVXXATMIAGGTITB
	GAG	GAGGCACGATCACGCGCATCAAGCAAACCAGTATCAACATTATCAAAAACGTTAAAAAGCAATAAGAGCGTTGAAACC	IKOTSINIIKNYKSNKSVETIKEI II NGIDG
	A C	A L CAAAGAGE TATATT GAATAGGAT COATCOTTATAACACCTTT GATCAATACCTCTATAACTTATGGGATAGCTCTT	YNTFDQYLYNLWDSSSVYHSKWVRPV
	2 5	TATTICATESCAGATESCAGA COLOTION OF THE TATTICATESCAGAT GAGA ACCCCATT	LALANYFMADEEKPHFIAMDAETOVEH
	¥ 2	PARTITION OF THE STATE OF THE S	ILPQTPKRGSQWNADFDKEKREEWVN
	8 <u>5</u>	GCATGCTTTAAAGGGGGATTTT	NIANLTLLKRKKNAHALNGDF
HP1072	1309 GGA	1309 GGACCCTCCTTATAACATTTCGGTTAAAAACAATTTTCCCACCCTAAAAGAGGCTAAAAAGGCAATAGATTTTCG	4240 CODY TOTAL WALL CONT.
	GGA	ATGGGATAAAAATTTCAAGCTTTTAGAATGGATCGCACGCTACGCCCCCTTAGTCGAATCCAAACGCTTCCAAA	MOKNEKI EMIABYADI WIDHOOMI
	ATT.	TIATTITITICCTCTTACAGGTTTATAAAGCTATATCGCTGATTITITAGAAGAAACGGCTTTGTGGTCAAAGACTTTATC	CSYRFISYIADFLEENGFVVKDFIQWVK
1101072	134	1344 CACCA ACT CATA LOCACIA COLORA	
2/01/4	990	GGGTGCGGATGATTAGTGAGCGTGATGATTGAAAAAAAAA	1312 ASVLSALLLVGLGAAPKHSVSANDKRM
	AAA.	AAATCTAGGGAGGATTTAAAAATGGTGGTTATTGAAGATCGGGACACTAAATAATAATAATAATAATAATAATAATAATAATA	CONLVSVIEKOTNKKVRILEIKPLKSSO
	GAT	GATGGTAATTTAATCATAGGGGTTAAGGAACATATTCTTTAGGAATAAAGCGGATGATGATGATGATGATGATGATGATGATGATGATGAT	DLKMVVIEDPDTKYNIPLVVSKDGNLIIG
	AAT	AATCAAAAAGTTCAAGCTCTTAACGCCCAACAAAATAGCGCGAAATTGAACTTTTAATGAATATAATAAATA	ATOOMS AND MAISNESS AND VOLVAE I NOKYOALN
	GAT	GATTATECGATAGAGTTGCCCTCTACTAACGCTGCAAATAAGGATAAAATCCTTTATATTGTCTCTGATCCATGTCC	NI CHI LI TOTO CON CONTROLLA CONTROL
	ξ C C	CCACATTGCCAAAAAGAGCTCACTAAACTTAGGGATCATTTAAAAGAAAACACCGTGAGAATGGTCGTGGTGGTG	DHI KENTYDANAACHACHACHACHACHACHACHACHACHACHACHACHACH
	GCT	SGTCAATTCAGCTAAAAAAGCGG	IOFEMAKABARGASV
	GTGGA	- 3	Approved
HP1072	1313 ATT	1313 ATTTATGCATCACTCACTGCCCTATAATTTGAGTATTGAATATCAAGGGAGTGATGATTTAGGGCTTATGATGATTA	1314 LCITSLPYNLSIEYQGSDDFRAYDDYLN
		THE CAN I BE I BY AND THE COLUMN TO THE COLU	WCKNWLKNCYFWGKEQARLCLNVPL
		THE STANDARD OF THE SECRET SEC	DTNKHGKQSLGADIIAIAKECGWKYQN
		ACCHAMMINGENTIALTIGGANIGAAAGCAATATICAAGACGCACCGCTTGGGGGGAGTTGGTTGCAAGCTAGCGG	TIIWNESNISRRTAWGSWLQASAPYAI
2000		AT GOOD TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL TOTAL TO THE TOTAL TOTAL TOTAL TO THE TOTAL	APVELIV
Z/0L4H	ASI CEL	1315 I CAAALCCI II I AAACCAI GOTAAAAAACT CAAAGCTTGAATGGGGTGGAGATTGTAGGGTTGGAGCATTTGGATAA	1316 OTLLNHAKKTOSLNGVEIVGLEHLDKVI
	AGIO	AGITALITATTACAGGAGCCCCCCATAGGCAAAACCCCACGAAGCAACCACTGCCACTTACACGGGAGTGATGGATG	YLDOAPIGKTPRSNPATYTGVMDEIRIL
	AGG.	AGGAGGGGGGT GCGAGAAATGCCAAGGCGATGGGGGACATTAAAATTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATTAAAAATGAAATTAAAAATGAAATTAAAAATGAAATTAAAAATGAAATTAAAAATGAAAATTAAAAATGAAATTAAAAATGAAATTAAAAATGAAATTAAAAATGAAATTAAAAATGAAATTAAAAATTAAAAATTAAAAATTAAAAATTAAAAATTAAAA	FAEGKEAKILGYSASRFSFNVKGGRCE
	CAA	CATGCGATAGCTGTAAGGGGCGCTAAATACAACCCCCCAAACTTTAGAAATCAAGGGCGCAAATCAATAGAAA	KCUGDGDIKIEMHFLPDVLVQCDSCKG
_	TGT	TGTGTTGAACATGAGCGTGGAAGAGGCCTTATGAATTTTTTGCTAAATTCCCTAAAATGCCCGTGAAGGTTAAAAAACGCT	AYEEEAKEDKIAVKI KTI MOVOI OVITI
	TATE	TATGGATGTGGGCTTAGGCTATATCACTTTAGGGCAAAACGCTACGACTTTAAGTGGGGGGGG	GONATTI SGGFAORIKI AKFI SKKNTG
	TAN)	AAATTAGCTAAAGAATTGAGTAAAAAAGACACAGGCAAAACCCCTTTATATTTTAGATGAGCCTACTACCGGTTTGCATT	KTLYILDEPTTGLHFEDVNHLLDVI HSI
	3	I I GAAGACGI GAATCATCTI TI ACAAGI CTI GCATI CITI AGI GGCGTI AGGCAATI CI ATGCI AGI GATI GAGCATAA	VALGNSMLVIEHNLDIJKNADYIJDMGPD
3.0	ATTI TO	TTAGACATTATCAAAAAGGCTGACTACATTATAGACATGGGGCCTGATG	
HP10/2	131/160	16116CCICTCT111GATAAGCGGTTGCAGTCTCTTTAAAAAGCGTAACACTAACGCCCAGCTAATCCCCCCTT	1318 LVASLLISGCSLFKKRNTNAQLIPPSAN
) L	COLOR CONTRACTOR CONTR	GLOAPIYPPTNFTPRKSIOPLPSPRLEN
	200	GCCTAATAATGCATTGAATTGAACGCCCGTCATGGGCATGGGCATGGCCTCCCACTAACGCTATCCAATTCAACGCCCCATTCTAACGCCCCATTCTAACGCCCATTCAACGCCCATTCAACGCCCAATTCAACGCCCATTCAACGCCCATTCAACGCCCATTCAACGCCCATTCAACGCCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACGCCAATTCAACAACGCCAATTCAACAACAACAACAACAACAACAACAACAACAAC	NDOPVISSNPTNAIPNTPILTPNNVIELN
	1299	GGCTCTAGCCAAGCGGGCGGCCTATCGTTGATGGCTACCGCCAGTTGGAAAAAATGTATAAGATTAAGAAAAAAAA	AWAWAWLQNPFHPLKPWL
	СТС	GCTCAAGACACCGTCAAAGACATGGTTTTACAAAATTCCGTGATTAAAACGAGGGTCAACGCTCTCGTTCGT	
	GAAA	GAAATCACTGAGACCATCTATAAAGACGGCTTGTGTCAAGTGAGCATGGAGCTTAAATTAGACGGCAGGATTTGGTA	
7	TCGT	NTITIGAGCGGAGCGAGAGGATAAACCCTCTTACTCTATAATCATGCGGGTATTTTAGAAGTGCTTTTTATA	

4
2

HP0608	1327/TGAAACTITTAGCGCTCTCTTTAGGTAAAGCCCCTTTGAGGAGTTTGAATTTAGAGGGGTATTTTAACCAGCTTTCTAA	1328 KLI ALSLGKAPI RSI NI FGIFNOI SNAA
	TGCGGCCTGGAGCGGGTAACAAGCCCCTATGAATTAGAATGGCTTAGAATGAACGAAGTGGCTTTAAAAATGCGAGAC	WSGNKPYELEWLRMNEVALKMRDHF
	TATTGGATAGGTCAAAAAAAAAAAAAAAAAAAAAAAAAA	PSIDFIDKFPRYLMOLIPEFDNIRLLDSS
	(TITABATI TITTABATI CONTINUE C	KTRFGAYLGTGGYTQMPGASYVNFNA
	GCACTCATATTGGGGGAAGGGGGAAGTGTGAAGAGGGGGGAATTTATAAAGAGGGGGAATTTATAAGAGGGGGAAGAGGGGGG	GAMGVCMNEGRISSSVVVGAGTDIGG
	ANATECTIFICATION OF THE PROPERTY OF THE PROPER	GASVLGVLSGGNNNPISIGKNCLLGAN
	TACTACE CONTROLLED TO THE CONT	SVTGISLGDGCIVDAGVAILAGSVIEIEE
	ATECTOR COGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	NEFKKLLEVNSALEKHANNLYKGKELS
	AGCIGATIFICITITA GEAGGGGGGGGGGGAACH I CUCHAAAAAA I GEGGGGGAA I GGAA I GAA I G	GKNGVHFRSNSQNGKLIAFRSVKKIEL
	AAGTTGTTATTG	NONLH
HP0608	1329 CAATCCTTTGCCCCCTATTGAAAACAAACAAGAAAAGAA	1330 NPLPPIENKÖEKKEKKILIIGSGPNRIGÖ
	CATICUS I CASICIONE I I I I I I I I I I I I I I I I I I I	GIEFDYCCVHASLALKDLNIKSVMFNC
	THE CAN I COMI I COM I COM I COM I COM I COM I COM I COM I COM I COM I COM I C	NPETVSTDYDTSDTLYFEPIHFECVKSII
	I GAGI GCGI GAAAAGCA I CCAAAGGGAGGGAGGGGATTATCGTGCATTTTGGGGGACAAACCCCTTTA	QRERVDGIIVHFGGQTPLKLAKDLAKM
	ACCOUNTY THE STATE OF THE STATE	QAPI GTPFKVIDIAEDREKFSLFLKELDI
	AGCTTARECTARTECTARTECTARTECTARTECTARTECT CARGED AGCT CARACTEG CONTRACT CATES A CONTRACT CAT	KOPKNGMAKSVDEAYSIANVIGFPIIVR
	ANTITY CONTROL OF THE	PSYVLGGQHMQILENIEELRHYLESVT
	CONTROL TO A TANK TO THE A CONTROL TO TH	HALEISPKNPLLIDKFLEKAVELDVDAIC
	CECTICIONE I PARTAMANA PROPERTIES I PROPERTI	DKKEVYIAGILOHIEEAGIHSGDSACFIP
	A CONTROL OF THE ACCOUNT OF THE CONTROL OF THE CONT	STLSPEILDEIERVSAKIALHLGVVGLLN
	TATCHE LANGUE TO THE MET IN THE MET TH	IOFAVHONSLYLIEVNPRASRTVPFLSK
	MAICCAGAGCGAGCGTTTTT	ALGVPLAKVATRVMVLEĎLKEALKFYĎ
	AAGECTITAGGCCTITGGCCAAAGTGGCCACTAGGGTTATGGTGCTAGAAGAAGAAGCCTTGA	KKNIVGYSKGVYKPKMPHFVALKEAVF
	AGILLAIGAIAAAAA	PFNKLYGSDLILGPEMKSTGEVMGIAR
		SLGLAFFKAQTACFNPIKNKGLIFVSIKD
		KDKEEACVLMKRLVQLGFELCATEGT
		HKALEKAGVKSLKVLKISEGRPNIMDL
		MMINGEISMAINTSOHKSOODAKLIRAS
		VLKNHVSYFTTLSTIEVLLLALEESSKE
	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	DELLALODYLK
HP0232	1331 CCA I GAAAAAAGCGATAAAGCCGCTTTGGGGCTTTATGAATTGCTAAAAGGGGCTACCACTAATCTTAGTTTGCAAG	1332 HEKSDKAALGLYELLKGATTNLSLQAQ
	Section Sect	ELSVKOAMKNHTIAKAMFLPTLNASYN
	Carterior in expensive traceria recentations and in the recentage of the recent of the	FKNEARDTPEYKHYNTQQLQAQVTLN
	ATTTAGAATATAGCCCCCAGAGCGTGTATTTCCAACTCAACAATACAATAATATAACAATATATAAAATATAAAATATAAAAATAAAAATAAAAAA	VFNGFSDVNNVKEKSA I YKSNVANLE
	TIGATOGOTH TOCARARARATA AGACCARAT TOCARA TOCARA A COCOTT	OKY DOWN TOWN THE THIN LAKINIAL
	CCACGATIGATITICAGE AND ANA AGE CECAAGE GAATITICA AGE ATATICA ATATICA CATATITICA AT	CAN LEGIN DINKVINLYUKGLI IIDDL
	TGGAGCAAAACCGCTTGACTTTAGAATACCTTACCAATCTCTGAAAAAAAA	יייייייייייייייייייייייייייייייייייייי
	CTAATTTGCAATTAAGAGAAAGGCAGGATTTAGTTTCTTTAAGGGAGCAGATTTCCGCAATCAGATACCAAACAAGC	DI VSLREQISARYONEN I IDAPINE CENERALI
_	AACTCAATTATTACCCCAAGATAGATGTGTTTGACTCATGGCTTTTTGGATCCAAAAACCGCTTATGCCACAGGGC	DSWLFWIOKPAYATGREGNEYPGOON
	GTTTGGGAATTTCTACCCCGGTCAGCAAATACGCCTGGGGTTACTGCGACTTTGAATATTTTGATGATATAGGCT	TAGVTATLNIFDDIGLSLOKOSIMLGOL
		ANEKNLAYKKLEQEKDEQLYRKSLDIA
	AAAAAAAAAAAAAAAA	RAKIESSKASLDAANLSFANIKRKYDAN
	CGGCCAAICII	LVDFTTYLRGLTTRFDAEVAYNLALNN
		TEVCKANTIFNSGHKIDDYVH

2/000201					
1334 GKTFAETDAEVSEAIDFLEFYPYSLRVL QEQNTKTQFTPKGVGVIAPWNFPVGI SVGTIAAPLATGNRVIYKPSSLSSVTGY KLCECFWDAGVPRDALIYLPSKGSDIS EHLLRDESIQFAILTGGEDTAYKMLKAN PTLALSAETGGKNATIVSKMADRDQAI KNVIHSAFSNSGOKCSATSLLVLEKEV YEDENFKKTLIDATLSLSVG	MASIPKACELVAT LEIN MASIPKANACH MASIPKACH MASIPKAN MASIPKA	1330 NELSOAMMETERITINGS OF THE ACT IN STATE OF	1340 EPNALKUYLKPEELKLY 11.1 KRYL-ASOL MODALFESOSVVACEKGEFKASGRK LLFDGYYRILGNDDKDKLL PULKENDPI KLEKLESNAHVTEPPARYSEASLIKVLE SLGIGRPSTYAPTISLLQN ADYIKVEKK OISALESAFKVIEILEKHFEEIVDSKFSA SLEEELDNIAQNKADYQQVLKDFYYPF MDKIEAGKKNIISQKVHEKTGQSCPKC GGELVKKNSRYGEFACNNYPKCKYYK QTESANDEADQELCEKCGGEMVQKFS RNGAFLACNNYPECKNTKSLKN	ILIKAFNSKNEVLKEETYYSGGGFVY LILKAFNSKNEVLKEETYYSGGGFVY TEKELDNLSEEDGNESIAYDFSSAKELL ELCQKHQKSIAEIVRLRENALKNHPDA TMVKIYHAMLECYDNGANSKERYLPG SLKYTRLAPSIKTRLEKHPTSGKDPLAL IDYISLYARAIAEENASGGKVYTAPTNG ACAVVPS	1344 GVGEGSPDINGGSVDRED SEIGAGDGG LMFGYACKETETLMPLPIHLAHGLTFAL AGKRKONTLPFLRPDGKSGVSVRYEN NKPVSIDTNISTGHSPEVSGKHLKEAVI EEIVYKVLSKEYLHDNIKFFVNPTGKFVI GGPQGDAGLTGRKII
1333 GGTAAGACTTTCGCTGAAACGGACGCTGAAGTGAGCGAAGCCATTGACTTTTTAGAGTTTTACCCTTACAGCTTAAGGCTTAAGGCGTTAAGGCGTTAAGGCGTTAAGGCGTTAAGGCGTTAAGAGGCTTAAGGCGTTAAGGCGTTAAGGCGTTTAAGAGGCTTTAAGAGGATTTCCTAGGCATTTTAAGAGCTTTTGAGCGAATTTCCTAGCGTAAAGGCTTTAAGAGTTTTAAGAGTTTTAAGAGTTTTAAGAGTTTTAAGAGTTTTAAGAGTTTTAAGAGTTTTAAGAGTTTTAAGAGTTTTAAGAGTTTAAGAGTTTTAAGAAAAGATTTTAAGAAAAATGTTTAAGAAAAATGTTTAAGAAAAAA	1335 GGGTGACGATGCGGCTTGTGAGGCTGTGAAAGGCCATTTCAACAACAATGGGGGGTTTAACCAAAAAAATGCGATGGGGGGGG	1337 AAAGAACTGAGCTCTGCGATGGAGACTGAAATCAATTTGCCCTTTATCACCGCGGACGCTACCGGGACGCTACCGGGACGCTACCGGGGCCTACCGGGGCCTACCGGGGCCTACCGGGGCCTACCGGGGACGGGGCCTACCGGGGACGCTACCGGGGACGCTACCGGGGACGCCTACCGGGGACGCGGGGACGCCTACCGGGGACGCCTACCGGGACGCCTACCGGGACGCCTACCGGGACGCCTACCGGGACGCCTACCGGGACGCCTACCGGGACGCCTACCGGGACGCCTACCGGGACGCCTACCGGACGCCGGGACGCCTACCGGACGCCTACCACCGCGGACCGCGGACCGCACCGCGGACCGCACCGCACCAC	1339 AGAGCCAAACGCTTTAAAAGACTACCTTAAGCCTGAAGAATTAAGGCTCTATACCTTAATTTACAAACGCTTTTAGAAGCCTTTTTGAAAGCCTTTTTGAAGCCTGGAAGAATTAAGGCTTGCGAAAAAGGCGAGTTTAAAGCCGGTTGGGAAAAAGGCGAATTGAAAGGCGATTGAAGGCGATTTGAAGGCGATTTTTGAAGGCGATTTTTGAAGAATTTTAGAAACTTAGAGAGCGCATTTACGAAGCGAATTGAAGGCGATTTCTGAAGCGAATTAGAAGCGAATTACGAAGCGAATTAGAAGCGAATTACGAAAACTTAGAGAACTTAGAGGCGATTTTAGAAGAATTAGAAAACTAGGCGATTAGGAAAACAGGAATTTTAGAAAAACGGAATTAGAAAACGGAATTAGAAAAACGAGCGTTTTAGAAAAACGAGAAATTAGAAAAAGCGAAAAAAGCGAAAAAGGAAATTTTAGAAAAATTGAAGGACATTTTAGAAAAATTGAAGCGGAAAAATTGAAGCTGAAAAAAAA	1341 GCTAACCAGCATCATATCCCTTTTGATTATGCTAAAGATTTTGATTTTTGACAAGCAGCAAGCCTTTAACAAGACCAAAACGAGCCTTTTAACAAAGCATTTGATTTTTAAAAGGATTTTAAAAGGATTTTAAAAGGATTTGTGTGGTG	1343 TGGCGTTGGCGAGAGGCCCTGATATTAATCAAGGCCGTGGATAGAGAGATGGCGGGGTTTGGGGGCAGGGGGTCA AGGGCTTATGTTTGGTTATGCATGCAAAGAGACTGAAACGCTCATGCCTTACCCATTCATT
HP0849	HP0849	HP0849	HP0849	HP0849	HP0849

-		
HP0849		1346 APLFSGGIEGIGPRYCPSIEDKINRFSE
_	1 AGE CANADA CONTROL OF THE LAGGE CONTRACT O	
	CACCICITIGCCCCTAGATGTGCAAGAAAAGGTCATCCATTCTATCAAAGGCTTAGAAAACGCGCTCATCACGCGCT	_
_	ATGGCTATGCGATAGAGTATGATTTTATCCAGCCCACGGAATTGACCCACACTTTAGAAAACCAAAAAAATCAAAGGG	_
	CTITATITGGCCGGGCAATCAATGGGACTACCGGCTATGAAGAAGCGGCGCGTCAAGGGCTTATGGCTGGGATTA	GYEEAAAGGLMAGINAVLALKNQAPFI
	ATGCGGTATTAGCCCTAAAGAATCAAGCCCCCTTTATTTA	LKRNEAYIGVLIDOLITKGTNEPYRMFT
	ATITAATCACTAAAGGCACGAATGAACCTTACAGAATGTTTACCAGCCGAGCCGAATACCGCTTGCTT	SRAEYRLLLREDNTLFRLGEHAYRLGL
	ACAACACGCTTTTAGATTAGGCGAACATGCCTATCGTTTAGGGCCTTATGGAAGAGGGATTTTATAAGGAATT	MEEDFYKE
HP0849	1347 CACCCCGGCCGTGTTTTTGAAGAATTAGGCATTAACTATATAGGGCCTATTAATGGGCATGATTTGAGCGCGATTAT	1348 TPGVFFEELGINYIGPINGHDLSAIIETL
	TGAAACCTTAAAATTAGCCAAAGGCTTAAAGAGCCGGTGCTAATCCATGCGCAAAGCGTAAAGGGCAAAGGCTATA	KLAKELKEPVLIMAQTLKGKGYKIAEGR
	AGATCGCTGAAGGGCGCTATGAAAAATGGCATGGGGTGGGGCCTTTTGATTTGGATACCGGCTTGTCTAAAAAATCC	YEKWHGVGPFDLDTGLSKKSKSAILSP
	AAAAGCGCAATCTTATCGCCCACTGAAGCGTATTCTAACACCCTTTTAGAATTAGCTAAAAAAGATGAAAAAATCGTA	TEAYSNTLLELAKKDEKIVGVTAAMPS
	GGCGTAACCGCGGCGATGCCTAGCGGCCACAGGATTAGACAAACTCATTGACGCTTACCCTTTTGCGCTTTTTGATGT	GTGLDKLIDAYPLRFFDVAIAEQHALTS
•	CGCTATCGCTGAGCAACACGCTTTAACTTCTAGCAGCGCTATGGCTAAAGAGGGGTTTAAACCTTTTGTGAGCATCT	SSAMAKEGFKPFVSIYSTFLQRAYDSIV
	ATTCTACTITITIGCAGAGGGCTTATGATTCTATTGTGCATGACGCTTGTATTTCTAGCTTGCCGATTAAATTAGCCAT	HDACISSLPIKLAIDRAGIVGEDGETHQ
	TGACAGGGCTGGGATTGTGGGCGAAGATGGCGAGACGCACCAAGGGCTTTTAGACGTGTCGTATTTGCGCTCTATC	GLLDVSYLRSIPNMVIFAPRDNETLKNA
-	CCTAACATGGTCATTITTGCCCCACGAGACAATGAGACTTTAAAAAACGCCGTGCGTTTTGCCAATGAACACGATT	VRFANEHD
HP0849	1349 GGCATGCCTGTGATTGAGGGCAGTGATGGGTTGCTTAAAAGCTATCAAGAAGCTGAAGAAATCGCTGATAAAATCGG	1350 GMPVIEGSDGLLKSYQEAEEIADKIGYP
-	CTACCCTGTCATCATTAAAGCAGCCGCTGGTGGGGGCGGGAGAGCGATGCGTGTGTGT	VIIKAAAGGGGRGMRVVGDKSKLKNLY
	AAAAACCTTTATTTAGCCGCAGAAACGGAAGCTTTGAGCGCGTTTGGCGATGGGAGGCGTGTATTTAGAAAAGTTCAT	LAAETEALSAFGDGSVYLEKFINKPKHI
	CAACAAGCCCAAGCACATTGAAGTCCAAATTCTAGCCGATAAGCATGGCAATGTCATTCAT	EVÓILADKHGNVIHVGERDCSVORRÓ
	GCTCGGTGCAAAGACGCCAACAAAAGCTCATTGAAGAAACCCCGGCAGTGGTTTTAGAAGAGGGCGTGCGT	OKLIEETPAWLEEGVRERLLETAIKAA
	GTTTGCTAGAAACAGCGATCAAGGCCGCTAAATATATCGGCTATGTGGGGGGGG	KYIGYVGAGTFEFLLDSNMKDFYFMEM
-	TCTAACATGAAAGATTTTTATTTCATGGAGATGAACACTCGTTTGCAAGTGGAACACCCATTAGCGAATGGTGAGC	NTRLQVEHTISEMVSGLNLIEWMIKIAQ
= =	GGGTTAAACCTCATTGAGTGGATGATTAAAATCGCTCAAGGCGAAAAATTGCCCAAGCAAG	GEKLPKGESFSLKGHAIECRITAEDPK
	GGGCATGCGATAGAATGCCCGCACAGATCCTAAAA	
HP0849	1351 AGGAACGCAAACTAAAGAAGAAGTCATAACCACCCAAAAAATCTATGAAAACCCCCTAACCACACCCACAAACTAAAG	1352 GTOTKEEVITTÖKIYENPLTHPÖTKEÖP
	AACAGCCTAAAGAACAAAATAAAAGGGGATACGGCCACCACCACAAAGCGGTTACGGAAAATACTACATACCCCAAAGC	KEONKSDTATPQSAYGKYYIPQSTILK
_	ACCATITIAAAAAATGCAACGGCTTTATTCACCACGGACAAGATGGCTTAACTTTTATTCTCAAAACCCTG	NATALFITDKIENGLIFYSONPVYANM
-	I G A I GCGAA I A I GGGAGCGTAACCATACAAACTTTCTGCCTTATAATTTAAACAATGTTGAACTGAGTTT	VNGSVTIONFLPYNLNNVELSFKDAGG
-	I AAAGAGG CAAGGG GG CAAI I I AGGCG IGA AGAGACCAI CCCI AAACAAI I ACCT I GCCTG	KVVNLGVIETIPKOSOITLPASLFNDSEF
	CARGCITETTARTERITCAGATTTEGACCAGCTGATACCAACAACAACTTCAAGCCACCACTTT	EQADSFNYQQLQATATQFSDANTQSL
-	ICTERACECTARGECTARGETTER ICARARGETTER GARACEC	FOKLSKITTNVTMSYENADTNNFKGNC
	CCATACCACACTITIAAAGG AATTGCCATGATTGTGTGTGTGTGTGCCCCACACCCCCACACGCACACCCACAC	
	ATCAGGETT TETAGGCCTAGGGTATGAACTT GATGATGATGGTAATCTGGGGGATAGAAGCTTCTGCCTTAAATC	
	CTGAAAAATTGTTTGGTAAAACTTTGAACAAAGTTGATATTGTGGAATTAAGAGACATTATCCATGAATTTAGCCACAC	LRDIMEFSHTKGYTHNGNMTYQRVRL C
	IAMAGGCIAI	COENGGAIQECEGGKEELV

HP0849	1353	1353 AGAGCTAGAAAAGTGCATCAAATTTTAGATAACGCTAATTCTTTGTGCCTAAAATGCAATTGCATAAAGCTTTAGAG	1354 EL EKVHÖLL DNANS FVPKMOLHKALFF
		GAATTGTTTAATGTTTTTTTTAAACAAACTCATCGCTAAAGAAGAGGCCATGGGTTTTGCACAAAAACAACTAGAAAAACTAGAACTAGGGTTTTGATGCGTTTTGATGC	LFNVYDFLNKLIAKEEPWVLHKNNESE KI FALLSI JANALI OSSELI VAENDKSA
		CAAAGAGCGCTGTGAAATTAGCGAATGCTTTCAACACAGAAATCACGCCCGATAATTACGAAACGCTTTTTTAAAGCTA	VKLANAFNTEITPDNYEIZFFKAKKLQD
		AAAAATTACAAGATATGATTTTACAAGACACCGAGCCTTTATTTTCCAAAATGGAGAAATTGAAAAGACGGAAAAAG	MILADTEPLFSKMEKIEKTEKAGEASPE
		CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	KNEKEKKDAKEKAPLKQENYIGIEDFK
		CIATALCECCATTERECATTICAAAAAAGICAATTIACAAAAAGICECCATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	KVEIKVGLIKEAORIEKSNKLLRLKVDL
		TGAGCCTGAAAGCTTGGTGGGTCAAATGGTGTGCGT	GEGRLRUIISGIALDYEFESLVGOMVC
HP0849	1355	1355 AAGGGAATTAGAGGGAATTTTAGCCCCAAAAAGAGAACGCAGAACAAAAATATAACACTCTTTCAGTCAAAAATAAGCA	1356 RELEGILACKENAECKYNTLSVKNKOL
		ALI AGAAGCTGAGTI AGATATGCTTAACGAAAAATTTGAAAAACTGAAAAATTAGTATGCTGGGGTAGAGGATTTTGA	EAELDMLNEKFEKLKNNYAGVEDFEK
		AAAACGCCAAAAAATATCAAAGAACAAATTGTAAAAACCAACC	ROKNIKEQIVKTNPKVL(3APSNEVEEL
		AGAATTAGCGTTTTAAAAAAACCACCTATATAGCAAGAGTTCAATGTTTTCTATCCAAGCGTTTATTGTATATTATTGTATATT	AFLERIEKGMOEFNVFY PKRLLYMFHT
		GAACTGCCCAAGCTCTATGTGCATTTTGGGGGGTTTTTTTAAGCATTGCTGTTGCTGCGTGACTAATTGCAACTGCAAATTGCAAATAAAT	ALKS I SLSPLSVLSGVSG I GKSELPKL
		AGAATCGTTGATGGGGTATTTTCATGCGATAGAAACAAATTTGATGCGACAGAGTTTTACGCTTTTTATCCAGAC	YEHAIENKEDATER REFIOTTI SNNFE
		CACTTTGAGCAATAATGAAGAACCATACGGCTTAAAAGAAGCGATGAGTATTGTGTTGCTTGATGAAATGAATCTAGC	PYGLKEAMSIVLLDEMN_AHIELYFAEF
	1	CCACATTGAATTGTATTTTGCAGAATTTTTGAGCAAGCTAGAGATTAAGTGCAGTCAAGAAACTAATATCAGCATTAAA	LSKLEIKCSQETNISIKLGTGLT
		CTAGGCACCGGCTTAACT	
HP0849	1357	AACCCCCTAAACCCTAAAACCAAAACCGAAGAATACGACTTGAAAAATGACCCCTATTTGTTAGCGCAATCTAGCCCC	1358 NPLNPKTKTEEYDLKNDPYLLAGSSPL
	~	CTAGACAAATTCAAGCAAACCCAAACGGGCGCGTATATGCGTCTTTTAAAAATTTTTAGACATTCAAAAAAGGCTTTG	DKFKQTQTGAYMRLLKFLDIQKNALDN
	<u></u>	GATAACGCCTTAAGAACGCTTTTTATCCATGAATTAGAGCAGCCCTTAAACAGCGAACAGCAAAATTTAGCCAAAGAG	ALRTLFIHELEQPLNSEQQNLAKELLNE
			PVDKKENFESLCQEIADI-TTHGEYTKRL
		A I ALACCAAACGCC I GAAA I AGI GGAALI I CI I A I GI I A I I AGCC I A I GGAT I I I GGAT A GCAAAGAAA	KLVEFLMLLAYADGILDSKEKELFLDVG
	<u> 1</u>	AGAATTTAACGAGCTTTTTTTTTTTTTTTTTTTTTTTTT	VFLQIDNQDFNELYDNFERFN
		1,000 I	
HP0849	1359	1359 CGCTATCGTGATTTTAAAGGCCACGCCTCCTAAAGGCATAGAGCCTGTGGGTAAGGATTAAAGTCCCCCAAAATGAGGT	1360 RYRDFKGTPPKGIEPVVIXIKVPQNEVIG
	- ·	GALLIGELLITAA IGACGGGG TAAA GGGGGAAA GGGAA TAGACGATTTAT CGCCAGGA	FNDGVKGEVKVNTNELDDFIIARSDGT
	`	SCIENTISSERIACECECACITIST IS TO THE STANDARD STA	PTYNFVYTIDDALMGITDVIRGDDHLSN
		SALICATOR I L'ARCACCCCI AVACAA I CEI I CI II ALAGESCI II GAA I II I AAAA I CCCI AATI II I I I CCATGI	TPKQIVLYKALNFKIPNFFHVPMILNEE
			GCKLSKRHGATNVMDYQEMGYLKEAL
		TOCANGALTICATION ATTACKS AND ATTACKS TO THE GOOD TO THE TOCANGALTICATION TO THE TOCANGALT	VNFLARLGWSYQDKEVFSMQELLELF
	- 	GOCTCAACGC	UTRULNSSPSCFSWERFINWEN
HP0849	1361	1361 GAAAGCAAGATCAAAGAATTITTGAATTITTGCAAAGAAATGAAGTGGAATTTGTGGATTTTAGATTCAGCGATATTA	1362 ESKIKEFFEFCKENEVEFVDFRFSDIKG
		AAGGCACTTGGAATCACATCGCTTATTCTTTTGGGGCTTTAACGCATGCTTAAAGAGGGGGATTCCTTTTGATG	TWNHIAYSFGALTHGMLKEGIPFDASC
		CONTITUE CON	FKGWGGEMSDMILTPDLVRYFIDPFSA
	<u>. r</u>	ACCOUNT ACCOUNTED TO CONTROL OF THE	DVSVVVFCDV TDV TRVC PYEKCPKSIA
		SAGATTETTATOTTEATOCATTAAAATTAAAATTAAAGACGCTTICCAATTACAAGAAGAAGAAGAAATTAAAAAATTAAAAAATTAAAAAATTAAAAAA	DOLKINDAGUGUVAY FGAENEFFIF
		AGGCCGAATGGAATAGGGATAGAAGCTTTGAAAACGGCGTCAATTTTGGGCATAGACCGGGCGAAACAAGGGCGGTTA	BSEENG/NECHROCKOCCCAMING
	<u>-</u> -	TATECCTGTGCCGCCAACGGATACGATGGATATTCGCACAGAAATTGTGAAAGTCTTAAACCAAGTGGGGCTAG	DTMMDIRTEIVKYLNOVGLETFVYHHE
	<u> </u>	AAACTTTTGTCGTCCATCATGAAGTCGCGCAAGCGCAAGGCGAAGTGGGCGTGAAATTTGGGGATTTAGTGGAAGC	VAQAQGEVGVKFGDLVEAADNVQKLK
		<u>GGCTGATAATGTCCAAAAACTCAAATATGTGGTTAAAATGGTCGCTCATTTAA</u>	YVVKMVAHL

HP0849	1363 AAGCAACTGGATAGCACCTACCAAGAGACCAACCAACAAGTGCTCAAAAACTTAGATGAGATTTTTTCAACCACTAGC CCTAGTGCTAATAATGAAATGGGTGAAGAAGATGCTCTAAACATCAAAAAAAGGGGCCATTGCTTTGAGAGGGGGGATTT AGCGTTATTGAAAGCCAATTTTGAAGCGAATGATGTTTTTTCATCTCAGAAGATGTGATTTTCAAAACTTATTATGTCT AGCCCTGAACTTTTAATTAACCTATATGAAAATCAATCCTTAG	1364 KQLDSTYQETNQQVLKNLDEIFSTTSP SANNEMGEEDALNIKKAAIALRGDLALL KANFEANELFFISEDVIFKTYMSSPELL I TXMKINDI
HP0849	1365 GAAGATGATAATATCACGCATGTGAACGACAGATTGATCCTTTGAATATAGAAACTATTGAATTGGAGTTGATTT TAGCGGATATTGCCGCTTTAGACAAAAGGATCGATCGCTTGCAAAAGCCTTAAAAAAGCCTCAAAAGACGTAAAAATTAGCCGATTTAGAATAGCGAAAAGCCTTTAGAATAGCGAAAAACCATTTAGAAAAAGCCTTTAGAATAGCGAAAAAACCAGCGGCGAAAAATAGCGAAAAAAAA	1366 EDDNITHVNDKIDPLNDIETIELELILADI AALDKRIDRLQKALKSSKDAKNLLECAL SLKTHLEELKPAKTFPLNTSEAFLELDK ELRFLSHKKMIYVANVGEEDLNEH AKKVKNHAKEQNSEFVALCAKLEEEM VSMSGDEVKEFLQSLGVEESGLEKTIR LSFKELGLINYFTAGVKEVSWTIKKGS SAPVAAGVIHKDFEKGFIRAETISYDDFI AYKGEAGAKEKGALRIEGKDYNQDGD VLHFRFNI
HP0849	1367 AAAACCACTTTTGAAAACGCAAAAGCTGAATGCAGTTTAGTTTTTTTT	1368 KTTFENAKAECSLVFIINKDFSHAWVKN KELLETFKYEGEGVFLDÖENKILYAGV KEDDVHLLRESACLAVRTLKKLAFKSV KVGVYTCGAHSKDNALLENLKALFLGL KLGLYEYDTFKSNKKESVLKEAIVA
HP0849	1369 TTAAACGATGACGCCCCCATTAAACTAGTGCATTGGCAAAATGCATTAAAAGAAGTCCAACGTCGATTCAAACGGTCCAGTCCAAACGCTCCAGTCAAACGCTCCAGTCAAACGCTCCAGTCAAAACGCTCCAAAACCCAAAACCCAAAACCCAAAACCCTTTTGAAAAAACGCTTTTTAAAAAAACGCTAAAAACGCTAAAAACGCTAAAAACGCTAAAAAACGCTAAAAAACGCTAAAAAACGCTAAAAACGCTAAAAAACGCTAAAAAACGCTAAAAAACGCTAAAAAACGCTAAAAAACGCTAAAAAAACGCTAAAAAACGCTAAAAAAACGCTAAAAAAACGCTAAAAAAACGCTAAAAAAACGCTAAAAAAAA	1370 LNDDAPIKLYHWÖNALKEYÖPÖSNAP ATPPIKAVÖTTLTFETPFNKTPKIMEVE GÖKVIVLKNAKLDSKKTMDFKEASLNA LEMFSYÖNDIYLLSKKAKVELEIQASNS KÖKRLRFLFLPKGFHLAPPPNLKEKS ÖQTNLAÖKDTNEOPÖSPLNTLELKPPL NLSHAYKALAVIAALLLILYVIKKKIVPTÖ GSFSAKÖFKLEISVLGRVDANHKIISIET NKERYLVLLSÖKYGLLLÜKISPKTSKEE LIKEAENNIKNSKLĞNLYAĞKF

DVBUGI	1371]CCCCGATAACGACCCTAATGGAGCATTAATTAATGATTAATTA	SECTATT 1373 DONING NAMED NICE AND SAVE CARACTEC	MAYTOVE
2	TTGGAGTTACTAATCCTTACACAAAGTGGATTATCCGCCTGTGGGTATGTTTGGCGTTTTTCACAAAATACGA		FSONTI
	TACAAAAACACATTGATGAGGGGGGGGGGTTTGCTTTAAAAAAGAGCATAAGGATAATGAAAGGGGGCTTTATTTA	-	FIYKRYL
	GCTATTTAAAGGATTTAAAAACCACGCAAAAAACTTTTGATAGTTTGATATTTAGCGATAATTGTTATGAACCAAGC		NOAATK
	GGCGACTAAAGAACTTTTAAATTTGGGAATGGGAAATATTTACTTATCCAAAAGGCGTAGAATTTATGAAAAAATC		KKIILHST
	ATTCTGCATTCAACCACGCCAAACGAGGCCACATCATCTTAGATTTTTTGCTGGGAGGGGACAACCGTGCATGC	·	MELNA
	GGTGATGGAATTAAACGCAGAAGATAAGGGTAATAGGGAATTTATTT		AYDFCK
	1 GAAAGCGCTTATGATTTTTGTAAGAAGGGTTTAGCGATTAGCGATTAGCATAGGAAAGGGT		DKISOLS
	AAAAGAGCCCCCCAAAAA AAGCCAA I A CAAAAGA AGCGG I I I GGA I I AAGGC I TAAAGI I TATACCTI ACA		NOKEEIT
•	AGACAAAGTGCAAATTATAAACGACAAAGAAATAACGCTTTTTAACCGATCGGATTTAACGCCTTTGACAAAGC		KTLNOA
	CCTAAATTTAGCCCTACAATGCGGCAAAACGCTCAATCAA		EAGEYL
	CGAAGACGCTTACTTTTGTATCGTGTGCGATGAAGAGCGCAAGAGTATTTAGCCAAAAGCAAAAACGAAATGATATT	\TGATATT AKSKNEMIFLDGYEEIDLEAFLNLNASF	NLNASF
	TITAGACGCCTATGAAGAGATTGATTTAGAAGCCTTTCTCAATCTCAACGCTAGCTTTAAAGAGCGTTTAAGCGTGGT	CGTGGT KERLSVVY	-
	GTATTGATTT		
HP0849	1373 CATTGGAGCCCCAGGGAGTGGTAAAAGCACTGATGCAGAGCTTATCGCTAAAAATAACAGCGAAACAATCGCTCATT	GCTCATT 1374 IGAPGSGKTTDAELIAKNNSETIAHFST	TAHFST
	TITCTACCGGGGATTTACTCAGGGCTGAGAGCGCTAAAAAGACCGAGGCGAGGCTTATTGATTG		SOGEL
	CAAGGCGAATTAGTGCCTTTAGAAATTGTGGTAGAAACGATCCTTTCAGCGATTAAAAGCTCTGGTAAAGGGATCATT		GYPRS
	TTAATTGATGGTTATCCTAGGAGCGTGGAACAAATGCAGGCTTTGGATAAGGAATTGAACGCTCAAAACGAAGTGAT		VIEVEV
	CTTAAAAAGCGTGATTGAAGTAGAAGTGAAAAACACTGCTAAAGAAAG		KVFHNR
	GATGATAATGAAAAGGTGTTTCATAACCGCATGCGGGTGTTTTTGGATCCGTTGGGCGAGATCCAAAATTTTACAAG	TTACAAG MRVFLDPLGEIQNFYKNKKVYKAIDGE	KAIDGE
	AATAAGAAGGTGTATAAAAGCGATCGATGGGGAGAGGGGCATTGAAGAGATTGTGGGCGAAATGCAAGAGTATATCTT	'ATATCTT RSIEEIVGEMQEYILSFGN	
_	GTCTTTCGGTAATTAAAATGCACTCTCAAGGAGAATAGCTGTGATTTCTGTTTATATCATTTTAAAAGAAAG	AGTCAA	
	AGGCGTTTGGATACTGAAAAGCTCGTTTCAGAATCCAATGAGAATTTAAAGGCCGTTGTGTTTTTCAAATCTTTGAC	TTGAC	
	GCIÁTIAGCCCTAAACACGAAGATTIT		
HP0849	1375 TTGATTGAAAAAGCGAAAACCTTCTATGGCGAAGATAAGGAAAAATTGAATGTTTTGATTGA	1376	SSALER
	GAAAGGGAATTGAAACAAAAGAATGAACATTTAGAGAACGCTTTAAAAGGAGCAAGAATATTTGAAAAACGCATGGCT		AWLLE
	TTAGAAATGGAAAAACAAAAAGAAATCTTTCACAATAAAAATTGGAATTGGAAAAAGTCCTACCAACAAGCCCTAAATA		ALNILKS
	ICTTAAAAAGCGAAGTCGCTTCAAAAGATACTAGCTCCATGCATAAAGAAATCCATAAAGCGAGCG		KHKTN
	AACACAAAACAAACCAAGAGATCCCACAAATCATAACGAACTTTCAAGCCAACGAAAAAGCGCGCTACAAGAATGAA		VLIVAIL
	AGCGTGCTGATTGTACAAATTTTAGACAAGGGCTATTATTGGATAGAAACCGAGCTTGGCATGCGTTTAAAAGCGCA		LKKIQK
_	ITGGGAGTTTGTTGAAAAAAATCCAAAAACCCCCTAAAAACCAAAATTCAAACCCCTAAAACAAC		LDLRG
	AGAAGCGAGCTTGCGCCCTTGATTTAAGGGGGCCAACGCAAGAAGCCCTGGATTTACTAGACGCTTTTTAAAC		FEEVLIC
HP0849	1377 GGGGCGTCTAATAGGGGGATTGATGATGTCCGTAATCTCATAGAGCAAACGCGCTACAAACCAAGCTTTGGGCGCT	1378	SFGRYK
•	ATAAAATCTTTATCATTGATGAAGTGCATATGTTCACCACCGAAGCGTTTAACGCGCTTTTAAAGACTTTTAGAAGAGC		EPPSHV
_	CTCCTAGCCATGTGAAATTCCTTTAGCGACAACAGACGCCTTGAAACTGCCCGCTACCATACTCAGCCGCACCGAG		RFKKIP
	CATTICAGGITTAAAAAAATCCCTGAAAATTCCGTTATTICICATTTAAAAACCATTTTAGAAAAAGAACAAGTGAGTTA		ALEKLA
	TGAAACAAGCGCGTTAGAAAACTGGCTCACAGGGGGCAAGGGAGGCCTAAGGGGATACGATCACTTTTAGAACAA		NAITES
	GCCATCAATIATIGCGATAACGCTATCACAGAAGCTGGCTGGAATGTTAGGAGCGATIGACAGAGCGTTTT		NODEA
	AGAAGATTTTTCCAAAGCCTAATCAACCAAGATTATGAAGGGCGTTATGAAAAATTATGA		ALFLKAK
	AACCGAGAGCGIIIIAGAAGAAAIGAIGAIGAIIIIIIGAAAACGGAAAIIAIIGAGCCCIGAIIIIIIAIICIA	LLSPUFTS	

HP0849	13/9 TAAAAAC	13/9/111AAAAAACAGCGCGCTGTTTGTAAAGAATCTCAAGCCCAAAGCGCTAGACGCGATGCTCAATTACATGGCTTATACT	1380 Ft	1380 FKKORAVCKESQAKALDAMLNYMAYT	
	TATGAAAAG	TATGAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA	포	KDEIKSMILEOLEEELEAQKSALIRRYE	
_	GTAATTATGC	GTAATTATGCGGCAGAGAAGAAGAGCTCGTATTGCTTTGCCTTGCTTATATATCGCTCGTCGACAAAAAAAA	<u> </u>	KEAKEEGKKKSYAILAEATARFAGNYA	
	ACGGGAAAA	ACGGGAAAAATATTGAAGCGTTTAAAAAGGTCAGCGGGGTGGATATAGAATTTAGCGAAGATAGCGAAATAGCGAATAGCGAAGAAAAAGGTAAAAAAAA	₹ ₹	AEKKYSCYDIEESEDSSEI OI SSENI X	
	TTGTCCAGTT	TTGTCCAGTTTCAATCTTTATCGGCGTGAAGTAGCGAGCG	<u> </u>	REVASETI KII IEDGRIODNIRIEKAN	
	GCCTAACAG	GCCTAACAGGATTGAAGAGGTTTATCATAGAGTCGCGCGCAACCTGGAAAAAAAA	<u> </u>	RVARNLEKELI SEGESVVI EI EI GAME	
	G1GG1GT1AC	GIGGIGITAGAATTAGAGCTTGGAGCTATGGAAGATGAGCTTAAAATTTTAATAGGCAAAATGCGTTATCGCTCCAGT	<u> </u>	DELKILIGKMRYRSSFGO	
3,00	111GGGCAAA				_
HP0849	1381 GAICGCICG	1381 GALICECTICATE CAPATION OF THE CONTRACT OF THE CAPATICA OF	1382 0	1382 DRSLYVDILDLTAKDYOVNAKLANRDV	_
		CTTTCCATTACT I CAST I CESCAL I GECT I GAAAGCTATAACTAACTAACTAATCT TCTGTAGAAGTGCGTATCC	Ľ.	FNAFEFGIGSESYNSSTNLSVEVRIPLP	
	19973911131	CALITICATE OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CANAGE CONTROL OF THE CONTROL OF	<u>5</u>	VTPKNIYQKRKFLDLQSGTLAQNEVMK	
		WOLCAND IN SAN I CANCECCAN I CONTRACTOR CONTRACTOR AND CONTRACTOR IN SAN I CANTERNAL IN SAN I CANTERNAL IN SAN I CANTERNAL I C	<u>~</u>	RNIRINANSYLNOLKTKEAYIETÖKEAIA	_
		ACCENTANT STATES OF THE SECRET STATES OF THE	Ž	NKKRLMEMGRIAYEAQKIGLFEYLIYON	_
	GC1111GAA	CCTITI I GAZIALI I I GALI I I I CAAAATICTI ACATGGACGCTCTTATTACTCTAGCGGAAGCCAAGATTGAATACATT	<u>8</u>	SYMDALITLAEAKIEYIDISALLEETLGE	
	16A1A1 A6C6	CALTO CALCACTOR I AGAGGGGGGGGGGGGGGGGGGGTTTGGCGGGGGGGGGGG	<u>18</u>	SLTRLGELH	_
	Aliceologia	ILE LECCITATE LA LEGECCETT LITICAAT GEGTGTTTTAAAAGCCAAAGAGTATTCAGAAATTATTTAGAAG	•		
•	AAAAAACTT	AAAAAAACI I GCAACCCATGGGGTT AAAGGTGGTT AAATTAGATAAAGAAATCTTTAGTAAAGGCTTCCTTTTAACG			_
	CITAIAITGA	CLIALIGATITICATARA AAAA GCTCTGTGGTGCAGAGCTTGAGTTTTGATGCGTCTGTGGCGCTGTTTATAAAA	•	-	_
	Josephon,				_
HP0849	1383 ATTTTGATG/	1383 ATTTT GATGAAAAGAGTCGTTGAGCGAGCGGTATTTGCAGCATAAGGTTAAGGACTTTTTGACTAGAGGGGGGT	1384 IFC	1384 FDEKESI SERVI OHKVKNEI TREGVY	
	TTATGATCTG/	TATEATCTGAGCTTTGAGCCTATTTTAGCCTTGAATGCGAAGGCGAGCAAGCCCCATGCTTTGCCTAGTGCGAAGG	O	DI SFEPII AI NANASKPHAI PSAKDEI K	_
	ATITITAAAA	ATTITITAAAAGCGGAGCACCACTTCTTTGGATATGGGGATCAAATACGAACGCTATTGCTCGATAGGACTCGCA	AE	AEHSILI DMGIKYERYČSDRTRTAFED J	
	CGGCTTTTT	CGGCTTTTTTGACCCTAAAGATTTTGTCTTTAAAAGAGAGAG	Ϋ́ X	PKDFVFKRFÖSFKDKFRÖKIYDIVKFA	_
	ACATTGTGAA	ACATTGTGAAAGAAGCGCAAGAAAAGGCTATTTCAGGCATTAGAGCGGGCATGACCGGTAAAGAAGCGGACAGCTT	0	OEKAISGIRAGMTGKFADSI ARGVISD	
	GGCTAGGGG/	GGC1AGGGGAGTGATTAGCGATTATGGTTATGGGCAATATTTCACTCAC	<u>\</u>	YGYGQYFTHSTGHGIGLDIHELPYISSR	_
	AICCAIGAGO	A I CCA I GAGO I COCTATATO TO A TOTA GAGA GAGA GAGA GAGA GAG	SE	SETILEEGMVFSVEPGIYIPGFFGVRIF	_
	GATTIATATC	GATTIATATCCCTGGGTTTTTTGGGGTGCGCGTTTGAAGATTTAGTGGTGATCAAAAATTCTAGGTCTGAGCTTTTGTG	<u> </u>	DLVVIKNSRSELL	_
	ATGCGAGAGA	A I GCGAGAGA I COTTACTAGC CGTTTTTCCCTAGACCTTTTTAAAAAAGGCTTGATTTTCTAACAGGGTGGTTTTA			
	G6611666A1	GGG I I GGGGA I CITAAAAA TCCTTTAAAAA TATTAAAAAATTGTTTTTGTATTTTAAAAATCATAGTAAAATCGG			
	GAAAATTTTTT	GAAAATITITITCTCGCCCATTTATATCAATCCGCCTTTTGGTTACACTAAGCAACCTATTATAAACGCTACGATC		•	
	AICCI I AAAA	ALCCI LAAAACAI CI II AAGII I GCGCCAI II II II II GCTCI GGTTTI TATAGAAAGGCGTTTTGGCCGCCAAAGGA			
	AGCGCGALLI	AGCGCGATTT PAAGGCGCCCAAGAACTTTAGACATTGATATTATCGCTTTCAACCCAAGTCATTTTAAGACAGAATG			
	ALLIGGCILIACC	20			_

HP0849

HP0849

Š

≺	۲
v	٦
_	j
•	7

- III I I C W -	101 05 30	12.0	
I HINVEEAIAFADILMSLR TO TERHNTP IFASLKDYGNAYCITQORLKAHAKNKE VIILHPGPVHRDIDIESAVLEDERSKVLE QVKNGVAMRMAVLEFLLLD 1394 TPLVDVMLVLLAILMYTTPTLTYKEEIAL PSGSKTARATQDKMIEIRMDKDAKIYID SQTYEYNSFPDTFNLLSKKYDKDTRVS IRADKRLTYDKVIYLLKTIKEAGFLKVSLI TSP	1396 ELIHNVAYKHNGYSVFAGVGERTREG NDLYFEMKEGGVLDKVALCYGOMNEP NDLYFEMKEGGVLDKVALCYGOMNEP GARNRIAFTGLTMAEYFRDEKGLDVL MFIDNIFRYAGSGAEMSALLGRIPSAV GYÓPTLAGEMGKLÓRRIASTKNGSITS VQAVYVPADDLTDPAPASVFAHLDATT VLNRKIAEKGIYPAVDPLDSTSRILSPÖ MIGEKHYEVATGIQQVLQKYKDLQDINI LGLDELSEEDKKTVERARKIEKFLSQPF FVAEVFTGSPGKYVTLQETLEGFGGIL EGKYDHIPENAFYMVGSIQEVLEKAKN MKNS	1398 ELAOKSLEETCTLYEEIFTPHQNELFFK ESOGIVFNERLLÖLLKNOYFDEIKGIES SALSERNYFNEIARKISEAHSEFSLEEI ELSLEKVKKTEIRRMIIKDKIRPDKRALE EVRPILIESDLLPMAHSSILFTRGOTOS LVVGVLGTDNÜAOTHESLEHKAPIKER FMFHYNFPFCVGEASSIGAASRRELG HGNLAKRALETSIKNKEOVIRLVSEILE SNGSSSMASVCAGSLALYASGVEIYD	1400 EWIHGIPTDYVLQEGDIIGLDLĞVEVD GYYGDSALTLPIGAISPQDEKLLACSKE SLMHAINSIRVGMHFKELSQILESTITER GFVPLKĞFCGHGIGKKPHEEPEIPNYL EKGVKPNSGPKIKEGMVFCLEPMVCQ KQGEPKILADKWSVVSVD
² €		<u> </u>	140
TACGCCCATTITICGGAGCTTGAAAGATATGCCTATTGCATCACCAACACCCCAACAAGGCTCAAAGCCTCAAAGCCTCAAAAAAAA	GAGCTTATCCATAATGTGGCTTATAAGCATA GGAATGATCTGTATTTGAAATGAAA		
HP0849	HP0849	HP0849	HP0849

2/066501			PC 1/EP01/13428
1402 SQGDFSDFFEDLGSFFEDAFGFGARG SKRQKSSIAPDYLQTLELSFKEAVFGC KKTIKYQYQSVCESCDGTGAKDKALET CKQCNGQQQVFMRQGFMSFAQTCGA CQGKGKIVKTPCQACKGKTYILKDEEID AIIPEGIDDQNRMYLKNKGNEYEKGKR GDLYL 1404 GYVGEDVENILTRLLQASDWNVQKAQ	KGIVFIDEIDKISRLSENRSITRIJVSGEG VQQALLKIVEGSLVNIPPKGGRKHPEG NFIQIDTSDILFICAGAFDGLAEIIKKRTT QNVLGFTQEKMSKKEQEAIL-LVQTHD LVTYGLIPELIGRLPVLSTLDSISLEAMV DILQKPK 1406 LQKEKSKVHQKMEQTNKEVFLKEQLK	GIGKELGTDKGRDEDLNQYYGKLESIN PFLKEEAFKEIKKGIDRLSRTHADSSDS ATLQNYIETMLDVPFGQYGKKALDIKH VREQLDKDHYSLKRPKERIVEYFATMQ LLEMRRKKPEKKDKTKGTILGFYGPP GVGKTSLANSIAKAIERPLVRIALGGLEA DVNELRGHRRTYIGSMPGRIVQGLIEA KKMNPVMVLDEIDKVDRSVR3DPASA ILLEILDPEQNTAFRDHYANFSIDLSQVIF IATANNIDRIPAPLRDRMEFIS/SSYTPN EKEEIAKNYLPQELEKHALKFSEVEISH ECLKLIIEKYTREAGVRDLRRQIATIMRK VALETMYTEDNPHQKGRTKKGKNEKSED QXEEDQKSENQKSENKGIVIGLAW KEYLERNPHGKGRTKKGKNEKSED OVMKESAIIAFSVVKVLLDNETLKVPKIP SETDAEGKKKKKVLLKVNAYIJLHLH SETDAEGKKKKKVLLKVNAYIJLHLH SETDAEGKKKKKVLLKVNAYIJLHLH	ERLDIEKVLERLGMLSGIIKDYGSIMHA KERLGHVKNELHNLKEIDSHCIETYHKEI ERLKTECLKLCEEISGFRKEYLAGFNAL LSAKAKDLLLKSPSLVLEDAP MSEKGA QKLVLNLQNSQLETLSSGEYSRLRAF MLLEMELKDFKQLVLDEMDSNLSG EESLAVSKALETLSSHSQIFASHOVHID ALAKNHILVFKENHKSLAKTL NNERVL EIARMIGGSENIESAISFAKEKLKAOE
ATTTAGGCTCGTTTTTGAAGACGCTTTTGGGTTTGGCGCTAGGGGG GATTATTTGCAAACCTTGAATTGAGTTTCAAGAAGCGGTTTTTGGC GCGTTTGTGAAAGTTGCGATGGCACGGGCGCTAAGACAAGCCCT 3GCAGGTGTTTATGCGTCAAGGTTTTATGAGTTTGCGCAAACTTGTG AAAACCCCATGCCAAGGGTGCAAAACCTATATCCTTAAAGA CATTGATGAACATGGTGGAGTGGA			1407 CATAGCGCGGAGTTTTTAAAAAGCGCTTTATTAGAAGCGGCGCTCTATTGGAAGAGATTGGAAAAAAGTTGAAAAAAAGGATTAGGAAGATTGGAAAAAGGTTTGGAAAAGGTTTGGAAAGAATTGCGAAAATTGCGAAAATTGCGAAAATTGGCAAAAAAATTGGCAAAAAAATTGGCAAAAAAATTGGCAAAAAAATTGGCAAGAAATAAGGGGTTTTAGAAAAGGCGTTTTAAGGCGGTTTTAAAAAAGCGGTTTTAAAAAAGCGGTTTTAAAAAAGCGGTTTTAAAGGGGTTTTAAAGGGGTTTTAAAGGCGTTTTAAAGGGGTTTTAAAGGGGTTTTAAAGGGGTTTTAAAGGGGTTTTAAAGGGGTTTTAAAGGGGTTTTAAAGGGGTTTTAAAGGGGGTTTTAAAGGGGGTTTTAAAGGGGGTTTTAAAGGGGGTTTTAAAGGGGGTTTTAAAGGGGGTTTTAAAGGGGGTTTTAAAGGGGGTTTTAAAGGGGGTTTTAAAGGGGGTTTTAAAGGGGGTTTTAAAGGGGGTTTTAAAGGGGGTTTTAAAGGGGGTTTTAAAAGGGGGTTTTAAAAGGGGGTTTTAAAAGGGGGTTTTAAAAGGGGGTTTTAAAAGGGGGTTTTAAAAGGGGGTTTTAAAAGGAAATTTTTAAAAGGTTTTTAAAAGGGGGTTTTAAAAGGGGGTTTTAAAAGGGGGG
1401 A A T A C C C C C C C C C C C C C C C C	1403 (1405	1407
-IP0849	HP0849	HP0849	HP0849

HP0849	1409 TAAGAGTTGGCAAGATGAAGAAGTGAAAAAATACACAGGAAGGCCGCACGGTGATCTCTAATAAAGCGCTCACCCAAC AAGCTAACCAACAAGTGTAAGAATTAAGAATTAGAATTAAGAATTAAAAAGAAG	1410 KSWQDEEVKKYTGSRTVISNKALTQQ
	TATGCCTACTATCCAAATCCGTGGCTTTGGAGCTGGGGGGTTCAGGGCATGCGATGCGACGCTGATGTTAGTCAAT GGTATTCCTGTTTATATGGCCCCCTACGCTCACATTGAGCTAGACATTTCCCCGTTACCTTTCAAGCCATTGATCGC	Transport Control of C
	ATTGATGTGATCAAGGGTGGAGCGTGCAATACGGGCCTAACACTTATGGGGGGTATTGTCAATATCATCATAA GCCTATCCCTAATCAATGGGAAAACCAAGGGGGCTGAAA	GSSQYGPNTYGGIVNIITKPIPNOWEN
HP0849	1411 CCTTAATCGCGCTAAAAAGCCTTGCATTGTTTTGAATAAAACGATTTAGCCCCAAAACTGGGGCTTGAAATTTTA	1412 LNRAKKPCIVVLNKNDI APKI FI FII KS
	AAATCTTATCTTAAAATCCCTTATACTTACTAGAGACCAACACCCTAAATTCCAAGGCTTGTTTGAAAGATTTGAGCC	YLKIPYTLLETNTLNSKACLKDLSOKISA
	AMMAMATICACCICATACTGAAATTGCAAAACTAGACACTCAAAACAAGCTCTTACTCACTTCCCTAGCCCAAAAAATTGCCC	FFPKLDTONKLLLTSLAOKIALENAITEL
	CGCGATAGAAACTTGAACTTGCTCACCCGCCCTTATGAAACCAGCCAAATGCTAG	CNAKNHLE I LELFSYHILSAIENLNLLTR PYFTSOMI
HP0849	1413 GAAGTGTATCGTTTGAAAAAGCTTTCCACTTTCAAGAGCTTGTGAGCGTGTATTACGGCATGGTGTTAAACGCAGAA	1414 EVYRLKKLSTFQELVSVYYGMVLNAEV
	GENERAL FINE GARAGA GARGA GARARA GARATA TATA GARA A A GARATA GARATA GARATA GARATA GARARA GARA G	AETLEEVEKGHYKHFQNALKMÖKVG
	GOLDAN GOOT GOOT GOOD GOOD GOOT GOOT GOOD	IARVETLGAQVAYDKAHIASVKAKDVLE
	AGATCCGCACGGAGAAAATCTGCCCGATCTGAGCTTTTTTGTTTCTCCACGCTCAATTCCTACCCGGTTTTAAAAA	VSQLSFNSILSSKDDLVPSSKLEIRTEK
	CTTTAGAAAATCAGATTCAAATCTCTAAAGAAAACACGAAATTACAGATCGCTAAATTCTTGCCCCAAGTGAGTTTTTT	SKENTKLOJAKFLPOVSFGSYJMKON
	TGGCTCTTATATTATGAAGCAAAACAATTCGGTGTTTGAAGACATGATCCCTAGTTGGTTTGTGGGCGTGGCCGGGC	NSVFEDMIPSWFVGVAGRMPILSPTGR
	GAATAATAATAATAATAATAATAATAATAATAATAATAAT	IGKYGASKLAELQVSSEGIGAKKNMEL
	ACARACHI CHESCULLE AND ACARACHICAL TO THE TOTAL PAGE CONTINUED TO THE TOTAL TO	LVNKTYKETLSYLKEYKSLLSSVELAKE
	IGCACGAACGCTCAAGTCATTGATGCCAACAAAAAAAAAA	NLKLQEQAFLQGLSTNAQVIDARNTLS
HDARAG	1415 GCGCGCGCTTGATTAAAGATGCCTTTTAAGCGTTCAAAACATGCGCTTCAAAACATAAGAAGAAAAAAAA	SIVVEU
2	GTGTTTTGGATAAAGACAAACCAAAAAAGACAAAAAAAAA	1416 RALIKDGFLAFKQAHYAEALRLFSEVLF
	AAGCCCATAGCTTATGAATTCAAAAGCTTGATTGAAAAGCTAAAAAAAA	CLUKUNUKAKVGALLSUJAKDFPKEAHS I
	AAATCATCATTTGATCACTTCTTTTGATGAGGGGGTTAAAACCAAAAAAAA	PIELICOLINIMORROLINIO DE COLONIO
	AAAGCGAAGAATTGAATGGCGTTTTGTATGCGGATTTCAAACGCTTGAAGCTTGAAGCTTTGAAGCTTTGAAGCTTTTAAAGGAAACGAAACGAAATTAAAAGGAAAAAAAA	STDEGLNUMAEKIDVQISQKSEELNGIL VADEKBI STEROFITAFITA MISSON
	GAAGATTTGATGTTCAGCTCTAGGGTGATTTTTGACAGTGATTTTTTATGAATTTTTATAGAAAGAA	
14	ATGGCTATTAGGAATTAGCAATAAATTA	LOW BOLIETCHELING TELAIN
HP0849	۲.	1418 VTDGÝVKVSĽVAĎERELLLĎOVLÓEAČI
	CAAAACCIIIIAGAACATCGTATTGAGCCTAAAGATATTACCATTTTATGCGCCACTAATGACGCCTTTAGAAATCA	NLLEHRIEPKDITILCATNDDALEIKNYL
	CTAAAATTATTAAAATTAAAAAATCATTAAAAATAAAAAA	QERLSAIRPSTESSAKLSOFVESKIIKN
	AACTC6CTG6ATACTTGCATGATGATGCGATCGCTTTAGCGGATCTTTAACCCTAAAAAAAA	ALEYALAEEPYKPFYKHSVLKLAGYLH
4 4		ような人の日といったこうなっていてつ
HP1015	1419 TGGCAGAAGTGTCTAAAGAAGATTATGTGCGTACCGCTAAAGCTAAGGGGTGTAGCTCCTTTAGGGTGATTTTTGTG	1420 AEVSKEDYVRTAKAKGCSSFRVIFVHT
	CACACITIECEIAAIGCITIAAICCCIGTAACGACTATCGCAGGCTTGATGTTGGCCGGGCTTTTAGGGGGGGG	LANALIPVTTIAGLMLAGLLGGSMITET
-	GRI PACT GRANGESTITION OF TRATECT AT STATE OF TAXABLE STATES OF	VFSWPGIGKWIVNALNORDFPIIQSMS
	GATCCTAGAATAAGGTTGTCATAATGGAGTCTTTTAGAGAGTTTATCCAACAATTCAAAAAAAA	LIIAMIMYIGANLLVDILYAFIDPRIRLS
	TIGGGCTTGGATTGTGCTTTTATTGGTAATTTGCGCGATTTTTGCGCCCCTTTTAGCCCCGCATGATCCTTATGTCC	
· .	AAAACGCGCAAGATCGCCTTTTGAAGCCTATATGGGAGCATGGAGGGAATGCTAAAATACCTTTTAGGCACCGATGAT	
	LeGesceceda All LeGesceced All LeGesceced All Legesceced All Legesceced All Legesceced All Legesceced All	

HD1015	1421 CGCAAAAAAGCGACCTTGAAAATTCCGTTAAAGATGTGATCATCAACAAAAAGGTAAAAGATAAAAGGTAAAAAGATAAAAGATGAAAATGAAAATTCAAAAATTCAAAAATTCAAAAAATTCAAAAAATTCAAAAAA	MINOVALINATION FINANCIAL INDIVIDUAL PROPERTY IN INCIDENTAL PROPERTY INCIDENTAL PROPERTY INC
2	TOANTO CONTACTOR	
_	TATTO AND TO THE CONTRACT OF T	CAVSVAKAMGDFSKVECVL*DLKNFS
	11 CAMAGGAGGAGCAA I I GGCI CAACAAGCA I I GAAGAA I I GAAGAAA AA I I I GAAGAAAAA I I I GAAGAAAAA I I GAAGAAAAA I	KECLACCACKNEDFNTGKNSELYCSV
-	CCG11AAGAA1AG1G1AAA1AAAACCC1AG1CGG1AA1GGGT1A1C1GGAA1AGAGGCCACAGGTCTCGCCAAAAAT	KNSVNKTLVGNGLSGIEATALAKNFSD
	TTTTCGGATATCAAGAAAGAATTGAATGAGAAATTTAAAAATTTCAATAACAATAATGGACTCAAAAACAGCACAG	KKELNEKFKNFNNNNNGLKNSTEPIYA
	AACCCATTTATGCTAAAGTTAATAAAAAGAAAACAGGACAAGTAGCTAGC	KVNKKKTGQVASPEEPIYTQVAKKVNA
	CTAAAAAGGTAAATGCAAAAATTGACCGACTCAATCAAATAGCAAGTGGTTTGGGTGGTGTTAGGGCAAGCGGGG	KIDRLNOIASGLGGVGQAAGFPLKRHD
		KVDDLSKVGLSASPEPIYATIIJDLGGPF
	CTACGATTGATGTCTCGGCGGACCTTTCGAAAAGGCATGATAAAGTTGATGATGATCTCAGTAAGGTAGGGGGA	PLKRHDKVDDLSKVGRSRNQELAQKID
	TCAAGGAATCAAGAATTGGCTCAGAAAATTGACAATCTCAATCAA	NLNQAVSEAKAGFFGNLEQ1'IDKLKDS
	AACCTAGAGGAAACGATAGACAAGCTCAAAGATTCTACAAAAAGAATGTTATGAATCTATATGTTGAAAGTGCAAAA	TKKNVMNLYVESAKKVPASLSAKLDNY
	AAAGTGCCTGCTAGTTTGTCAGCGAAATTGGACAATTATGCTATTAACAGCCACACACA	AINSHTRINSNIQNGAINEKATGMLTQK
	AATGGAGCAATCAATGAAAAAGGGACCGGTATGCTAACGCAAAAAACCCTGAGTGGCTTAAGCTCGTGAATGATAA	NPEWLKLVNDKIVAHNVGSVSLSEYDK
•	GATAGTTGCGCATAA	IGFNOKNMKDYSDSFKFSTKLNNAVKD
		IKSGFTHFLANAFSTGYYCLARENAEH
-		GIKNVNTKGGFQKS
HP1015	1423 TTATAGGGGGGGGGGGGATAGTTCGCCCTTCGAAACCTTTGTGTTTTCCCATTCTCAAGAAGCGGTGGATAAAAGC	1424 IGGGGDSSPFQTFVFSHSQEAVDKSV
	GTGGAGAATTTGAAAAAATTCTTATTAGAAAGCCCTGAATTAAAAGGCAAGGTTGAAAGCTATCATACAAGCACGAGC	ENLKKFLLESPELKGKVESYHTSTSES
	GAATCGCAACCGCAATTGCAACTCAAAATCTTAAGACAAAACGCTAACAAATACGGCGTGAGCGCTCAAACCATTGG	OPOLOLKILRONANKYGVSA2TIGSVV
	ATCAGTGGTGAGCTCTGCTTTTTCTGGGACTTCTCAAGCGAGCG	SSAFSGTSQASVFKEDGKEYDMIIRVP
_	TCATTAGAGTGCCTGATGACAAGCGCGTTTCTGTAGAAGACATCAAAAGGCTTGCAAGTGCGTAACAAATACGATAAA	DDKRVSVEDIKRLQVRNKYD< LMFLDA
	TIGATGTTTTTAGACGCTTTAGTGGAAATCACAGAAACTAAAAAGCCCGTCCAGTATTTCTCGCTATAACCGCCAACGC	LVEITETKSPSSISRYNRQRS\/TVLAEP
	AGCGTTACGGTGCTTGCTGAGCCTAATAGGAATGCGGGCGTTTCTTTAGGCGAGATTTTAACGCAAGTGAGCAAAAA	NRNAGVSLGEILTQVSKNTKE:WLVEGA
	CACTAAAGAATGGTTGGTTGAAGGGGCGAATTACAGATTTACCGGAGAAGCGGATAACGCCAAAGAGGGAAAGGGG	NYRFTGEADNAKESNGEFLVALATAFV
		LIYMILAALYESILEPFIIMVTMI?LSFSGA
	CTITIATCATCATGGTTACCATGCCTTTAAGTTTTTCAGGGGGGTTTTTTGCTCTAGGTTTAGTCCATCAGCCTTTGA	FFALGLVHQPLSMFSMIGLILI.IGMVGK
	GCATGTTCTCTATGATAGGCTTGATTTTGCTCATTGGTATGGTGGGTAAAAACGCCACGCTTTTAATTGATG1GGCGA	NATLLIDVANEERKKGLNIQE/AILFAGK
	ATGAAGAGCGTAAAAAAGGTTTGAATATCCAAGAGGCCATTTTATTTGCCGGCAAAACCGTCTAAGACCGATTTTAA	TRLRPILMTTIAMVCGMLPLALASGDG
	IGACGACCATTGCGATGGTTTGCGGGATGCTGCCTTTAGCGTTGGCGAGTGGGGGTGGAGCGGCGATGAAATCCC	AAMKSPIGIAMSGGLMISMVLSLLIVPV
HP1015	1425 CTTGAATACCGAGCTTTTATTAGACGAAATTGTCAGGCTTTATTCTCAAAATACTACAAATAATGAAAACATAAAAGTC	1426 LNTELLLDEIVRLYSQNTTNNIENIKVPS
	CGGTCTCAAAGCTTTAAGGAGTCTTTAAAATACAGCCAGAGGCGCTCAAAGAATCGCTCAATTAGTGATCAGTGAAAAC	QSFKESLKYSQSAQRIAQLVISENQQN
	CAACAAAACGCGAGTTTTGAACACACTTATAAGATTGATAAAGATTTTAATGCACAAAGCGTTATGGGATTTTCATTTTT	ASFEHTYKIDKILMHKRYGIFIIFLGFMFII
	TAGGGTTTATGTTTATCTTTTTCCTTGAGCTTTTTAATAGGGGGGGG	FSLSFLIGGGVQKALETGFKFLSDGIKE
		INVANEDLASLVGDGIIGGVGATVSFLPL IVVI YFGISI I F
		וויירוו טוטבנה

^	_
	Ľ
v	٦
^	ď

HP1015	1427 CG(GAA	1427 CGCACCTTTAGATTTTATCACGAAGTATTTCAAGTCGTTTGTGCTGTTACTCATTGTATTAGTCTTTTTTAGCGCTAAA	1428 APLDFITKYFKSFVLLLIVLVFFSAKESA PSAPPNLAKLYLNGAIFSTEDFDKEVD
	107	CAAAGAGGIGGAATTGAGGGAAAAAAAAATTGGTTTGGTT	KILKTPSIKGVLLLIDSPGGAVSASVELS EKIADLKQKMPVLAYARGVMASGSYY
	1991	GG11A1GGCGAGCGGGGGGCTATTATGCGGGCATGCAAGCGAGCGA	AGMOASEVYASKASLIGSIGVIFSGANV
	757	TGCGGCGAATACAAAGAAATAGGCACTTTCACAGAACGTTTAG	ENLLNKVGVATQGVHAGEYKEIGTFTR
	TCA	TCAATGAGCAATACCAAATGTTTGTGAATGATGATGACCCAAAAGCTAGGAAATTAGACGCTAAGGATTATAAGGATTTTG	KARKLDAKDYKDFAEGKVFSAQKALKL
	CTG		KLIDKISTIKQAQDRLMELSKVKKAYWL
	X X	CAMBATUSCTTMTTGGAGCGCTTCATCACAAAAAGCTTTGGCTACAAAAAGCCTAGGAAAAGCCCTATGAGGCGCTTCATTGAA AAAGCCACGCAATCAGCCACAACATCATCACACAAGCCTTTGGCTATCAATTAATT	EKSPMERFIEKATOSATNIITOAFGYOL
	ATT.	TTATTTAAAAATTCAAGCTAGAGACTCTAAAGGCTTGGTGAGCACGATTAGCACTATCGCTAACAACAAGGGCTATA	
	ACA	ACATCGTCAAAAACGATGAATTTGTTGATCCCTTAAAACAGCGTTTTTCATGCGGTTAAAAATCCAAAAAGAAATCAA GCCCTTGAATACTGAAA	
HP1015	1429 ATT	1429 ATTAGCTTTAGGCTGGGTGGGTGAGCCCGCTATCGCAAAATTGTTAGCCGCGCTGTTTGAGTCTATGGATTTGAGAG	1430 AI GWYGEPAIAKI LAAI FESMOI REN
:	AA A	AAAATCCTATTTTTATCCATTCAATGAGCGTGGTCATAGCGTTTTTAAGCATCACTTTTTTGCATGTCGTGTTGGGCCGA	PIFIHSMSVVIAFLSITFLHVVLGEIVPKS
	GAT	GATTGTGCCTAAATCTTTAGCGATCGCTAAATCTGAAAAGCCACCCTTTTTGCCGCACGCCCTTTGCATGTTTTG	LAIAKSEKATLFAARPLHVFWWFYPW
	199	GGIGGIGIIIIAICCGGIGGIGGIGGTGTTGATGTGATGGCTCATTTTTTTTGAAAAGATGGGCATCAATCCTAA	RLFDVIAHFFLKKMGINPKEHDGTHSE
	£ (AGACCA I CACCECCALI CLIGARGAGORI I CI GAGAGGGGCA I ATTIGATI	EELKIIVGESLREGIIDSVEGEIIKNAXDF
	9 0	CAGI GEAGGGGGAAA I CA II AAAAACGCAGGATI I I I I I I I I I I I I I I I I I I	SDTSAKEIMTPRKOMVCLDEENSYEEN
	2 P	GACATEGE GEGETETETAAGGAAAACAGCTATGGGGAAAATATGGGCATTGTTTGAAGAAGGCCATTTCACGGCCATTTCACGCCTAC	IDIVLKGHFTRYPYCKGSKONIIGMVHIR
	3 2	でです。」で、「大きな人もなる」、「して人もなるな」なんでは、「大きな人」、「大きなな」、「「なって、「大きな人」、「して、「して、「しん」、「しん」、「しん」、「しん」、「しん」、「しん」、「しん」、「しん」	DCLSKSIP I PKMHUPNOIVKKMIIVPES
	Z T A		ASISQLIKMIKKEQIMI ALVIDET 661 AG
	499 9	GGAAGACATCATTGAAGAGATCATGAGCAGATTAGCGACATTAGCGAATTACAATTAAAAACAAGAGAGAG	LLIMEDIIEEIMGEISDEYDLYGEGINKL
	AAG	AAGAGGGCGTGTTTGAATTAGAGGCCATGCTGGATTTAGAGAGCGTAGAAGAGCGCTTCACATTGAATTTGATAAA	CEÓVT GGÝVFSLLERMPMEGĎTIVSH
	GAA	GAATGCGAGCAGATAACGCTTGGGGGCTATGTTTTAGCTTGTTAGAGCGCATGCCTATGGAGGGAG	GYSFEVLSVDGARIKRLKAVKODOGE
1	TITE	IT CGCATGGGTATICT	
HP1015	1431 GGG	1431 GGGGGTAGAGGTGAAAATCAAATTCAAAGGATTGGACTATCAGGAGCAATGCCGGGACCAAATTTTAGGGGTGTTTA	1432 GVEVKIKFKRLDYÖEGCRÖĞILĞVFKGI
	D A C	AGGGGGGTTTATTATTAGGAAATATTGAGAATTTGCGATCGAAACAAAAAAAA	ULKEPENDACKISNPVFEIGAIKULLE
	LE S	GTTAAACTGCGGATATTTTAATGGAAACAGGCACCGGGAAGAACATTTGCTTTTGCTTTTGGAATGTGTTTATGCCTTGCAAACAA	MIENTANDA MENDA GEORGIA DE LA COLLA MENTE DE LA COLLA DEL COLLA DE LA COLLA DE LA COLLA DEL COLLA DE LA COLLA DEL COLLA DE LA COLLA DEL LA COLLA DEL COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DEL LA
	AAA	AAACCACCATTTGTCAAAATTCATCGTTTTAACGCCAAGCAACGCCATTAAATTAGGGGGTTTAAAGAGCGTTGAAAT	VLTPSNAIKLGVLKSVEITREFFKSEYS
	S	CACCAGAGAATTTTTAAAAGCGAGTATTCTAACACGCCATTTAGAAAGCTATGAAGATATAGAAAGATTTATTCTAGCG	NTHLESYEDIERFILASNHKCCVLVMTF
	AGC	AGCAACCATAAATGTTGTGTGTTGGTGATGACTTTTTCTGCCTTCAATAAAGAGAAAAACACTATTAATAAATCATGCC	SAFNKEKNTINKSCLENTNLFNGATSY
	P A	TAGAAAACACGAATCTATTCAATGGTGCAACAAGTTACATGCAAGCTTTAGTGAGTATGCGGCCCATCGTCATGG	MQALVSMRPIVIMDEPHRFLGDKTKKY
		NOCONOCIONAL III III III NOCONO III NA NATORO NOCONO NA NANA NOCONTITA NA NATORO III NOCONOCO NA NANA NA NA NA ROGO CERTA NA NA NA NA NA NA NA NA NA NA NA NA NA	CERCENSEL LAFTGALINOLINICIT ILD
	AAA	ους ουχήτη της περιοχήτησης του Την Του Του Του Του Του Του Του Του Του Του	
	\$35 50 50 50 50 50 50 50 50 50 50 50 50 50	GCAATTAACTACACGGATTTAGAAAATAAAACTCAAAGCGTCAAAGTCAAAGAGCATGATGATAATTTAGGGGTGGTAACT	DNLGV/TQISALEDYIVEKITKTEIRFLN
	CA F	CAAATCAGCGCTTTAGAAGATTACATTGTAGAAAAATCACTAAAACTGAGATTCGTTTTCTCAATGGCTTTAATTTGT	GFNLLLDÖKEPFSHLLEGEGEVMLKEA
	1 Y	ופטאוראא	Licy

HP0167	1433 ATCCCT	1433 ATCCCTCAAGAATTTGCAGAAATTTACAAACTGGCCAAACAAA		
<u> </u>	CAATTG	CAATTGAGCCTGGAATTGATGCCTTTACGCATGCGCGAAAATTCCGTAACGATTAAGCGTTATTTAGAGAAAGTGTTC	1434 IPUEFAEIYKLA	1434 IPUEFAEIYKLAKOSGMKPSHLDEIMOL
	CGCAAA	CGCAAAATGATCTTGTGTTGCCCTGAAGATTTGAATTTAAGGCAAAAACGCATCTTAATGCTTGTAGGGCCAACAGG	ILCCPEDLNLR	LCCPEDLNLROKRILMLVGPTGVGKTT
	CG1GG	CG1GGGGAAAACGACGACTTTAGCTAAATTAGCCGCGCGCTATTCTAGGTTTTAGCTAAAAATACAAGGTGGGCA	TLAKLAARYSR	TLAKLAARYSRMLAKKYKVGIITLDNYR
	000000	A SECRET TO A CALLANCE CAN I GEOGRAPH GOOD TO A CALLAND T	IGALEQLSWYA	IGALEQLSWYANKMKMSIE, AVIDAKDF
	CAGGGC	CAGGGCATTCGCAATACGATAAAGAAAAATTGCCGGTTTGAAAGAATTATAAGAGGGGTTATAAGAGGGGTTATAAATAAAAAA	ACHEREALEYCD	AKEIEALEYCDFILVDTTGHISQYDKEKI
	CCTTAG	CCTTAGTGCTTTCAGTTACCACTAAGTATGAAGACATGAAAAGATTATTATTAACAATTAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAATTAAAT	AGLKEFIUGGY	AGLKEFIUGGYNIDVSLVLSVITKYEDM
	CTTTAA	CTTTAATCTTTACGAAATTAGATGAGAGTAGGGGGTTAGGGAATTTGTTTTGTTTAGTGCATGAAAGCCAAAAACCTA	I FSI VHFSOKP	NDITUSFEVLEID LIFTRLDESKELGN FSI VHESOKPISYI SVÆDEVBADI KV
	TCAGCT,	_CAGCTATCTTTGGGCAAGAAGTGCCTATGGATTTGAAAGTGGCTACTAATGAATATTTAGTGGATTGCATGC	ATNEY! VDCM!	ATNEY! VDCM! DGESNDNKEOA
	TAGATG	1AGATGGCTTTAGTAATCCTAATAAGGAACAAGCATGAACAATCAAGCGAGCCGCTTAGATAATTTGATGAATATTAA		
	AAACCC	AAACCCTAAAAGTTTTTTGATAATAAAGGGAATACCAAATTCATCGCTATCACAAGCGGTAAGGGAGGCGTGGGGA		
	AAICCA	AAICCAACAITAGIGCTAATTTAGCCTACTCTCTATACAAGAAAGGTTATAAGGTGGGGGGTGTTGATGCGGGATATTG	-	
10101	1134 TOO O O O O O O O O O O O O O O O O O	ONAL INTERACTION OF A STATE OF A		
41014	TATOTAT	1437 AAACCI AGI CAGCGGCGGGCGGGGT I GGCAAGGGGGTTTGTACGCTTCGCTCAAGCGGCGTGAA	1436 TLVISGATRGIG	1436 TLVISGATRGIGKAIFVRFAGSGVNIAFT
		CONTROL OF THE STATE OF THE STA	YNKNVEEANKII	YNKNVEEANKIIEDVEQKYSIKAKAYSL
	SCCARA ACTOR	SCHAMBELLIALICIALITIAGAGCCTGAGCAATACAGGAGCTTTTCAAGCAATTGACGTGATTTTGAC	NVLEPEQYTELI	NVLEPEQYTELFKQIDADFDRVDFFISN
	AGAGIG.	AGABLEGALITITIALITICIAACGCTATTATGGGCGTTCTGTCGTGGGGGGATTTGCACCGTTTATGCATTA	AIIYGRSVVGGF	AIIYGRSVVGGFAPFMRLKPKGLNNIYT
_	AAACC1/	AAAUCI AAGGGGTTAAACAACATTTACACAGCCACCGTGTTAGCGTTCGTCGTAGGGGGCTCAAGAAGCGGCCAAAAC	ATVLAFVVGAQ	ATVLAFVVGAQEAAKRMOK GGGAIVS
	GCATGC	GCATGCAAAAATAGGCGGTGGGGCGATCGTGAGCTTAAGTTCTACGGGGAATCTAGTTTATATATGCCTAATTACGCC	LSSTGNLVYMP	LSSTGNLVYMPNYAGHGNSKNAVETM
	GGGCAT	GGGCA I GGCAATTCCAAAACGCCGTAGAAACCATGGTCAAATACGCTGCCGTGGATTTAGGCGAATTTAACATTAG	VKYAAVDLGEFI	VKYAAVDLGEFNIRVNAVSGGPIDTDA
	AGIGAA	AGI GAA I GCCGG I AGI I GGCGGGCCTATT GATACGGACGCTTTGAAAGCCTTCCCTGATTATGTGGAGATTAAAGAAA	LKAFPDYVEIKE	LKAFPDYVEIKEKVEEQSPLIKRMGNPN
	10000000000000000000000000000000000000	AND REARCED CONTROLL ADVANCE OF THE SECOND TO THE SECOND TO THE SECOND THE SE	DLAGAAYFLCD	DLAGAAYFLCDETQSGWLT(3QTIVVD
	GAGACC	GAGACCCCAAAGGTTGGCTTACAGGGCAAACGATCGTTGTAGATGGCGGGACTACTTTAAATAAA	GGTTFK	
	127775 017771	SCHOOL 1 ALCACH LOCAL CARCARAGE GEORGI LECAL LOC		
	101011	TI STANTING THE ST		
	GCTTCT	GCTTTCTAAAATCAC		
HP1014	1437 GCAAAAA	1437 GCAAAAAAGACGCTTGCGGGTTCATCTATGAGATCAGCGAGTTCATGAAAGCCTATACCGCATTGCTAAAAAAAA	1438 KVDACCEIVEICI	1438 KVDACCEIVEISEEAUANTALLI KKODON
	GACCGA	GACCGATACGTCTATTTATTGAGGTATCTCCCCTCTAGGTATTGGGCCAGCATTTTAACGACTGCCCTTTATGTCAAA	VYI I RYI PSRVV	WIND AND PSEYWASH TTAL VYKYDDED
	TACCCTE	TACCCTGATTTTGACGCTTTGAAAAAGCTTTTGGTGTCTTATTACCAAACTTGGATTGCAGGGGGGCACGATGACG	AI KKI I VSYYYC	AI KKI I VSYYYOTWIAGGTITBIKOTSIN
	CGCATC	CGCATCAAGCAAACCAGTATCAACATTATCAAAAACGTTAAAAGCAATAAGAGCGTTGAAACCATCAAAGAGCTTATA	IIKNVKSNKSVE	IKNVKSNKSVETIKELILNSIDSYNTFDO
	TIGAATA	11GAATAGCATGGACTCTTATAACACCTTTGATGAATACCTCTATAACTTATGGGATAGCTCTTGTGTTTATCATAGCA	VI YNI WOSSSV	YI YNI WOSSSVYHSKWYRPWI AI ANY
	AATGGG	AATGGGTGCGTCCTGTCTTAGCCCTAGCTAATTATTCATGGCAGATGAAGAAACCCCATTTTATCGCTATGGATG	FMADEEKPHFIA	FMADEEKPHFIAMDAETOVEHII POTP
	CCGAAAC	CGAAACCCAAGTGGAGCATATTTTGCCACAAACGCCCAAAAGAGGCAGTCAATGGAACGCGGGATTTTGACAAGA	KRGSQWNADFL	KRGSQWNADFDKEKREEWYNNIANLT
	AAAAAGA	AAAAAGAGAAGAATGGGTAAATATATATGGGGAATTTAAAGCGTTTTAAAAGGTAAAAAGAAGGGCATGCTTTAAACGG	LLKRKKNAHALN	LLKRKKNAHALNGDFDEKRKIYGGKDT
	166A1111	GEALTI I GAT GAZAZAZAZAZAZAZAZAZAZAZAZAZAZAZAZAZAZAZ	SKVISCYDITKEL	SKVISCYDITKELYSNYRKWNEKSLQE
	TOTAL TOTAL	ALLETTAGE AND LA RESEARCH DE LA RESE	RYKSLYNTITPVI	RYKSLYNTITPVLHIEGQEDDFEDDFD
	HOI I I A	I ELLI I ACACA I AGA GG GCAAGAAGA I GA I I I GAAGA I GA I		

¢	•	2
١	Ī	5
		ū
		٠,

02/066501	PCT/
1440 KEWIVAFDEDAPKFEASGEYCVSTDSF VITPLIFNGGDIGKLCVCGSANDVSVQ GGEPLYLNMGFILEEGLEISLLKOILQSI GKELFKANLKLLSLDTKVVPKGSVDKL FINTTCIGKIIKPGISSYHLQQGQAIILSD TIANHGASLFAMRNEIKLKTNLESDCQL LYPLLKPLFLSDLKIDALRDATRGGLAS VLNEWANSSRVKIVIEEEKIPLKEETKGI CEILGLEPYALANEGVFCHNOKDAP KALEILKSNEKAKNACVIGKVFENPYPS VVLKNAWGFERILEVPEGELLPRIC	1442 LNILLSQIPKOLGVCKDCLREIRDKNSPY FHYAFNSCAKCGARYSLLNALPYDRE NSALKPFKLCDFCASIYODPTNKRFHIO GISCKKCGIALNYKRFKNDDALLECAK DIOKGKIIALKGLGGFALLCDGRNFQTI ERLRLLKNRPLKPFALMFKDLNTAKOH AFLNALECESLISTSAPILLARKKPDIKL APNIAKNSPFYGVILPYTPLHALLLDLLD FPIVFTSANFSSLPLASDEAEIDALSFIF DFKLTHNRAIIHRIDDSIVQHVDNAIRPM RLARGAPLYTLTPKRSNGSPKKILALG AQOKGHFSLLDSGTSILLLSPFCGOLS VLENEKHFKETLNFFLKTYDFKPTILAC DKHQINYTTTOMAFDFNTPLLQVQHHH AHFLASVLDALLQDPHLNHPFIGIVWD GSGAYENKIYGAECFVGDLERIEETAR FEEFWLLGGQKAIKEPRRLVLEIALKHO LINKLLKRVOKHFKEDELEIFQQMHDKK IQSIATNSIGRLFDIVAFSLDTGTISFEA ESGQVLENIALQSDEIAFYPFEIKNSVV CLKEFYQAFEKDLGVLEPERIAKKFFN SLVEIITALIVPFKEHVVVCSGGVFCNO LLCEQLAKRLEGLKRGYFFHKHFPPND SSIPIGQALMAYFNPTIIKKG
1439 AAAAGAATGGATTGTTGCATTTGATGAAGAGGGTGCCTTAATTTTAATGGGGCCCCTTAATTTTAATGGGGCCCAAATTTTAATGGGGCCCAAACTTTTTATTTTGCAATTTTTACAATTTTTGCAATTTTTGCAATTTTACAATTTTTACAATTTTTACAATTTTTACAATTTTACAACTTTTAATCAACTTTAACAAC	1441 CTTGAÁTITIGCTCAGCCAAÀTCCCTAAAGATTTAGGCGTGTGCAAGGATTGCTTGAGGAATACAGCTTTGAAAACTTTAAAAACTTTGCCCTATTCACCCTATTTAAACGCTTTGCCCTATG CCCCCTATTTAAACGCTTTCAAACCCTTCAAACCCTTGCAAAACGCTTTGCCCTATG GCAGAAACTCCGCCCCAAAACCCTTCAAACCCTTCAAGCGATTCAAGCGATTCAAGCGATTCAAGCGATTGGCCTTGG GCTTCCACATTCAAGGCATCAAGGGTAAAATCATCGCCAATTACAAGCGATTCCAAGCGATTGCAAGCGATTGGCGTTGGC GTTTTAGAATGCGCTAAAGAGATTACGGCTTTTAAAAAACGCCCCTAAAGGCTTTACACAGCGCCCCC GATGGAAGAATTTCAAACCATACAGCGCTAAAAATTACACCCCCCCTTAAAAACTTTACAGCGCCCCCCCC
HP0047	HP0047

02/066501	Ţ		PCT/EP01/15428
1444 VEKEHGATPPKEAKIGVRKI-YRHKKW VDADVWQMEKLLPGNEVIGPAIVESDA TTFVIPKGFATRLDKHRLFHLKEIK	1446 ESLENGTKFKKRFVFELQNI)LIFLRTKR NTYSAKTEHENFGERLLAAKOTFRLIKA NDFKTKIYPYQITLRLKTKHI. VFRWLKK EIIKRFVKKOLFTETLSIKITD KGGKYA LIANYNHASDIIELMLDDKTYTTTLYYQK PLFDLIKNSNFNLTIKONTLEINQAKKRL	1448 LSDLVKNTSSVAINFDKEEEF-LNLNTLK DYELAVQILKKRANG	1450 NEIILITGAYGMVGONTALYFKKNKPDV TLLTPKKSELCLLDKDNVQAYLKEYKP TGIIHCAGRVGGIVANMNDL3TYMVEN LLMGLYLFSSALDSGVKKAINLASSCAY PKFAPNPLKESDLLNGSLEPTNEGYAL AKLSVMKYCEYVSAEKGVFYKTLVPCN LYGEFDKFEEKIAHMIPGLIAI3MHTAKL KNEKEFAMWGDGTARREYLNAKDLAR FISLAYENIASIPSVMNVGSGVDYSIEE YYEKVAQVLDYKGVFVKDLSKPVGMQ OKLMDISKQRALKWELEIPLE:QGIKEAY
1443 CGGTTGAAAAAGGCCATGCTACGCCCCAAAAGGAGCCCAAAATAGGCGTTAGAAAATTCTATCGGCATTAAAAAAATTCTATCGGCATTAAAAAAAA	1445 ACGAATCTTTAGAAAATGGCACGAAATTCAAAAAGAGGGTTTGTGTTTGAAATGCAAAATGATTTATATATTTTTGAGAAC AAAAAGGAATTGCTATAGCGCTAAAACCGAGCATGAAAATTTTCAAGAAAGA	1447 CCTTAGCGATCTTGTGAAAAATACCTCTTCTGTCGCTATCAATTTTGACAAAGAAGAAGAAAAACCTAAACCCTAAACCCTAGCGAACTCCTAGCGAACTCCTAGCGAACTCCTAGCGAACTCCCTAGCTAG	1449 TGAATGAGATTATTTTAATCACTGGTGCCTATGGCATGGTGGGGCAGAACGGGCGTTGTATTTTAAAAAAAA
HP0047	HP1497	HP1496	HP0045

_	
•	٠,
٠.	-
V	
_	7

02/066501 PCT/EP01/15428					
1452 VFKDSKKDACGFIYEISEFMKAYTALLK KQDRYVYLLRYLPSRYWASILTTALY KYDDFDALKKLLVSYYYOTWIAGGTITR IKQTSIINIIKNVKSNKSVETIKELILNSIDS YNTFDQYLYNLWDSSSVYHSKWYRPV LALANYFMADEEKPHFIAMDAETQVEH ILPOTPKRGSOWNADFDKEKREEWN NIANLTLKRKNAHALNGDFDEKRKIY GGKDTSKVIS 1454 VAKAMGDFSRVEQVLADLKNFSKEQL AQQAQKNEDFNTGKNSELYGSVKNSV NKTLVGNGLSGIEATALAKNFSDIKKEL NEKFKNFNNNNNGLKNSTEPIYAKVNK KKTGQVASPEEPIYTQVAKKVNAKIDR LNQIASGLGGVGAAGFPLKRHDKVD DLSKVGLSASPEPIYTQVAKKVNAKIDR KNOMINLYVESAKKVPASLSAKLDNYAI NSHTRINSNIGNGANEKATGMLKDSTK KNOMINLYVESAKKVPASLSAKLDNYAI NSHTRINSNIGNGANEKATGMLKDSTK KNOMINLYVESAKKVPASLSAKLDNYAI NSHTRINSNIGNGANEKATGMLTQKN PEWLKLVNDKIVAHNVGSVSLSEYDKI GFNGKNNMKDYSDSFKFSTKLNNAVKDI KSGFTHFLANNATKGGFOKS	1456 QHNRVSVESPAKLIEMLYEGILRFSSQ AKKCIENEDIEKKIYYINRYTDIFTELLU LDYEKGGEVAVYLTGLYTHQIKVLTQA NVENDASKIDLVLNVARGLLEAWREIH SDELA 1458 YFLKAPILGFEHINEVRLEKIDSLFSRLIS QTNSPMALDMVLVNIPYCLREYSFVIPK YIELLLELDSHSKVEVYCVVVLQKNLED SMVNFLAPLVFNSKNGFGAQVALSMM DYPOFGFRDPLKSFVIQERERA				
	1455 ACCAGCÁTAACCGAGTGAGTGGGAATCCCGGCAAAACTCATTGAAATGCTTTATGAGGGATTTTCAC GGCAACGCCAACGGTGATTGAAAATGAACAGGCGTGAAAAGGTTTATTATTATTATTAATGGGGTTACGGGATTTTCAC GGCAATTGTTGAATATTTTAGATTGAACAAGGGGGGGGAAGGGTTACGGGGTTAACGGGTTATCACGGGGTTAACGGGTTAACGCGCTTATACGAGGGGTTA TCAAAGTTTTAACGCAGGGCCAATGGGAAATGCGATCCTAACAATTGAAATCGCTCTTGATAAA TTACAAGCATTGGAGGCCAATGGAATCGGTTCTTAGAGCAAATAAAAGGTTTGGATTTACTGGAATTCGTTAAA AAAGGTTCTAAGGAAATGCATTCAGAAGCGCTTTCTTTAGAGCAAATAAAAGGTTTGGATTTACAAATGCCTTTAAAAGCATTCGTTAAA AAAGGCTTAAGGAAATTCATTGAAATTATTAGAAAAAGGTTTGGATTTGATTTGAAATACCAAATACAAAGGATTCGTTAATACGGCAAATTCATTTAGAAAAGCCTTTTAGTTTTAGTTTTAGTTTTAGTTTTAGTTTTAGTTTTGGGATATCGTTTAATTCGGGGAATACAG AGGCTTAATAATTAGCCAAACAATTCTTGGCTTAGAATTAGGGAATCCTTTAATTCCAAAAATTCCTTAAAAGGCTTTGGCGTTTTGGCGTTTTAGTTTTAGTTTTGGGAATTCGGCGCTTTTAGTTTTAGTTTTGGGAATTCGGTGGTTTTGGCGTTTAATTAGGAAAAAATTCCTAATAGCAAATTCCTCTAATTTAGGCGAAATCCTTTAATTAGGCGCAAAAAAAA				
HP0045	HP0601				

г	•	1	
۱	C	>	

2/066501 .		1. C O X I	1 4 H =
1460 FDVKAPILGFETIHKMRLCKIDEIFLRLN STEENSVVSFTLVNPFALRKYEFEVPT SPLANTIN OF THE STEENSVVSFTLVNPFALRKYEFEVPT SPLANTIALELEGAKSVLVANIN OV TOWN TANY LAPLIFILD KOLMGQVVLDSNKY DHYHLRENILSHTHE	1462 DKGLKKVFKDSKKDACGFIYEISEFMK AYTALLKKQDRYVYLLRYLPSRYWASI LTTALYVKYPDFDALKKL-VSYYYQTWI LTTALYKKQDRYVYLLRKL-VSYYYQTWI AGGTITRIKQTSINIIKNVKSNKSVETIKE KWYRPVLALANYFMADEEKPHFIAMD KWYRPVLALANYFMADEEKPHFIAMD AETQVEHILPQTPKRGS(WNADFDKE KREEWVNNIANLTLLKRYKNAHALNGD KREEWVNNIANLTLLKRYKNAHALNGD FDEKRKIYGGKDTSKVISCYDITKELYS	NYRKWNEKSLGERYKSLYNIIIPYLII EGGEDDFEDDFDLE 1464 RVLETIVALREYRKSLEESVGFVPTMG ALHKGHOSLIERSLKENSHTIVSVFVNP TAFGANEDFMYPRPLEKDLALCEKLG VNAFVPKIGEMYPYEAEGRLKLYAPK EI SSSI EGAMRKGHFDGVVQIVLKMFH	LVNPTRAYFGKKDAQQLLIIEHLVKDLL LDIEIAPCEIVRDDDNLALSSRNYLNA TQRKQALAIPKALEKIQCJAIDKGEKACE KLKKLGLEILETLEVDYLECCNHKLEPL TIIEPTNTLILVAARVGKTRLLDNLWV
1460	1462	146	
1459 GATTTTTGATGTGAAAGCGCCTATTTTGGGGTTTGAAACCATTCATAAAATGCGTTTGCAAAAGGTTGATGAAATCTTTTTTTT	TTTAATGAAGACGIGITITAACUSUSCATTITAGECTTGAGGGGTTTGACCCGGAAATGAGAAAGAAGATCGCCAAAACAAAAGAGTTCCACTGAGGGGGGTTCATGAGGGGGGTTCATGAGGGGGGTTCATGAGGGGGGTTCATGAGGGGGGTTCATGAGGGGGGTTCATGAGGGGGGTTCAAAAAAGGGGAAAAAAAA	1463	ATGTGAAAAATTAGGCGTTATAGTTAGGGGGGGGCCATGCGTAAAGGGCCATTTTGAAAAGGGCCATGCGTAAAGGGCCATTTTAGTTAG
HP0601	HP0601	HP1259	

			ı	١
1	١	١	3	<u> </u>
١	١			
ı		٠		

02/066501			PCT/EP01/1
1466 WTNGKFVSVKWVNGKYEEIKEDIKVSN NAGELLKQASTILTTLNEACPWLSNGG AGNVAGGNSLWAGIDKGDGSACGIFK NEISAIDDMIKNAEIAVEQSKIVTANAQN QHNLDTGKAFNPYKDANFAQSMFANA RAQAEILNRAQAVYKDFERIPAAFYKD SLGVCHEKGSDGNLRGTPSGTVTSNT WGAGCAYVGETVTNLKNSIAHFGDQA ERIHNARNLAYTLANFSGQYKKLGEHY	1468 FGGIQLAGTSWLNSQYVNLANVNNYY KAKINTSNFQFLFNLGLRTNLARNKRIG ADHSAQHGMELGVKIPTINTNYYSLLG TTLQYRRLYSVYLNYVFAY	1470 RGPKAVĎFSKLFETTGFFSYĎPGYSST AGCÓSKISÝVNGKKGELYYRGHRIEĎL VAKYKYVDVCKLLTGELPKNĎĎESLE FELELRHRSFVHESLLNMFSAFPSNAH PMAKLSSGVSILSTLYSTHONMHTEEĎ YQTMARRIVAKIPTLAAICYRNE	1472 LLGTGSSNAGSLDAANILKPVLTDGSL KCLGATTFEEYRSVFEKDKAFNRRFSV RYDESVFKACVLLKKIAPLYEEHHÜV RYDESVFKACVLLTSÖYMHÜKFLPÜK AIELLÖEVGSRKKISPKKGKKIGVÖDVK ETLALKKIPKMRLSSÖKKALLRNLEKS LKNKIFAÖAEAISLVSNAIKIÖHCGLSAK NKPVGSFLFVGPSGVGKTELAKELALN LNLHFERFÖMSEYKEAHSVAKLIGS
1465 ATGGACTAATGGAAAATTTGTTTCAGTCAAGTGGGTGAATGGGAAGGTATGAAGAAATTTAAAGAAGA		TCGTGGGCCTAAAGCGGTGGATTTTCCAA TACCGCTGGATGCCAATCTAAGATCAGGTF AAGATTTAGTCGCCAAATACAAATATGTAG AAAGCTTGGAATTTGAATTGGAATTGCGCC CTAGCAACGCCCACCTATGGCAATTGCGCC ATGCAACGAAGATTACCAAACTTG	1471 CCCI II I AGGCACAGGGAGCAG FACGCI I GGATGCGGCGAATATATTAAAACCGGTTTTAACGGATGG GAGCTTGAAAACTTTAGGAGCGACCACTTTTGAAGACGCGTGTTTGAAAAACGGTGCTTTTAATAGGC GATTTTCAGTCATAAAAAGTTTGAAGAGGCGTGTTTTAAAAAAGATCGCTCCCTTTATGA AGAACCCACCACCACGGTGCTTAGATGAGAGCCTGTTTTAAGGCATTTAACGGATGATTACATGCATG
HP1259	HP1259	HP1259	177259

V	7
V	3
C	١

	02/066501		PCT/EP01/	15
	1474 AEEKHAKENTKPLHFCFAGHIDVVPPG INHWQSDPFKPVIKEGFLYGRGAQDMK GGVGAFLSASLNFNPKTPFLLSILLTSD EEGPGIFGTRLMLEKLKEKDLLPHMAIV AEPTCEKVLGDSIKIGFRGSINGKLILK GVQGHVAYPQKCQNPIDTLASVLPLIS GVQCHVAYPQKCQNPIDTLASVLPLIS	1476 ASVLSALLLYGLGAAPIHSVSANDKRM GDNLVSVIEKQTNKKVIRLERPLKSSQ DLKMVVIEDPDTKYNIPLVVSKDGNLIIG LSNIFFSNKSDDVQLVAETNQKVQALN ATQONSAKLAAIFNEIPADYAIELPSTN AANKDKILYIVSDPMCPHCQKELTKLR DHLKENTVRMVVVGWI.GVNSAKKAAL IQEEMAKRARGASVEDKISILEKIYST	1478 TSLARGELKNPGFTQAJELRQLRDGA VRLQTSAIPLSYTLDILG:NKTATLLRESL KNNAQPSQPNQQPPQJNGPSNQALA NLEQSLGILGKLLDLSQQYSQGVIRPL VVDVGKEGIGITDSMLVAQNIVLALGG VDLSKIQQNNNEQLSQIATGMANFALGG GTNGAYNGVSVGDIATGMANFSSQTG LIGANSTVSELNALIKSGISLDRETLGLG SFIEKNICSGASSCFSGVQLYKKGLDR TINIINTYLGQFESSASSLYKISYIPNLFS LKDYQSASMNGFGAKMGYKQFFTHKK NVGLRYYGFLDYGYANFGDTNLKVGA NLVTYGVGTDFLYNVYERSRRRERTTI GLFGAQI 1480 INHMIMSRREAFGVRFVNKIGAMKELIK MYNQGNGLVGILVDONVVPKDGVVVK FFDRDATHTTASILSRRYNIDIQPVFID FNDDYSHYTATYYPSIRSQITDNAQNDI LECTQAQASICCEEVIRNHPESYFWFHR RFKSTHPEIYQR	
4/77/17/04/04/4/04/4/04/4/4/04/4/4/4/4/4/4/4/4	CTGGAAATCATTGGCAAGCGATCCTTTAAACCCGTTATTAAAGGGGGTTTTTATACCCCTAGGGCCAIAITGATGTGTGCCTC CTGGAAATCATTGGCAAGCGATCCTTTTAAACCCGTTATTAAAGGGGGGTTTTTATACGGCCGTTGGGGCGCAAGAC ATGAAGGAGGGGTGGGGGGCGTTTTTGGCGGTTTAAATTTTAACCCTAAAACCCTTTTTTGCTTTCTATTTTA CTCACAAGCGATGAAGAAGGGGCTTCTGCGAAAAAGTCTTAGGCGATAGCACAAAAAATGCCGAAAATGCCAAATTGTGTGCGCAAAAAATGCCGAAAAACCTATTTGAGGGGGTTTGAGGCGATAGCAAAAATGCCGAAAAAACCTATTTGAGGGGGTTTGAGGGGGGTTTAGACAATGGCGAAAAACCCTATTGAGGCGATAGTTTTGAGGGGGTTTAAATAATAATACCCGAAAAATTTTTGAGAAAATTCAAAAATTAATAAAAAAAA	1475 GAGCGAGTGTGTGAGCGCGTTACTTCTTGTAGGGGCAGCCCCTAAACATTCAGTTTCAGAAACGCGCCCCTAAACGCGTATTTTAGTGAAACCCTTTTAAACGCGTAATTTAATTCAGAAACCCGAAAAACGCACTAAATACAAAACCGTTAAGCGCTTTTAATTCATTAGTGCCGTAAACCCTTTCATTAGTTGCAGAAACCCTTTAATTCAAAAACCCTTTAATGCACCAACAAAACGCGTATTTTTTAATGAAAAACCCCTTTAATGCCCCAACAAAAACGCGCTCAGAAATGCCAAAAAACCCTTTAATGAAATACCCTTTTTAATGAAATACCCTTTGATCCTTTAATGCCAAAAAACGCGTTTAATGCCAAAAAAACGCGTTTAAATGCCAAAAAACGCGCTTTAAAAAAAA	1477 AGACGAGTITGGCCAGACAGGAATTGAAAATTCCAGGCTTCACCCAAGGGCAAGATTAGGGAATTAGGCAGTTCACAGAGTTGATCAGAGTTTAGGCAATTTGGAATTTTAGGGAATTAGGCAACTCTTTAGGGAATTAGGGAATTAGGGAATTAGGGAATTAGGGAATTAGGGAATTAGGCCACCACAAACGGATCTTTTGCGTGAACTCTTTAGGAAACTCTTTTTTTAGGAAACTCTTTTTTTT	ATTACCATITA
ייטייט		HP1259	HP1259	

۹	L	4	۴	۰
_	7	١		•
١	L	ı		
ı	3			١
1	г	٠	٠	ı

				1 0 1/11 01/13426
1482 SSSNGGNGSSTQTTATTTQDGVTITTT YNNNKATVKFDITNNAEQLLNGAANIM QVLNTQCPLVRSTNNENTPGGGDPW GLSTSGNACSIFQQEFSQVTSMIKNAQ EIIAQSKIVSENAGNGNNLDTGKPFNPY TDASFAQSMLKNAQAQAEMFNLSEQV KKNLEVMKNNNNVNEKLAGFGKEEVM TNFVSAFLASCKDGGTLPNAGVTSNT	1484	1486	1488	1490 TNSFNKNPHLMRMWSLDDVFNÖSELÖ LLYÖHGKLVKATTRGNGLEGELVSAN LLYÖHGKLVKATTRGNGLEGELVSAN LLYÖHGKLVKATTRGNGLEGELVSAN KHIANIPHAIAYNGEIERGEVIISKKDFD ALNÖERLNANEPLFANPRNAASGSLR QLÖSEITKKRKLÖFIPWGVGKHSLNFL SFKECLÖFIVSLGFSAIQYLSLNKNHÖE IEDNYHTLIREREĞFFALLDGMVIVVNE LNIÖKELGYTÖKSPKFACAYKFPALEK HTKIVGVINQVGRSGAITPVALLEPVEIA GAMINRATLHNYSEIEKKNIMLSDRVVV IRSGDVIPKIIKPLESYRÖGSOHKIERPK VCPICSHELLCEEIFTYCÖNLNCPARLK ESLIHFASKÖALNIĞGLGDKVIEÖLFEE KLIFNALDLYALKLEDLMRLÖKFKIKKA
1481 TAGCAGTAGTAATGGCGGTAATGGCAGTAGCACCAAACAACCACCGCAACCAGCAAGACGAGACGGTCACCCAGAGACGATAACCAAGACGATAACCAAGACGATCACCAATAACCAAGACAACAACACCGCAAGACCGCAAGACCACTAATAACCAAAACACCTATAATAACAAAACCACCTTAAATCAAGCAATGCCCATTCCACCAATAACGAAAACACTCCCAGGGGGTGGTCAACAACACATCATGGGGTTTAAACCAACAACACTCCCAGGGGGGTGGTCAACAACACTCAGGGGTTAATCAGCAATGCGGGAATGCTTAGTGAACAACAACAACAAGAAATTAGCCAAGAATTAGCCAAGAATTAGCCAAGAATTAGCAAGAATTTAGAAAACGCCCAAGAACAAGAAGAAGAAGAAGAAGTTGGAAGCGCAAAGCGCCAAGAATTTGGGAAGTTTTGGGAAGAATTTGGCAAAGAATTAGCAAGAATTAGCAAGAATTTGGAAATTAGCAAGAATTAGCAAAGAATTAGCAAATAGATAATGATAATGATAATGATAATGATAATGATAATGATAATGATAATGATAATGAAAAAA	1483 TGGCTAAAGAGGGGTTTAAACCTTTTGTGAGCATCTATTCTACTTTTTTGCAGAGGGCTTATGATGATTCTATTGTGCATG ACGCTTGTATTTCTAGCTTGCCGATTAAATTAGCCATTGACAGGGGCTTGTGGGCGAAGATGGCGAGACGCA CCAAGGGCTTTTAGACGTGTCGTATTGCCGTTTATCCCTAACATGGTCATTTTTGCCCCACGAGACATGAGACTTT AAAAAACGCCGTGCGTTTTGCCAATGAACACGATTCAAGCCCTTGCGCGTTCCGATACCTAGGGGGTCGTTTGCG TTAAAAGAGGGGGTTTTTGAGCCTAGCGGTTTTTGTTTTAGGCCAAAGCGAATTGTTGAAAAAAAGAGGGGCC	1485 TGAGTGCTAATCATTGCGTCTTGAGGGGGGGTATGGGGGGGG	1487 AATACCTIGICATCAAAAGAAAGGGTGTGAAATGGGTTTAAACGCGCGCTAAAACTCACCAAAAAGGCCCAACAAATCAA AGAGCTGCTTTTAAAAACATTACCCCAAACCACCAACCAA	1489 CACCAATÍCGITCAATAAAAACCCCCATITAATGCGGATGTGGAGCTTAGATGATCAATCAAAGCGGAATTGCA AGCGTGGTTCAATCAAAAACCCCCCATITAATGCGGATGTGGAGCTTAGATGCAACTTGATCAACTTGATGCAGGTTTTGC TCAATCTTTTGTATCAACATGGCAAGCTAGTGAAGGGCGAACTGGTGTTTAGC TCAATCTTTTGTATCAACATGGCTAATATCCCCACACTTAGAGGAGAATTAGTTAG
60	69	69	g.	o
HP1259	HP1259	HP1259	HP1259	HP1259

۰				
			1	
٠	4	r		

				PCT/EP01/
	1492 ASAEFLEREKEKAKNEKRPFIRYSDEW ATLEKOKHHAPVVRLKAPNHAVSFNDA® IKKEVKFEPDELDSFVLLRQDKSPTYNF GACACDOLLYKISLIIRGEOHVSINTPKQIL GACACDOLLYKISLIIRGEOHVSINTPKQIL IQQALGSNDPIVYAHLPIILDEVSGKKM IQQALGSNDPIVYAHLPIILDEVSGKKM IQQALGSNDPIVYAHLPIILDEVSGKKM IGNKVPKEVFSLDEAIEWFSLENLSSP IGNKVPKEVFSLDEAIEWFSLENLSSP IGNKVPKEVFSLDEAIEWFSLEREKIS SIKDKNLLGLRLFIEEGGTLLELREKIS IFLEPKDIVKTYENEDFKERCLAFNAL TSMDFQAYKDFESFKKEAMRLSQLKG TSMDFQAYKDFESFKKEAMRLSQLKG TSMDFQAYKDFESFKKEAMRLSQLKG TSMDFQAYKDFESFKKEAMRLSQLKG TSMDFQAYKDFESFKKEAMRLSQLKG TSMDFQAYKDFESFKKEAMRLSQLKG TSMDFQAYKDFESFKKEAMRLSQLKG KDFFKPLRILTGNSHGVELPLIFPYIQS HHQEVLRLKA NGVEIVGLEHLDKVIYLDQAPIGKTPRS NPATYTGVMDEIRILFAEQKEAKILGYS	ASRFSFNVKGGRCEKCGGDGDIKIEM HFLPDVLVQCDSCKGAKYNPQTLEIKV KGKSIADVLNIMSVEEAYEFFAKFPKIAV KGKSIADVLNIMSVEEAYEFFAKFPKIAV KLKTLMDVGLGYITLGQNA "TLSGGEA CRIKLAKELSKKDTGKTLYI! DEPTTGL HFEDVNHLLQVLHSLVALGNSMLVI HFEDVNHLLQVLHSLVALGNSMLVI 1496 APPSQARLWVVPPSKMDEGELINEGY YAIFGAAGARTEVPGCSLCMGNQARV YAIFGAAGARTEVPGCSLCMGNQARV	RDNAVES IS IN THE STANKEY GSAELGAACALLGRIPTKEEYMNLVS GSAELGAACALLGRIPTKEEYMNLVS 1498 TMINTMFCATMORGVAEIVAVEATFTR ALPAFVISGLANSSIGEAKURVOSALO ALPAFVISGLANSSIGEAKURVOSALO	NNDF I FFFLATION OF THE STATE O
267	-		- 00	
	HP1259	HP1259	HP1259	HP1259

		_
(×	0
١	•	3
ż	:	

02/066501		PCI
1500 AKNIMITLKQALSLSQDELETLKNEIDAK VRASDLNAYIKAPSLNGASAKGVPILIK DNISVKGWEITCSSKILEGYVAPYHASV MENLHQNSMAGFGLSNMDEFAMGST TESSCYGITKNPRDKNRVPGGSSGGS AAAVAGGLAVAALGSDTGGSIRQPASY CGCVGLKPTYGRVSRYGLIAYCSSFD QIGPITQNVEDASILFDAISGYDSKDST SANLKPTQTFKNLNRDKRFKIAVLMDHI KDASNEVQLAYENTLKALKE	1502 KEDLKRLGIQKEIFYISVNEENEKALLN CYPNAKNIAGFFHLETDYVGLGIDRÖM ACLAVNNGVVVDAGSAITIDLIKEGKHL GGCILPGLAQYIHAYKKSAKILEQPFKA LDSLEVLPKSTRDAVNYGMVLSVIACIQ HLAKNQKIYLCGGDAKYLSAFLPHSVC KERLVFDGMEIALKKAGILECK	1504 VSSHDÖYERMKKSGSLNTENLDSHIÖ ANSLGELNÖKLLÖFVGADRKYMPYTK AVOISLKINPRILKDLEVIÖTPGVNDPIAS REERTKALLKÖCDVVFIISSSNÖFLTES DMSLFÖRVSNKESLÖEIYFVASÖAĎSA VLSMSEVEKSRHHLPTALENAÖKSLSS SLNKTMEALIOTNPNORGIFEKAIKNÖV ILTSGAČFSMYKDFKNOASWESKKEE CYNAWRNLTNAYPLTLLTALINLKKAYY S
1499 GGCTAAAAACATGATCACTTTAAAACCAGCCCTTTATTCCCCAGGATGAATTAGAAACCCTTTAAAAACGAAATTGACGCCTAAAGGGCTGACGCCTAAAGGGCTGCCGAAGGGCTGCCGGCTAAGGTTTGAAGGGCTTGCGCCTAATTGAAGGGCTTGCGCCTAATTGAAGGGCTTGCGCCTAAGGTTTTAGGAAGGCTTGCGCGAAATCACTTGCTCCCTTGCTCCCTTGCTCCCTTGCTCCCTTTTTAGGGGCTTTTTAGGGGCTTTTTAGGGGAGCGATTTTTAGGGACGAGTTTTTTAGGGACGAGTTTTTAGGGACGAGTTTTTAGGGACGATACTGCCAAAAACCCACGGGGTTTAGGGGATCACTAGGGGTTAGGGGATCACTAAAAACCCACGGAGGCGTTATGCGGGCGCGTTAGGGGGCTTTAGGGGAGGCGTTATGGGGAGGCGTTATGCGGGCGCGTATTGCGGGCGCGTATTGCGGGCGCTTATGCGGGCGCTTATGCGGGCGCTTATGCGGGCGCTTATGCGGGGCGTTTAGGGGAGGGTTTTTATTTTGAGGCGTATTGCTCTAGTTTTGATGGGGGCGTATGAGGCGTATTGATTTTATTTTGAGGCGTATTGCTTAGGGGGCTTTAAAAACCCACTTAAAAACCCACGAAACGCTTAAAAACCCACTTAAAAACCCACGAAACGCTTAAAAACCCACGAAACGCTTAAAAACCCACGAAACGCTTAAAAACCCACGAAACGCTTAAAAACCCATTAAAAACCCCTTAAAAACCCCTTAAAAACCCCTTAAAAACCCCTTAAAAACCCCTTAAAAACCCCTTAAAAACCCCTTAAAAACCCCTTAAAAACCCCTTAAAAACCCCTTAAAAAA	1501 TAAAGAAGATTTAAAGCGTTTGGGTATTCAAAAGGGAAATTTTTTACATTAGCGTGAATGAA	1503 CGTTTCATCACACGATCAATACGAGCGCATGAAAAAAGCGGATCGCTCAACACGGAAAACTTAGGATTCGCACATTC AAGCCAACAGCTTACAAGAGCTGAATCAAAAATTGCTCCAATTGGAGGGCGCGGATAGGAAGTATATGCCCTACACT AAAGCGGTGCAAATTTCTTTGAATAACCCCAATCTTAAAGATTTGGAAGTGATTGACACCCCAGGAGTGATGACCC AAAGCGGTGCAAATTTCTTTGAATAACCCCAATCTTATTGAAAGATTGATT
HP1259	MP1259	HP1259

	ı.		
Į	ζ	5	١
1	۱	£	
í	è	₹	ĺ

	2/066501		PCT/	EP01/15428
	1506 IVYHPYHWIPIGFMLDIQNWTLKDIKKF HSLYYQPKNANLLWGDVNSQKVFELS KKHFESLKNLDEKAIPTPYMKEPKQDG ARTAVVHKDGVHLEWVALGYKVPAFK HKDQVALDALSRLLGEGKSSWLQSEL VDKKRLASQAFSHNMQLQDESVFLFIA GGNPNVKAEALQKEIVALLEKLKKGEIT QAELDKLKINQKADI:ISNLESSSDVAGL FADYLVQNDIQGLTIJYQRQFLDLKVSD LVRVANEYFKDTQSTTVFLKP	1508 LKAPKPNTPQIMAVI NLTPDSFYEKSR FDSKKALEEIYQWLEKGITLIDIGAASSR PESEIIDPKIEQDRLKEILLEIKSQKLYQ CAKFSIDTYHATTAQMALEHYFSILNDV SGFNSAEMLEVAKDYKPTCILMHTQKT PKDMQENVFYHNLFIDEMDRFFKEKLE VLEKYVLQDIILDIGFGFAKLKEHNLALI KHLSHFLKFKKPLLVGASRKNTIGLITG REVQDRLAGTLSLHI MALQNGASVLR VHDIDEHIDLIKVFKSI.EETD	1510 NMKNLVILSGAGISAE:SGIKTFRDADGL WERA 1512 SKESLMHAINSIRVGMHFKELSQILESTI TERGFVPLKGFCGHGIGKKPHEFPEIP	NYLEKGVKPNSGPKIKEGMVFCLEPM VCQKQGEPKILADKWS 1514 YSGGSSFSPTIQLTYHINNAENLLQQAA TIMQVLITOKPHVQTSNGGKAWGLSST PGNVMDIFGPSFNAINEMIKNAQTALA KTOQLNANENAQITQPNNFNPYTSKDK GFAQEMLNRAEAQAEILNLAKQVANNF HSIQGPIQGDLEECKAGSAGVITNNTW
1505/ATGTCTATCACCCTACCATTGGACGCCCATTGGTTTTATGGATGATATTCAAAATTGCAGTTATAAAAATTGCAGTTATAAAAAATTGGAGTTATAAAAAATTGGATGATTATATAAAAAA	ATTCCATTCGCTCTATTATCAGCCTAAAAACGCTATCGTTTGGTGGTAGCCAATTGCAATTCCCAAAAGGTTTTGAAAAAAAGCTATCCAAAAAAAGCTACCAAAAAAGCTACCAAAAAAGCTACCAAAAAAGCTACCATGAAAAAGGTTTTGAAAAAAGCTACCATGAAAAGGGTTTTTGAAAAAAGCTACATGAAAAAGGGTAAAAGGGTAAAAGTGGGTAAAAGTGGGTATAAAGTGGGTATAAAGTGGGTAAAAGTGGGTATAAAGTGGGTATAAAGTGGGTATAAAGTGGGTATAAAGTGGGTATAAAGTGGGTATAAAGTGGGTATAAAGTGGGTATAAAGTGGGTATAAAGTGGGATTTCAAAAAAGCTTCAAAAAAGCTTTCTCCAAAAAAGAAAG	1507 ACCTCAAAGCCCCTAAGCCCCACAGATCATGGCAGTTTTAAACTTGACTCCGGATAGCTTCTATGAAAG AGCCGGTTTGATAGCAAAAAAGCGCTTGAAGAATCTATCAATGGCTAGAAAAGGGTATCACGCTCATTGATATAG GGCGGCCAGTTCAAGGCCTTGAAGAATCTTGATCCAAAATGGAGCAAGATCGCTTAAAAGGATTTTATTAG CGCGGCCAGTTCAAAAACTCTACCAATGGAATTCAGCATAGACCCTACCATGCCTAAAAGAATTTTATTAG AAATCAAATC	1509 GCAACATGAAAAATTTAGTAAAGCGGGGGCTGGTATTTCAGCAGAAAGCGGGATTAAAAACCTTTAGAGACGGTTAGAGACGCTTAGAGACGGTTAGAGACGGTTAGAGACGGTTAGAGAAAAAGAAAAAGAAAAAGGAAAAGGAAAGTTTGGATTTTACAAACAA	TGCTTAGAGGCTATGGTGTGTGAAAACAGGGCGAGCCTAAAATAGCGGGATAAGTGAAAGAGGGGGATATTTTGCTTAGCGGGTAAATTGGAAAAGAGGGGGTATTTTGCAAAAAGAGGGCGTATGGCGGAAAAGAGGGCGAAAATTGGCGAAAATAGTGGGGGTTTTTGCAAAAGGCGTAATTAGTGAAAAGCGTGAAAAGCGTTTTTGCAAGGGGTTGCATGATCAAGGCGTAAAGCGTGGGGGTTGGATGAATGTGATGAATGTGAAGGGGTTAAAAAGCGCTAGCAATGTGATGAATTTTAAAAAGCGCTAGCAAAAGCGCTAGCAACAGGGTTAAAAAAGCGCTAAGAAAAGCGCTAAGAAAAGCGCTAAGAAAAGCGTAAAAGAAAAAAAA
HP1259		HP1259	HP1259	HP1259

(3)
	٠		
	•	۰	3
7			

0	02/066501	100	· · · · · · · · · · · · · · · · · · ·	PCT/EP01/1	5428
		1516 FKPFKDAFYRDFNHNEGKLLIGAAKSG CIGSSADKLAQLKTRLLYWQDKSVKVD WDKPILIKDFFKGNNYLYRRFCFLLGK HFWDRFLKNNAKASVKDFMSSKEFVA KYRYTPKGNTERAKKLGSYLENKRDFI GFVQALNSLKÖNPQDPFLPNEETSFLV FANEPTIVFNLRDYLLVLAQIFNOQAK	YGESKÇPI 1518 EPKTYAKWOEQQAFKRMQARKDNHG DFTLHÖGPPYANGHLHLGHALNKILKDI VVKREYFKGKKIYYTPGWDCHGLPIEQ QILERLEKEKTSLENPTLFREKCRDHA KKFLEIQKNEFLQLGVLGDFEDPYKTM DFKFEASIYRALVEVAKKGLLKERHKPI YWSYACESALAEAEVEYKMKKSPSIFV AFGLKKESLEKLKVKKASLVIWTTTPW TLYANVAIALKKDAVYALTQKGYLVAKA LHEKLAALGVVDNEITHEFNSNDLEYLV ATNPLNQRDSLVALGEHVGLEGGTGA VHTAPGHGEEDYYLGLRYNLEVLMSV	1520 NKVEGVTEILHVNERĞTLGFHKELKKG VEANNKIQVEHLNPHYKMNLNSKASVK ITPLGGLGEIGGNMMVIETPKSAIVIDA GMSFPKEGLFGVDILIPDFSYLHQINCKI AGIIITHAHEDHIGATPYLFKELQFPLYG TPLSLGLIGSKFDEHGLKKYRSYFKIVE KRCPISVGEFIIEWIHITHSIIDSSALAIQT KAGTIIHTGDFKIDHTPVDNLPTDLYRL AHYGEKGVMLLLSDSTNSHKSĞTTPS ESTIAPAFDTLFKEAQGRVIMSTFSSNI HRVYQAIQYGIKYNRKIAVIGRSMEKNL DIARELGYIHLPYQSFIEANEVAKYPDN	1522 FLDAMIKKOENAIKRIEARKCAVSÖDFK OGMKRNIKVINLVKA
GGCGTGATCACTAATAACACTTCGGG		1515 CCTTTAAACCCTTTAAAGACGCTTTTTACAGAGATTTCAATCATAATGAGCCAAÁAGTTACTGATAGGGGGCAGCTAAAA GCGGTTGCATTCAATCTAGCGCTGATAAAACTGGCCATACTCTGATACTGGCAAGACAATCTGTTA AAGTGGATTGCGATAAACCCATTTTAATCAAGGACTTCTTTAAAGGCAATAATTACCTTTATGGCAGTTTTTTTT	1517 TGAGCCTAAAACTTACGCCAACGGCATTTAAAGGCATTGCATTTGGGCATGGCATGGCATGGGAAGGCTAGGGAAGGCTAGGGAAGGCTAGGGAAAGACATGGCAACGGCATTTAAAAAGGCTTAAAATTTTAAAAGGGAACGGCTTTTAAAAGGCATTTTAAAAAGGGAAGACATTTTAAAAGGGAAGACATTTTAAAAGGGAAAAAGAAAAAGGCTTTACCGCTTGGGGTTTTTAAAAAGGGCGCGCTTTTTAAAAAGAAAAAGGTTTTTAAAAAGAAAAAGGAAAAGAAAAAGAAAAAGAAAAAGAAAA	1519 CAACAAGTACAAGGCGTTACAATTTTGCATGTGAATGAGGGGGCTTTAAGGCTTTCATAAGGGGGTTAAAAAAAA	CTTCAAACAAGGTATGAAACAGGAAAATGCGATTAAACGCATAGAAGCACGAAAATGTGCGGTAAGCGATGA
		HP1259	HP1259	HP1259	11L0307

PCT	/EP01	/15428
-----	-------	--------

VO <u>02/066501</u>			PCT/EP01/154
1524 KKRVEKVQESFKALDKAKKEWLKALEA PIDEREDELVRSLTLAYKROTI.KÖRLY OLEPTSKLINELVKTMETTLKSGDGFEK ELKRLEYKLPLENDTLANHKKILANITN MTKEDIJAQVPEATMVSVYMDLKKLFLT KEASEGFDLAPNKLKEILEQIKRGKLI SDRAKNKMAKSNLRLVVSIAK RFTSRG LPFLDLIQEGNIGLMKAVDKFE:HEKGFK FSTYATWWIKQAISRAIADQAIRTIRIPIH	1526 QILEPISSKRLKELADLKISCATIRNYFQI LSKEGMLYQAHSSGARLPTFKAFENY WQKSLRFETLKVNEKRLKSASSENFGLF TLLKKPSLERLERVIECEKRFLILDFLAF SCALGYSVKMEKFLLELVGRSVKEVRS IAASFNALSLARQLERLEYSNTGITRFN LMGLKTLLNSPLFFDILGGKVLERLSKG LHFIEPDCMLYTRPVEFQNKRMQLLCV GKLECDYEGFFGTISEE	1528 LGLLNGFILQSYKVEKEFKDYKALYEW VIEILPQAIWVVNENGSFFYKNSLANGS HEVFNKAKLENFNTEIEHENKISYLVQQ NSIQGKQIITATDISAQKRQER_ASMGK ISAHLAHEIRNPVGSISLLASVLLKHANE KTKPI	1530 LKGVFGHDNKEKINALLGEKKKFFIDD NLENKHLDTTMVSEFVGKTRAFIKIDD GCDFDCNYCIIPSVRGRARSFEERKILE QVGLLCSKGVGEVALTGTNVGSYGKD RGSNIARLIKKLSGIAGLKRIRGSLEPN QINDEFLELLEEDFLEKHLHIALQHSHD LMLERMINRTKSDRELLETIASKNF AIGTDFIVGHPGESGSVFEKAFKNLESL PLTHIHPFIYSKRKDTPSSLMTDSVSLE DSKKRLNAIKDLIFHKNKAFROLQLKLN TPLKALVEVQKDGEFKALDGFFNP
152	152	152	. 153
1523 AAGAAGCGTGTAGAAAAGGTTCAAGAAAGCCTTTAAAGCCCTAGACAAGGCTAAAAAAAGAATGGCTTAAAAGCCCTTGA AGCCCCCATAGATGAAAAGACGATTTGGTGCGTTCATTGACCTTACAAACGCCCAAACGCCCAAAGACA AGCCCCCATAGATTTAGAACCTACCAGCAAACTGATTAATGAATTAGTCAAAAACGATGGAAACCACTTTAAAAAAGCGGCG ATGGGTTTGAAAAAGAGTTGAAACGCTTGGAAAACGCTTATTCAATGACACTCTCTATCGATGAACCATTAAAAAAAA	1525 CAGATITTAGAACCCATTAGTICTAAACGCTTAAAAGAGTTGGCGGACTTGAAAATATCTTGCGCGACGATCAGGAAT TATTITCAAATCCTTTCTAAAGAGGGCATGCTTTATCAAGCCCATTCTAGTGGCGCTAGATTGCCCACTTTTAAGGCG TATTITCAAAACCTATTGGCAAAAGTCGTTGCGCTTTGAAAGCTGAATGAA	1527 CTAGGGCTITIAAACCAATTIAITITGCAAAGCTACAAGGTAGAAAAGGGAATTIAAAAGATTATAAAAGGCCTITATGAAT GGGTCATAGAGATTITACCTCAAGCCATTIGGGTGGTGAAAGAAACGGGGAGCTTITITATAAAAATTCTITAGCCA ATCAAAGCCATGAGGTGTTCAATAAGGCTAAATTAGAAAATTITAACACTGAAATTGAACATGAAAATAAAAAGGCTATTT AGTCCAGCAAAACAGCATTCAAGGCAACAATCATCACCGCAACCGATATTAGCGCTCAAAAACGCCAAGAGGGG CTCGCTTCTATGGGGAAAATCTCAGCGCATTTAGCCCATGAGAACCCTGTAGGTTCTATCTCTCTTTTAGCT TCAGTGTTATAAAGCATGCAAAAAGACTAAAGGCAATT	1529 TTTAAAGGGCGTTTTTGGCCATGACAATAAAGATAAAGATTAACGCGCTTTTACAAGAAAAAAGGGTTTTTTTT
HP0962	HP0962	HP0962	HP0962

HP0962	1531CA AA ATI GA	1531 CAGCCATTTAGTCGTTTTGATCGAACCTAAAATAGAGATCAATAAAGTTATCCCTGAAAGGTTATCAAAAAGAGTTTGAG AAGTCTTTGTTTCTCCAGTTGAGTTTTTTAGAGAAAAAGGCTATAGCGTTTCGCAATTTAAAGATGCCGAA AAGTCTTTGTTTCTCCAGTTGAGAAAAAGCGTTTTTAGGCAAATGGGGAATGTGGCTATCTTGGAAGATATTGTA ATCCCTCAAGAGACGATGCGTTGCTCGTTTTACGCATGGGATGGGGAATGTGGAAGAGAGAG	1532 SHLVVLIEPKIEINKVIPES FLOLSSFLERKGYSVSQI KEKALLVLRMDGNVAILE EEKVIDMSSGYLNLNFVLE GIDVSKKAVIEDVIEIDFY	1532 SHLVVLIEPKIEINKVIPESYQKEFEKSL FLQLSSFLERKGYSVSQFKDASEIPQDI KEKALLVLRMDGNVAILEDIVEESDALS EEKVIDMSSGYLNLNFVEPKSEDIIHSF GIDVSKKAVIEDIVEI DOT
нР0962	1533 177 1533 177 177 177 177 177 177 177 177 177 1	GCGCACCAA 1533 TTGGAATACGCTGATCCTAGCACTTCTAAAAAGGGGCTTAAAAAAGGGTGTTCAAAGACGCCAAAA AGACGCTTGCGGGTTCATGAGATCAGCGGTTCATGAAAAGGCTGTTCCAAAAAAACGCGAT AGACGCTTGCGGGTTCATCTATGAGTCTCATGCTAAAAGGCCTATAGCTAAAAAACAGCCGAT ACGTCTATTTATGAGGTATCTCCCCTCTAGGTATTGGGCCACACTTGCAGAGACCGATCCCCTG ATTTGACGCTTTGAAAAAGCTTTTGGTGTCTTATTATCCAAACTTGCAGGAGGCACCATCACCGCGCATCA AGCAAACCAGTATCAACATTATCAAAAACGTTAAAAGAGCGTTGAAGCCGTTCTTTTTTTT	1534 LEYADPSTSKK ACGFYEISEFN LLYSYYYQTM KLLVSYYYQTM VKSNKSVETIKI NLWDSSSVYH DEEKPHFIAMD SQWNADFDKE SKKNAHALNGI RKKNAHALNGI	1534 LEYADPSTSKKRADKGLKKVFKDSKKD ACGFIYEISEFMKAYTALLKKODRYVYL LRYLPSRYWASILTTALYKYDFDFDALK KLLVSYYYQTWIAGGTITRIKQTSINIIKN VKSNKSVETIKELILNSIDSYNTFDOYLY NLWDSSSVYHSKWVRPVLALANYFWA DEEKPHFIAMDAETOVEHILPQTPKRG SQWNADFDKEKREEWVNNIANLTLK RKKNAHALNGDFDKRKIYGGKDTSK VISCYDITRIKL LYSNYRKWNEKSLQERY
HP0962	1535 AAC 0 CA1 0 CA1 0 CA1 0 CA1 0 CA1 0 CA1 0 CA1 0 CA1 0 CA1 0 CA1 0 CA1 0 CA1	AGGATGATGAAGCATCAAGAAGAGGTATTAAAGATGATTTGATCTAGAATTGAAGATTGCCAAGCATCAAAAACAACA AAGAGGTGATCAATGAAAAAGAGCTATTAAAGATGTCTAGAAAGCATCAAAAGAACAACA AAGAGGTGACCGCC AAGGAGCACCGC 1535/AAGGAGAAGGTATTATAAAATCGCGCGCCTTAAGGATCATTATGTGATTTGTTACCACAATACCACATTTACCAATACCAATACCAATACCAATACCAATACCAATACCAATACCAATACCAATACCAATACACAATACCACTTAAACACAATACCAATACCAATACAATACACAATACCACTTAAACACAATACACAATACAATACAATACAAATACAAATACAAATACAAAAAA	1536 KEKGMİYKIARL KOFRSAQIPFV YPYYIIGDPHTN LSKILPVNVALM IIASAHSDEGLEI MAQRVSAMAVF	1536 KEKGMİYKIARLKÖHYVICYHNEYTIELS KQFRSAQIPFVVVÜNDPSFEEEAIKHK YPYYIIGÜPHTNLAMLKTHLSSARGVVA LSKILPVNVALMVSVRLFEKELKRKPYY IIASAHSDEGLEKLKKLGADMVVSPTKL MAQRVSAMAVRPÜMENILERFINKKÖT LLÖLEEVIVPKTSWLVLRKLKEAHFREI
HP0962	1537 1537	1537 ATGAGTACCCACAAATTTGAGCAATAACAAAATTTATCAAGCAACAACGAGAAATGAATTAGACCATTAACAAAATTTATCAACAACAACAACAATTTATCAACAA	AKAF 1538 MSNPÖNLSNNKNLSEFIKÖÖRENELD OMERLEDMÖEGAGANALKOIEELNKK GAEETIKQRAKDKINIKTDKPÖKSPEDI SIELSPSDSAWRTNLVVRTNKALYÖFIL SIELSPSDSAWRTNLVVRTNKALYÖFIL RIAQKDNFASAYLTVKLEYPÖRHEVSS VIEEELKKREEAKRÖKELIKÖENLNTTA YINRVMMASNEGIINKEKIREEKÖKIILD ÖAKALETÖYVHNALKRNPVPRNYNYY GAPEKRSKHIMPSEIFÖDGTFTYFGFK NITLÖPAIFVVÖYDĞKLSMTDAAIÖPNN TNSGLRWYRVNEIAEKFKLIKÖKALVT INKĞYĞKNPLTKNYNIKNYĞELERVIKK LPLVRDK	AKAF MŚNPÓNLŚNNKŃLŚEFIKÖĞRENELĎ OMERLEDMOEGAGANALKOIEELNKK GAEETIKORAKDKINIKTDKPOKSPEDN SIELSPSDSAWRTNLVVRTNKALYÖFIL RIAGKDNFASAYLTVKLEYPORHEVSS VIEEELKKREEAKROKELIKOENLNTTA YINRVMMASNEQIINKEKIREEKOKIILD OAKALETĠYVHNALKRNPVPRNYNYY QAPEKRSKHIMPSEIFDÖGTFTYFGFK NITLÔPAIFVVQPDGKLSMTDAAIDPNIM TNSGLRWYRVNEIAEKFKLIKÜKALVTV INKGYĞKNPLTKNYNIKNYGELERVIKK

2/066501		·	PCT/EP01/15428
1540 AKEDALKARKKLLNNTHDFLEÖLIFRKQ KIKELMDHRAKVLSDLENKYKKEKEAL EKETRGKILTAKSKAYGDLEQALKONP LYRKLLPNPYAYVLNGETFTKEDRERL SYYYPQVKTSSIFKKTTATTKDKAQALL QMGVFSLDEEQNKKASRLALSYKQAIE EYSNNVSNLLSRKELINIDYYLQLERN KFDSKAKDIAQKATNTLIFNSERLAFSM AIDKINEKYLRGYEAFSNLLKNVKDDVE LNTLTKNFTNQKLSFAQ	LAYLQIKEDEIKGPLVKFLSEKGLKNILE LAYLQIKEDEIKGPLVKFLSEKGLKNILE RTDAQVGDIVFFGAGIXKIVLDYMGRL RLKVAETLDLIDKDALINFLWVVNFPMF EKTENGYHAAHHPFTMPKNIECEDIEE VEAHAYDVVLNGVELGGGSIRIHKEEM QKKVFEKINIHEEEAQKKF	1544 KLNVLIENSSALEREL'GKNEHLENALK EGEYLKNAWLLEMEKOKEIFHNKKLEL EKSYOOALNILKSEVASKDTSSMHKEI HKASEILSKHKTNOEIPOITNFOANEKA RYKNESVLIVOILDKGYYWIETELGMRL KAHGSLLKKIOKPPKNKFKPPKTTIPKP KEASLLLKKIOKPPKNKFKPPKTTIPKP KEASLRLDLGGRSEEALDLDAFLND ALLGGFEEVLICHGK(\$\$GILEKFVK	VDSKRIDTAVLALFNGGYFKDVYATFE VDSKRIDTAVLALFNGGYFKDVYATFE GGILEFHFDEKARIAGVEIKGYGTEKEK DGLKSQMGIKKGDTFDEGKLEHAKTAL KTALEGGGYYGSVVEVRTEKVSEGAL LIVFDVNRGDSIYIKQISIYEGSAKLKRR MIESLSANKQRDFMGWMWGLNDGKL RLDQLEYDSMRIQDVYMRRGYLDAHIS SPFLKTDFSTHDAKLIYKKRKDVFN IEHLRADAQILKTEIATNGYAFAVVKPD LDKDEKNGLVKVIYRIEVGDMYYINDVII SGNQRTSDRIJRRELILGPKOKYNLTKL RNSENSLRRLGFFSKVKIEEKRVN
1539 TGCAAAAGAAGACGCTCTTAAGGCTCGCAAGAGCTCTTAAACAATACGCATGATTTCTTAGAAGACTTGATTTTTAGAAGAAAAAAAA	1541 CGTTAAGGGGGCTGATGCGCTTTTTAGCCGCAGCGTTTTAAAAGAATTAGATGAATTTGTGCGCCAALTTGGGGCCAALTTGCGAAATTAGCAAATTAAAGAAGGGCCTTAAAAGAAGAGCTTTAGAAATTAGTTAAATTAGAAATTAGGGGCTTAAGGGGGCTTAAGAAAAAGGGGCTTAAGAATATTTTAGAAAAGGGGCTTAGGGGCGTTAGGTTAGATTAGGGGCGTTTGCGCTTGATGCGCGGGGATAAAAAAAA	1543 AAATTGAATGTTTTGATTGAAAATTCCAGCGCGCTAGAAAGGGAATTGAAACAAAGGAATGAACATTTAGAGAACGCT TAAAAAGAGCAAGAATATTTGAAAAAACGCATGGCTTTTAGAAAATGGAAAAACAAAAAAATTAAAAAGAGCAAAAATTTTTTGAAAAAAACGCTTGGAAAAATTGGAAAAATTGGAAAAATTGGAAAAATTGGAAAAATTGGAAAATTTTAAAGCGAAATTTTAAGCCAAAAATCCATAAAGCGCGCTACAAAATTTTAAGCAAAACCAAAACCAAAGCGCGCAAATTTTAAGCAAAACCAAAATTTTAAGCGAACTGCAAAACCAAAATTTTAAGCGAAAATTTTAAGCGAAAATTTTAGAAACCGAAAATTTTAGAAACGCGCGTTAAAAGAAGCGGCGTTTAAAAGCGGGGCTTTAAAAGCGGGGCTTTAAAAGCGGGGGTTTGTTGTTGAAAAAATTTTAAGAGGGGGCAACGCGGGGGGGG	1545 AGTCAAGTCCATTICTTATGTCGGGCTTTCTTACATGTCTGACATGCTCGCTAAT GAAAAT I GAAAAAT I GAAAAAAT I GAAAAAATTGTCGGGGTTTTTGATGAAAAAATGACGCTGTTTTGATCAAAAAAATGCCGGGGTTGATGCCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGGTTGCGGGTTGCGGGTTGCGGGTTGCGGGTTGCGGGGTTGCGGGGTTGCGGGGGTTGCGGGGGG
HP0962	HP0962	HP0962	HP0962

HP0962	1547	1547 CCGCTCTAAAGAGCCTTCAAAAGGCTGAGATGGAGCGCCAAATGATCGCTTTAAAAAAGAGTCTTGAAAAAATGGTAAACGTGTAACGAAAAAAAGCGTTCGAAAAAAATGGTAACGAAAGGCGATCATTTTAGAAAAGCGAACATTTTTTTT	1548	1548 RSKELOKAEMEROMIALKKSLEKNRNE SLAOEKVLTNYRKSLDHLOKKRSFLOK RVFDTLLODFLFSOALKGONLASSNDV VLQVAFENLHOSTLSKMSQLSOEEKEL NTOALKVKNSIQKISSIIDEQKTREVTLK SLKTEQDKLILSMQKDYAI
HP0962	1549	1549 AGCGAACACTTAAAAAACACTAACAAACACGAGCTATACGAACTCTTAGGCTTTTATCAAAAAGAATTAGATAAAAAAC AAAACCATTCAGCCTTTAAGAATTTGCTATTCTCAATGGTTTAGACAGAGACTTTGAAAGAGAGCTAATGGCTATTC TGTTTTAAAGAAAAAGAAATGCTTTTAAATAAGCTTGAACACCTAGACAAACGCCTTTTAGAAAAACCACTCTTA CTATTAGCCCAGCTAAGAAATGAAGTTAAAACCAAGCAAAACACCCTAAACAAAC	255 250 200 200 200 200 200 200 200 200	1550 SEHLKNTNKHELYELLGFYGKELDKKG NHSAFKNFAILNGLDRDFERETNGYSV LKKKEMLLNKLEHLDRRLLDKNSHLLA GLRNEVKTKGNIGYNTLTNPILLAKALE LSKDKRPTLKTFKNA YFSARKYGFMLE SFKTKGNDPTYKLNDNTYELVSKGLQD YGNTMLLLAKERLLFLEGDLKQKEEEF ERAKEHYVKSSKHYRETSLSPKEKGG FLKQIRGFSKISKDILYTCNEIIGANRFLT HYDNLNLEKVLEHAKDT
HP0962	1551	ISSI IGATTCCTAAAGAAGGAAAGGGCTTTAGGCGGCGGTAATCATTTCTAAAGAGGCGGCTATATTGTAACTAATAA CCATGTGATTGATGGCGGCGATAAGATTAAAGTTACCATTCCAGGGGAGCGAATAAAGAATTCCGCCACCTCTAGTAG CCATGTGATTCGAAAGCGATTTAGCGGTGATTCGCATCACTAAAGAATCTCGCCACGATTCTAGTAGCGATTCTA ATGATATTCAGTGGCCGATTTGGTTTTTGCGATTGGTAACCCTTTTGGCGTGGCGAAGCGTTACGCAAGCGTTACCAATCCT GTTTCAGCGCTCAATAAAAGCGGGATTGGTAACCGTTATGAAACAGCGTTAATCCATCAATCCT GGAATTCCAGCGCTCAATAAAAGCGGGATTGGTAACCGTTATTGAAAACAGGCGTTAATTCCATCAAAACTGG GGGCAACTCCGCCGCGCGTTTGCTAGCGTTAGCTGTAGAAAAGAAGAATTTGAAAAACGAAAAAGAAAG	52 52 52 54 54 54 54 54 54 54 54 54 54 54 54 54	ISSZ IPKERMERALGSGVIISKDGYIVTNNHVII DGADKIKVTIPGSNKEYSATLVGTDSE SDLAVIRITKDNLPTIKFSDSNDISVGDL VFAIGNPFGVGESVTGGIVSALNKSGIG INSYENFIQTDASINPGNSGGALIDSRG GLVGINTAIISKTGGNHGIGFAIPSNIMV KDTVTQLIKTGKIERGYLGVGLQDLSG DLQNSYDNKEGAVVISVEKDSPAKKAG ILVWDLITEVNGKKVKNTNELRNLIGSM LPNGRYTLKVIRDKKERAFTLTLAERKN PNIKKETISAGNGAGGUNGLQVEDLT QETKRSMRLSDDVGGVLVSGVNENSP AEQAGFRGGNIITKIEEVEVKSVADFNH AI EKYKGKPKRFI VI DI NDGYRIII VK
HP0962	1553 1 1 1	1553 TGTGAGCGAAAACGCCAGCCAAGATCAAAAATCCTACCGCCGTTTAGCCCGACATACCACCCGGATTTGA ATAAAACCAAAGAGAGAAATTCAAAGAAATCCACCCGCTTTAGAAATTTTGAGCGATGAAGAAAACGC ATAAAACCAAAGAAGAGAGAAATTCAAGGAAATTCAAGCCGCCTTTTGAGCGATGAGAAGCCCTAG CGCCAATACGATCAGTTTGGCGATAACATGTTTGGCGGCGGCAGATTTTCAGCGATTTTTGCCAAAGCTCGCAAGG TGAAGATTTAGACGATATTTTAAGCTCTATTTTTGGAAAGGAGGCTTTTCGCAAAGATTTTCCAAAACTCGCAAGG CTTTTCTGGCTTTAATTTTTCCAATTTTCGCCCCTGAAAATTTAGACATTAGACCCCCCCC	22 24 >=00xxxx	1554 VSENASQDEIKKSYRRLARÖYHPÖLNK TKEAEEKRKEINAAYEILSDEEKRRÖYD OFGDNMFGGQNFSDFARSRGPSEDL DDILSSIFGKGGFSORFSONSOGFSGF NFSNFAPENLDITAALNVSVLÖTLLGNK KÖVSINNETFSLKIPIGVEEGEKIRVRN KGKTGRTTRGDLLLEIHIEEDEMYRRE K

	7
-	
٠	7
•	۷

12	T	PCT/EP01/15428
1556 ISVVAKILGVHPOTLR(JYEKEGLIEPSR TDGKMRLYSORDMDI(KTILRLTRDMG VNLAGVDIILRLKEKLCELDNLMKELQD ALHKHSKNTKTPTKNI.NTPTNFYELILF KK	1558 QDKSKQAEKENQINWWKYSGLTIATSL LLAACSVGDIDKQIELE;GEKKEAENAR DRANKSGIELEGEKQKTIKEGKDLVKK AEQNCQENHGQFFMFKLGIKGGIAIEV EAECKTPKPAKTNOTFIQPKHLPNSKQ PHSQRGSKAQELIAYLQKELESIPYSQ KAIAKQVNFYRPSSVAYLELDPRDFKV TEEWQKENLKIRSKAQAKMLGNEKPT SPPFNLSKPFVRSKNIC	1560 IQELDVINIKPLLTTKGYDLNAYLEAKK QMDSQAYFDALRTISRAFKNYPQTMF KKOLYLLEIIALGOLGIKKSLLIDIGTQWI KNYPTDPNIPEALYYVAKALDENNHYK QAMRYYKRILEYKNSIYAPLAQMRLA IEAAEGSDLSNANMLFIEAFSNAKDKE SASEIALNWAEAEINYONFNNAKYLIDK VVQSNPDYISTHSESALDLKLLKKNO MNASAIEIAHLLNQDD JLKAKEQALYD LGALYARIKDFKNAHLYNLQYLQDHAE LDKASVYRADEKALFISMEGNTQEKIA HYDKIIQNFPNSNEALKALELKAQLLFE NKRYAEVLSMQKNLPKDSPLIQKTLNV LAKTYLENHRCEEALKYLSQITTFEFSP KEEIQAFDCLYFASLKEKAQIIALNAFKT AKAPSEKLIWLYRLGRNIYYRLGDFKNS TLASKDALLAQSLNKKI:FYDIAFVLFSD YMQNNEKELALHLYAFI.EKHFKGDKR MALVYFKLENEKDPKSVKIYATSLLKL
1555 AATCAGCGTCGTGGCTAAAATCTTAGGCGTGCACCCTCAAACCTTGCGCCAATACGAAAAGGGGGTTTGATAGAGC CTAGCAGGACTGATGGGAAAATGCTTATTAGGCCTTCCCAACGAGACATGGACAAATGAAAAGGATTTTACGCCTTACA AGGGATATGGGGGTTTAATCTTGCGGGCGTGGATATTATCTGCTTTAAAAGAAAAGCTTGATGAATTAGACCCTACA AGGGATTTACGAAGAGGCTGGCACAACACTCTAAAAATACCAAAAGCTTGAAAATTTAAAAACCCAAGAACCCTTGCACTATTAAAAAAAA	1557 CAGGATAAATCCAAACAAGCTGAAAAGAAATTCAAATTCAATTGGTGGAAATATTCAGGATTAACAATAGCGACAAGT TATTATTAGCCCCTTGTAGTGTTGTGTGATATTGAAAACAGATAGAAAAAAAA	1559 CATTCAAGAGGTTAGATAACAAACCCTACTCACCACAAAGGGCTATAAACGCTTATTTAGAGGCTAA AAAACAAATGGATTGCAAGCCTATTTGCGAATTAGGACATTAGGCGTTAAAAAACTACCCCCAAACGA TGTTTAAAAAAGATTTGTATTTGCAAATTATCGCATTAGGACATTAGGCGTTAAAAAACTACCCTCAAAGGA TGTTTAAAAAAGATTTGCAAAATTACCAAATTACCAAATTACCCGAATTAGGACATTAGGACATTAGGACAAAGCTTTAGAAAATTACCAAAGCTTTAGGACAAATTACCAAAGCTTTAGAAAACAATTAGGAAACCAATTAGAAAATTACCAAAGGCTTAATTAGGAAACCCTTAGAAAGCCTTTAAAAAAGAGCCTTTAGAAACAACCCTTAGAAAGCCTATTAAAAAAATTACCAAAGCCGTTAATTGGACAACCCTTAGAAACTACCAAATTAGAAACAACCCTAGATTAAAAAAACCGCTAAAATTAGAAAACCCGTAAACAATTAGAAACAACCCTAATTGGAATTAGAAACAAATTAGAAACAACCTAATTAGAACAACCAATACCTCAATTGAAAAAAAA
HP0962	HP0962	HP0962

)2/066501			
1562 GVNYPLYQFKHPNYTENFTPEFRSFID 1562 KHYNHSFEPLEVLGYIYALLYSPNYRK PYEDFLKNDYPKILFTNNKDLFRALSLL GIELIGLHVLNQESLNYSFGKLKDATIG GESCYKEEHNPIIKKPSHNEPDQRLYINH SAYFRGVSQEIYDYRIGGYGULDKYLK SHKNEPCDFDHVTNIIKVIARTIEIQKTL GFLTSDLPHLKGNDSKALMQEILQNPP PPPPJ	1564 VPFGQYGKKALDIKHVREQLDKDHYSL KRPKERIVEYFATMQLLEMRRKKKPEK KDKTKGTILCFYGPPGVGKTSLANSIAK A	1566 ADPSTSKKRADKGLKKVFKDSKKDAC GFIYEISEFMKAYTALLKKQDRYVYLLR YLPSRYWASILTTALYVKYPDFDALKKL LVSYYYQTWIAGGTITRIKQTSINIIKNV KSNKSVETIKELILNSIDSYNTFDQYLYN LWDSSSVYHSKWVRPVLALANYFMAD EEKPHFIAMDAETQVEHILPQTPKRGS QWNADFDKEKREEWVNNIANLTLLKR KKNAHALNGDFDEKRKIYGGKDTSKVI SCYDITKELYSNYRKWNEKSLQERYKS LYNTITPVLHIEGGEDDFEDDFDL	1568 KTLCKQLKISNFRASISQIKNGMMDLS MQDSECYKAYELYQNALKKDNLVDFD DLLFLSLKILQDNETJAKETSERYHYIMV DEYQDTNALQLEFLKKLSFTHHNLCVV GDDDQSIYGFRGADISNILNFSKHFKG AKIVKLETNYYRSSAEILACANSLISHNQ HRHIKTLQSFK
1561 GGGGTCAATTACCCCCTTTATCAATTCAAACACCCCCAACTACACCGAAAATTTTACGCCAGAGTTTAGAAGTTTTATA GACAAGCATTATAACACTCTTTTGAGCCGCTAGAGGTTTTAGGCTATATTATGCGCCAGAGTTTTGTATATA GACAAGCGTTATGAAGACTTCCTTAAAAACGATTACCCTAAAATCCTTTTCACAAACAA	1563 ATGTGCCTTTTGGGCAATACGGGAAAAAAGCGCTTGACATTAAGCATGTGAGAGAACTAGACTAGGCAAGGATCATTAT TCCTTAAAAAGGCCTAAAGAGCGCATTGTAGAATACTTTGCCACCATGCAGCTTTTAGAAATGCGCCGCGAAGAAAA GCCAGAAAAAAAAAA	1565 CGCTGATCCTAGCACTTCTAAAAAGAGACCGATAAGGGATTAAAAAAGGTGTTCAAAAGACAGCAAAAAAAGGCCTTTTTTTT	1567 AAAACGCTGTGCAAACAGCTCAAAATTTCAAACTTTAGAGCCAGTATTTCTCAAATCAAAAACGGCATGATGGATTTG AGCATGCAAGATAGCGAATGCTAAAAGCGTATGAGCTTTACAAAACGCGCTCAAAAAAAA
HP0962	HP0962	HP0962	HP0962

-	
•	٠,
•	

02/066501		PCT
1570 LAKL GLNEREINKL FVELENSNALEFDE TNNAYKIIAPICETMÖNNEERIKDFLSD EEYHAVLSAFKMAENPTNKRDGIINAN QPÖEKVKIRÖNLAKEFKELWOTINAGS OLSYGNIGKTKLIESIAKAFNESHVSAE VIKFESKRYDPOTNRIITEGSSTLKIRDY ANALQKEINALLLDFAKDERLPLKFTLE LYNALNKEHFTNSPKKAFKLLKGIIKDK LHENLLSCVSYGFCQNAFSNTAFDKTD PLYCEDGSPKNEIEKHKIGKYKSAOTP SPNYLYETIIYDSKIEEEVSEEGVQTLE GKSIEVFAKLPKFKIPTPYKNYEDDFAY LLKDEKGAKIFFVCETKGYEKESDIPPD EKRKIEYAKKFFETLSQNLKNAKKEIRV VFATRINKODI FNTI KNAI KETP	1572 IFDVKAPILGFETIHKMRLGKIDEIFLRLN STEENSVVSFTIHKMRLGKIDEIFLRLN PLKILLELEGAKSVLVANIMVVQTPIELS TVNYLAPLIFNLDKQLMGQVVLDSNKY PHYHLRENILSHTHE	1574 DEVKRGSRDETINSARDVWCAAKSOA TLAKETYKRVQDLYDNGVASI.OKRDE AYAAYESTKYNESAAYGKYKWALGGA SSESKIAAKAKESAALGQVNEVESYLK DVKATAPIDGEVSNVLLSGGELSPKGF PVVLMIDLKDSWLKISVPEKYI.NEFKVG KEFEGYIPALKKSTKFRVKYL3VMGDF ATWKATNNSNTYDMKSYEVEAIPLEEL ENFRVGMSVLVTIKP
1309 A I I AGCCAACI I AGI I GAGGGGGGGGGGGGGG	GATTÍTIGATGIGAAAGCGCCTATITIGGGGTTTGAAACCATTCATAAAATGCGTTTGCAAAAGGTTGATGAAATCCTTT TTGCGTTTGAATAGCACAGAAGAGAATTCCGTGGTCTTTCACGCTGGTCAATCCCTTTAAGAAAATACGAA TTGCGTTTGAATAGCACAGAAGAATTCCGTGGTCTTTTAGAATTCCGAATCCTTTTGCAATACCTTTGAATACCATGGTC GTTCAAACCCCCATTGAGCTTTCCACCGTGAATTATTAGAGGGAGCCAAGGGCGTTCTAGTCGCTCATGGGG CAAGTGGTTTTGGATTCTAACAAATACCCACTACCATTTAAGAGAGAATATTCTAAGGCCACACGCATGAATGA	1573 CGATGAAGTCAAAAAGGGCTCAAGGATAATTCTGCGGGGGGGCTTTGGCAAGCCGAATCCCCAA 1574 GCCACTTTAGCCAAGAGGCTCAAGGACGATTAATTCTGCGGGGGGCTTTGGCAAGCCCAAATCCCCAA GCCACTTTAGCCAAGAGACTTATAAGCGCGTTCAAGAGTTTGATGCGGCGTTTAGGGGGGTTTAGGGGG TGAAGCCTATGCGGCTTATGAAAGCACTAAATACAAGAGAGGCGCTTTAGGGCAAGTGAATGAGGGG GGGCGAGCTTTAAAAGTGCGCTAAGGCTAAAGAGGAGCGCGCTTTAGGGCAAGTGAATGAGGGG CTTATTAAAAGACGTCTCAAAGCACTAAGGCTAAAGAGGAGTGGCTTTAAAGGGCTGCTTTAAAGGGTTATAAGGGTATTAAAGGGCTAAAGTAT AGCCCTAAGGGTTTTAAAGTGGCTAAGGCTAAAGGATAGTTGGTTAAAAAAAGTAT AATTTGAACGAGTTTAAAGTGGAATTTGAAGAGTATTAAAGGGTTAAAAAA
TSOS AT LIAGCCARGE LIANTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1571 GATTITIGATGTGAAAGCGCCTATTTTGGGGTT TTGCGTTTGAATAGCACAGAAGAAATTCCGTG TTTGAAGTGCCTACCCCTTTAAAAATCCTTTAGGGTTTAGGGTTTTGAACCCCATTGAGCTTTCCACCGTGAAT GATCAAACCCCATTGGACTTTCCACCAATACCCACCCAAGGGTTTTTGGATTCTAACAAATACCCACCGTTTCTTGAAGGGTTTTTTTT	1573 CGATGAAGTCAAAAGAGGCTCAAGAGAGCGAAAAGGCTCAAGGACTTATAGCCAAAGAGACTTATAAGCGCGTT GGAGCCTATGCGGCTTATGAAAGCACTAAATA TGAAGCCTATGCGGCTTATGAAAGCACTAAATA GGGCGAGCTCTGAAAGTAAGATGCCGCTAAG AGCCCTAAGGTTTTCCTGTGGTTTTACGACTTTGAA ATATTTGAGCGTTACAAGTGGGGATTTGAAAAGGATTTTTCCGACTTGAAAAAAGGATTTGAAAGGGTTTTAGGAAAAAGCCATGCTTTAGAAGAGGTTTTAGGAAAAAAACTCTTTA GATAAGACCACGAAGCCTTTTAGAAGTGGCTTTTAGGGCATGC TTTGTTTAGGGGTTTTAGGCCACGCAAGCGTTTTAGAACTCCTTAAAAAAAA
45 50 50 50 50 50 50 50 50 50 50 50 50 50	HP0194	HP0194

10000	4676/17	*** * * ATTOTOCOT*******************************		
48 O L	71 6/61	TTARGERACE CONTRACTOR AND AND AND AND AND AND AND AND AND AND	15760	1576 OKLSLKNAWTRVLSNHEGLHAQEYAIK
	1	CITITETA ACCOUNT TANKED THE SECRET HE SECRET HE SECRET THE SECRET	<u>~</u>	RASKMKLAAKLSFLPQIDLSAFYVYLSN
	AA .	ANGECT TO TAKE TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL TOTAL TOTAL TO THE TOTAL	<u>a.</u>	PIKMDFASOKQPGVQKATNQIHQGIQN
	A A	ATGCARGETITIEGEGETTTEAGEAGGGGTG	<u>o</u> :	IQQNIPSQVLTPQIQAGMQGVMQGFG
	<u> </u>	THOUSE OF THE TRANSPORT	<u>₹</u>	ALSSTLEAPLLFSKONVVIGALSIIYPLY
	110	CTAATGAAGTETATCETTTEAAAAAAAAAAAAAAAAAAAA	Ξ_	MGGARFTMVRIADLMQKDANEVYRLK
		CCCACA CACACACACACACACACACACACACACACACA	록_	KLSTFQELVSVYYGMVLNAEVAETLEE
_). 4	CTGGGGCAAAACCTTGCTTAAAAAAAAAAAAAAAAAAAA	<u>></u>	VEKGHYKHFÖNALKMÖKVGÖJARVET
	2	CONTRACTOR AND AND AND AND AND AND AND AND AND AND	<u> </u>	LGAQVAYDKAHIASVKAKĎVLEVSŐLS
	3 2	CAAATTAGAATOLOGIA AAAAO I UGAAATTAGAGAAGAATTAGAGAATTAGAGAATTAGAGAATTAGAGAATTAGAGAATTAGAAAAAA	Ĺ	FNSILSSKDDLVPSSKLEIRTEKNLPÖL
	<u>i</u>	TITARA GAGACITTA GALANATE AGALANATE	<u> </u>	SFFVSSTLNSYPVLKTLENDIQISKENT
	AG	46THTH TEGETOTT ATATTATATATATA A COCCANA CATATATATA A COCCANA CATATATATA A COCCANA CATATATATA A COCCANA CATATATA A COCCANA CATATATA A COCCANA CATATATA A CATATATAT	<u>¥</u>	KLOIAKFLPOVSFFGSYIMKONNSVFE
	- 25	GCCGGGCCATGCCT	٥	DMIPSWFVGVAGRMPILSPTGRIQKYQ
-,-	<u>. </u>		¥.	ASKLAELOVSSEGIOAKKNMELLVNKT
			<u>*</u>	YKETLSYLKEYKSLLSSVELAKENLKLQ
			<u> </u>	EQAFLOGLSTNAQVIDARNTLSSIVVE
			<u>ă</u>	QKSVAYKYIVSLANLMALSDHIDLFYEF
10000	4573	CONTROL OF THE PROPERTY OF THE	ν۲	
TF0047	// // // // //	TAGECTIETALGAIGAGCATTTCTTGCTCACTAAAACGAAAACTTAGTGGGCATCCTCCGTTTAGAAGGGGGTTAGC	1578/LG	1578 LGLYDEHFLLTKNENLVGILRLEGVSYT
	- C	ACACCCAI I PASCACACAGAGCAI I GCAAGATCTI TI CACCGAGCCCAGATGGCGTTGGATTCTTTAGAAAAGT	<u>로</u>	HLSTEGLÖDLFTEROMALDSLEKVVAR
	2 6	Celegococci igi 6611 AAAA 66 GCGTAAAATT GATCA CCAACAAAA CATTCAATCT GAATA CTTGCAAGC	<u> </u>	LVVKRRKIDHQQNIQSDSQYLQAILNQ
	¥ (GATTTTFAGAAAAGAAAGAAGTGTATGAAATCAGTATTTTTTAGAAAAGCACTCATTTGCAT	Щ	FENKEVYENOYFLVLESTHSLHGVI FH
_	9	GCC61111GGAGCATAAGAAAAATCTCTCATGCATGCTAATAGGGAAAATTTTAAGGATATTCTCTTATAAAGCG	<u> </u>	KKKSLMHANRENFKDILSYKAHFI DET
	₹ [<u> </u>	LKSLEIOLKNYAPKLLSSKEVLNFYAEYI
	<u> </u>	STILLEAN I II LA I GCGGAA I ACATTAA TGGGTTT GATCT CCCCTTAAAA CCCTTAGTAGGGGGGTATTT GAGCGAT	<u>Z</u>	NGFDLPLKPLVGGYLSDSYJASSITFEK
	2 6	TCATTORIC COLOR INCOME TO THE ANALYSIS OF THE	<u>ձ</u>	DYFIGESFNORTYNRLIGIKAYESERITS
	2 1	TING TO THE TOTAL TO THE CARGE CARAGEA FOR THE TANGE OF THE TOTAL TO T	₹	IAIGALLYQETPLÓIIFSIEPMSVHKTLSF
	ATA	ATTICLE AND AND AND AND AND AND AND AND AND AND	<u> </u>	LKERAKFSMSNLVKNELLEYÖELVKTK
	<u> </u>	GCCCTAAACATTCTTATCAAAGCCCCTAATTAAAAATTAAAAATTAAAAACAAAC	포	RLSMÖKFALNILIKAPSLENLĎAG
	, ,			
HP0042	15/9 AA	15/9 AAATTI AGGGCTAAAAA GACCCCTAGGAATTITTI TIATTCTTAGAATATATAGAAATAGGAAAGCCATAAAGCCATAAAGCCAGAAATT	1580 NL	1580 NLGLKDPRNFLFLEVIEIVKAIKPEIFIIEN
	- E	CTTTAGE AND CANACTOR CANACTOR CONTINUED TO CONTINUE AND CONTINUED TO CANACTOR CONTINUED TO CANACTOR CONTINUED CONTINUED TO CANACTOR CONTINUED CONT	<u>\{ \}</u>	VKNLISCAKGYFLEEIKERLNALGYQLS
	Ė		<u>X</u>	YOILNAKDYGVPONRERAFIVGASRFS
	Č	GGGTTTAGGGTATCTTTTATTATCAGGGGGGGGGTTTTATTATTATTATTATTATTATTATTAT	0.	FDFNLLEPSGSVNVQDAISDLAYLCSN
	E	CTITAATGCGAAAAGGTAGCCCTAAATTATAAAACAATAAACAATAAACAAATAAAGAAAAAGGAAAAAGGAAAAAAGGAAAAAAAA	ָ פַּ	EGAFESDYLNPIQSSYQALMRKDSPKL
	AAC	AACTCATTAACAAGAAGAAGGCGAAGGATGCTTGCCTAAAACTTGCATGGCAAACAGCAATTCAA	Ž a	YNHQATNHSQAALEKLKLINKEQGKEC LPKNLHGKQÓF
HF0042	1381	ACGATGAGATCAAACGGAATTCTTTGGTGGTTGAAAGCATTGATTG	1582 ND	1582 NDEIKRNSLVVESIDLIKOIKPRFFILENV
	- 0	11 AGAMAN GI CCCI AGI I I I I I A AAAA CA GGTT GTATA GA CAAAAA T GA TAATT GCTA GAAATA GGAT CTATGATA	PSI	PSFYKTGCIDKNDNLLEIGSMIEQNLSG
	A CA	BASCHWANTTIBAGIGGCGATTCAAGCCCATTCAAGCCCGA	<u>O</u>	DYMLYDEVINFKNFGANSSRTRTLVIG
	AAG	AAGAAAAAACTTAAAAAGAAGTGATAACAATAAAAAAAAA	<u></u>	_
	ATA	ATAGITITAGAACITATCCAAAGCATATGCAAGAAACAACAACIIGCIIGGGGGGGGGG	SS:	GSLKPLAWGEYDNTDFYHSFRTYPKH N
			Q N	MOEW

HP0042	1583 1 4 4 4 6 0 0 T 0	1883 TCATTGATGGGCAAAAAGAAGGCGTCTATGGCGGGATTGCGTGCG	1584 IDGGKEALYGGIACANLLHKNSGITIDIG GGSTECALIEKGKIKDLISLDVGTRIKE MFLDKDLEVKLAKAFI DKEVSKLPFKHK NAFGVGGTRALSKVLMKRFCYPIDSL HGYEIDAHKNLAFIEKIVMLKEDQLRLL GVNEERLDSIRSGALI LSVVLEHLKTSL MITSGVGVREGVFLSIJLLRHHYHKFPP NINPSLISLKDRFLPHEKHSGKVKKECV KLFEALSPLHKIDEKYI FHLKIAGELAS MGKILSVYLAHKHSAYFI
HP0042	15851 A T	1885 GCCCTATATCGCTAGAAATTATCCTTTGGAAAAATCCGTCCTCAAAGAACCGCATGAAGCCCTTTTTGGGGGGGG	1586 PYJARNYPLEKSVLKEPHEALFGGVKG DEILKEIVFLAAKLKIPFLVCEMGYDQLK SLKECLEFCGYDAEFYKDLSGFDRGFV GVLKSFLR
HP0042	1587 C C C C C C	TGCATGAAAAATACCCTAACGCTTTTGATGTCATTTTTTGCTTAGGGGTGCTATACCACAGAAAAAGGCCCGCTAGAGG CTTTAAAAAGCCTTGTATCACGCTTTGAAAATAAAAGGGGGGGCTGGTTGGATACCTTAATCATTGATTCGCCTTAG ACATCGCCCTTTGCCCTAAAAAACTTATGCTAAAATGAAAATGTTTTTTTT	1588 HEKYPNAFDVIFCLGVLYHRKSPLEAL KALYHALKIKGELVLD־LIIDSPLDIALCP KKTYAKMKNVYFIPSVSALKGWCERV GFENFEILSVLKTTPKEGRKTDFILGQS LEDFLDKTDPSKTLEGYDAPLRGYFKM LKPSKR
HP0042	1589 A C C C C	1589 ACTGGGGACAGGGGGGGACGATTGCAGGGAGTGGTGGGGGGGG	1590 LATGGTIAGSGASASLGSYKSGELGIK ELLKAIPSLNRLARIQGEQISNIGSQDM NEEVWFKLAKRAQELI DDSRIQGVVIT HGTDTLEESAYFLNLVLRSTKPVVLVG AMRNA
HP0042	1591 A G T,	1591 AGATGAAATTTTAGACTCTTTGGCAGAAAATATGTGGAGTATAGTTTATACTACGCTTTGATTGA	1592 DEILDSLAEKYVEYSLYYALIDSLAAEH SARMQAMDTATNNAKDLVKTLTISYNK ARQEAIT
HP0042	1593 893 803 808 808 808 808 808 808 808 808 80	1593 AGACAGCCATTTGAAAGAAAGGGTGGCGTGGAGTTACCTAAAAGTATGAGGGGGCCTAATCTCTTCTTTTTTTT	1594 DSHLKEKGSVELPKRYESINSHNLYLY VKHYLSSARANTAKSK'NRAEVSGGGR KPWAQKGGGRARAG SITSPVFVGGGV SHGATNNRNYNLKINK'KOKRLALEYAL EEKAQANKLFVVEKIAIKGVVEDNKRK HLTKEANOMFQALEQ 3DTLFVCMNMD EYTELAFSNLKKCLIVCWSELNAYLLAA FSSVVMEEAAFOHVV'QDKTEE

c	>
O	o
Ċ	٧

0 02/066501	PCT/EP01
1596 RLEMIPKKANLMILDKEKCVIEAFRFND RVAKNDILGALPPNIYEHGEEDLDFKGL LDILEKDFLFYQHKELEHKKNQIIKRLNA QKERLKEKLEKLEDPKNLQLEAKELOT QASLLLTYQHLIHKHESRVVLKDFEDK ERAIEIDKSMPLNAFINKKFTLSKKKK KSGFLYLEEENLKEKIAFKENGINYYKG AGESVLEMFMPSKNSKIKRPMSGYE VLYYKDFKIG TOWNDINDNEEAPKNTPLKYYKNLSALA QDNALDPVIGREEEIRVEILGRRKKN NPLLIGEAGVGKTSIAFALAKIAQKEV PEFLQEYEVYSLDLALMVAGAKYRGDF EKRLKKTLKEIQONGRIILFIDEIHTLGT GSSNAGSLDAANILKPVLTDGSLKCLG ATTFEFYRSVFEKDKAFNRRFSVIKVE EPSKEACYLILKKIAPLYEEHHQVRYDE SVFKACVDLTSDYMHDKFLPDKAIELL DEVGSRKKISPKKGKKIGVDDVKETLA LKLKIPKMRLSSDKKALLRNLEKSLKINK IFAQAEAISLVSNAIKIQHCGLSAKNKPV GSFLFVGPSGVG 1600 ĞENA	1602 AYLCSNEGAFESDYLNPIOSSYÖALMR KDSPKLYNHOATNHSOAALEKLKLINK EOGKECLPKNLHGKOOFKSTWGRLN WNKISPTIDTRFDTPSNGTNSHPELHR SITPREAARIOSFSDNYIFYGNKTSVCK ÖIGNAVPPLLALALGKAILK
3 3	1601
HP0042 HP1493	HP1493

0.00/0//50/			DCT/	ED01/16/20~~
1804 GKDYLPPKAKVYSSKNKNAGEAHEAIFO PTSIILEPNALKDYLKPEELRLYTLIYKRO FLASOMQDALFESQSVVVACEKGEFKS ASGRKLLFDGYYKILGNDDKOKLLPNLS KENDPIKLEKLESNAHVTEPPARYSEAS SLIKVLESLGIGRPSTYAPTISLLQNRD'C IKVEKKQISALESAFKVIEILEKHFEEIVD SKFSASLEEELDNIAQNKADYQQVLKD FYYPFMDKIEAGKKNISQKVHEKTGQS CPKCGGELVKKNSRYGEFIACNNYPK CKYVKQTESANDEADQEL(EKCGGEM VQKFSRNGAFLACNNYPECKNTKSLK NTPNAKETIEGVKCPECGGDIALKRSK KGSFYGCNNYPKCNFLSNHKPINKRC EKCHYLMSERIYRKKAHECIKCKERV FLEEDNG	1606 TYARLASLHNLHFYLELVKNARNAILEK RFLSFKKEFLEKYNSRSH	1608 VLKEILSSYGKRALKLTKRVRKKIFKND PTENQKKAIKIALNTPDIAIICGPPGTGK TTVINAICERLFEEYPKDKNIKGQILLCA QGHDATNNARERIKVGGLFTFKFGAK KNAKEEQYKQDERLNERLFIEFAETLIE SVRKKLOKLGDYENIEKILDLEEALRRY YSSPISELEFLKEIEKNESFF	1610 NADNVFLEFVRNSKELSEHSSPKNNEK LIKIMOTLKDGOSKDDLPESILRPKSGYI NTYAKMWWEKPAPTITRNI'STPSSSR CIHPRDSRALSIREGARLQSIFPDNYKF CGSGSAKRLQIGNAVPPLLSVALAQAV FDFLKG	1612 FVNNIKTSEGGTHEAGFKMGLSKALLCE YIGNNIKTKESRPISEDIKEGLIAVVSLKG MSEPLFEGOTKSKLGSSYARALVSKL' YDKIHOFLEENPNEAKIIANKALLAAKAD REASKKARELTRKKDNLSVGTLPGKLD DCQSKDPLESEIFLVEGDSAGGSAKQ
180	16(16	16
1603 ATGGCAAAGACTATTTACCCCCTAAAGCCAA ATCAGGCCCACTTCTATTATTTTAGAGCCAA TTAATTTACAAACGCTTTTTAGCTTCTCAAAT AAAGGCGAGTTTAAAGCCAGTGGGAGAAAG CAAATTGCTCCCCAATTTGAAAGAAAATGAC TCCAGCACCCTTTTACAAAAAAAAGAAATGAT TCCAGCATTTCCCTTTTACAAAAAAAGAAATGAT AGGTGATAGAAATTTTAGAAAAAGCGACTACCA ACAATATCGCTCAAAATAAGCCGACTACCA TCGGGAAAAAAATGATCATCTCTCAAAAAGT GTCAAAAAAAATGATGATCATCTCTCAAAAAGT GTCAAAAAAAATGATGATGAGGGGAGTTTA AGCGCTTTTTAGCTTGCAAAAAATTGCCGAGCTTCGAAAATTG	1605 CACTTACGCTGTTTGGCCAGCTTGCACAATTTGCATTTTTAGAGCTGGTGAGAGAACGCCAGAAACGCCATTTT AGAAAAGCGGTTTTTGAGATTTTAAAAAGAGTTTTTGGAGAAATACAACTCCCGCTCTCATTGAATGGAGGATGCAA AAATACTAAAAAAGCGTTTTTTACCATCAATAAAAAGTTTTCTTAAAAATAAGGCTTTAGTTTTTAATTTTTACCATCAATAAAAGTTTTCTTAAAAATACTAAAATTTTTAAAAAGGGTGGTTTTTAAAAAGGGTGCTTTTAAAAAAGGGTTTAAAAAAAGAAAAAGAAAAAAAA		1609 AAAATGCGGATAATGTTTTTGGAATTTGTGCGAAATTCTAAAGAATTAAGCGAACGTAGCAGTCCTAAAAACATGA AAAACTGATAAAAATCATGCAAAACGCTAAAAGACGGACAGAGTAAAGATTTGCCAGAAAGTCGCGCCCAAAA GTGGTTATATAATACCTATGCCAAAATGTGGTGGGAAAAACCAGCCCCCACTTACAGAAATTTTTCTACCCAAA GCAGTTCTAGGTGTATCCATCCAAGAGACTCTAGAGCGTTAAGCATTAGAGGGGGCCAAGATTTCTAAAGGACTCTAGAGCGTTAAAGGCGTTTCCT GATAATTATAAAATTCTGTGGGAGTGGTAGCCTAAAAGATTGCAAATTGCCATGCCGTGCCGCCTTTATTGAGGATTTCGAAAAATTGCGAAATTCTGAAAAATTCGAAAATTCTGAGGGGGGGAAATTTTTAACGAATTTTAAACGCGCTCAAAAAATGCGTTTAAAGGGGTTAAAAAA	1611 GCTTTGTGAATAACATTAAAACTTCTGAAGGTGGCAGCATGAGGCGGGCTTTAAAATGGGCTTGTCTAAAGCAATTTT TGCAATATTTGGCAATAATATTAAAACCAAGAGTCACGCCCATCTCTGAAGATATTAAAGGGGTTGTCTAAAGCGTG TTGTGAGCTTGAAAATGAGCGAGCCTTTGTTTGAAGGGCAGACTAAATCCAAACTCGGCAGTTCGTATGCGCGCGC
HP1493	HP1493	HP1493	HP1493	HP1493

1104 400	4643		
284 LL		TTAGAAGAAAAAAAAAACCAAAAAAAAAAAAAAAAAAAA	1614 TOAAQNRDGSLNNFKNIALTDSLDYLE
		GCCAACCAAAATATTAGAGTCATCATCATCATCACOCCTTATTCACCCCCCAAAGAGGCAAGAGGAAGAGGAAGAGGAAGAAG	EKTNKGVLPLYEDLKENKGIKDTLANQ
		AAACCTCTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAA	NIRVIIGNPPYSAGAKSONDNNONLSH
<u>:</u>		ACCECTOR CAN ACCOUNT OF THE CONTROL	PKLEKLVYEKYGKNSTSRSVGKTTRDT
		GTGGTGAAGGGGGGGTTTTATTGACTCTTAAAAGGGGGGGG	LIQSIRMASDVVKDRGVIGFVVNGGFID
	-	TATE TATE TO A THE CANADA TO COMMENCE OF THE COURT OF THE	SKSADGFRKCVAKEFSHLYVLNLRGN
-		SCOULABOR SOURCE CONTINUE CONT	QRTSGEVSKKEGGKIFDSGSRATVAIIF
_		ANCETEC NOT TENDESCRIBED AND THE STREET OF THE STREET AND THE STREET OF	FVKDKSTPDNTIFYYEVEDYLKREAKL
	_	AND SECTION OF THE PRACTICATION OF THE SECTION OF T	NWLANFENLDFVPFEKITPNDKGDWIN
		CANAMA I CAUCUCARA I CA I ARAGGCIGA I I GIGAT CAACCAAA GGAAT GACGCTTTT GAAAAACT CATCCTTTAAAAA	QRNDAFEKLIPLKRDKTLONDSVFDINS
		FATAL CHARACTOR CONTROLL CONTR	LGVVSGRDPWVYNFSPNILTOSVOKCI
		TO CONTROLL OF COMMENT OF THE CONTROL OF THE CONTRO	DTYNADLKRFNARFREAFKORAGSVK
		A SOCIO EL LA SOCIA DEL LA SOCIA DEL LA SOCIA DE LA SOCIA DE LA SOCIA DEL LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DE LA SOCIA DELLA DEL LA SOCIA DEL LA SO	AGDLYKQLNDKEITTDKTKIAWTDGLK
1707700	107	いたのからいない	
1483 2483	CIO	INTERNATION OF STREET S	1616 FLACASPKILAPSMNTNMLNSPITOSNL
		CONTINUE MANUEL I BANAGA I I CENACE I I ATTITA GA CACCANA A GOCCTITITA GCAT GCACACTANA G	KRLKDSNHIILDTKNALLACDTKGÓGA
		SCURI EGGECEA I GECT GAGCCTTT AAAGCCGCTCAAACGCCCTTAAAAGACGCTTATTTGAA	MAEPLEILFKAAOTLLKDAYFENREVIV
		ANCASAGA GENERAL CATEGEGEGEGEGEGEGEGEGEGETA A GAAT GACAGEGET TEGA A CENTRECANTE CATTEGE A CONTROL OF THE CATTEGE A CONTRO	MGGASIEKIDSVRTISNLSSGIQASALA
		COSCALI CARGUGAGUCULI I AGUTI TIGGO GITATATTI TAAGGGAGCCAAGATACTI TGAT CGCATCAAACTT CC	LALYFKGAKVTI JASNEPTPI PKFITSVI
_		CACCCCCT I GCCTAAAGAAATCACAAGCGTTTTAGTTAGCGACACCGCTTCTTATGAAAACGCCCTGAATAGTGCCG	VSDTASYENAL NSAANNI OKHAI KPI I
		CTARCARCT I GCAAAAACAT GCCTTAAAACCCCTGCTTCAATTTAGCCGCCATTAGCGATTATGTGCCTAAAACTT	FNI AAISOVVPKTSENYKI KKSEIGETI
		CITITAATTATAAGCTTAAAAAAAGCGAGATAGGCGAAACCCTAAACATTGAATGCGTTCAAAATAAGGATTTACTGGT	NIECVONKOLI VSINDNOEVRICEKAEO
_		TTCTATCAATCCTAATCGTTAAAATCGGTTTTAAAGCCGAAGATAATCAACAAAACGCTATCAAAAACGCTCAA	NOONAIKNAONI I KPEKDNOKOCKA
		<u>AATCTTTAAAACCTTTAAAGGTAACGGCAAGGATTGCTCTGTTGTCGCTTTGAATCTCATTAAAGATTCACGCCCTT (</u>	AI NI IKUSRPECSI ENEI WI ESHHKTO
	-	TGGCTCATTAGAGAATGAATTGTGGCTCTTTAGCCATCATAAAACCCAAAAAATCCCTTCTATGAACAAATTAGAAG	KIDSMNKI FASEKII DEIKONAI
		CGAGCITIAAAAICCTIGATTTTATCAAAGACAACGCCCTTTAATGCTAGAAGCCCTAAAAGGCCCTAAACGAGCTTAA	
		ATTCCAAAACGCTACGCACC	
		AAAGAICII	
HP1493	1617		1618 KPDLKELEEYYHKNKVSYLDKEGKLOD
		CANTATOLICATATION CONTRACTOR I CANTATOLICATION OF THE CANTAGORAT GAAAAAGCCTTAAGGAG	FKSVGEQVKHÖLSMÓKANEKALRSYIA
		TO A TO SOLICITATE AND ANALOG CONTROL TO A CACCACACATITICA A CACCACACTCCCCTATACTCC	[LKKANAONYTTODFEENNSPYTAEITO]
		CACCOCAGAGAGAC CACCOCITICAAACCCCTTGAAATCCTAAAGCCCAGAGCCTTTTAAAGATGGTTTTATTGT	KLTALKPLEILKPEPFKDGFIVVOLISOIK
		TEAS SCHOOL CALL TOWN I AVAIGACEAN I I I CANAN I I I I AN I GAAAA I I I I I AN I GAAAA GCGCT TTAAAA CCGCCTAAAC	DELONFNEAKSALKTRLTGEKTLMALO
	- 7	10-construction of the contract of the contrac	TLAKEKLKDFKGKSVGYVSPNFGGTIS
		A STANDARD TO SEASOCACTATIAN I SANCE I TANCEARGA GA A A GOTTA TO SANCE CONTINUE OF THE SANCE OF	ELNOEESAKFINAL

02/066501			
1620 KAGEELIEPIITKKIDCYGCDDFTNEGLK DKCFKRNDAYLNTLL TPIIGKGERRFSC SDFHNPELKEGCMDKTNAYEKGKDRG KRLINLVQLEAFEKEYAGYKPYIIPYFTK ECVKNAPHLANKERLCGKEVHEKFDD PYSSKELSVQSAIS-CIKKVDAKLEKA ALMNGVYISPYKKSTHCORTHLENKSL KEIALNMNPKLEKGSPFIDADKMAMGS AGLLRKNKGVLIAFATDICMERNEHKK EEFISLKDSCTGOSGAKIYNNKERFDKFI QDYGKOLKTCLLUTSNTKEEVEONFS GCGKEGLRDDNKGLGFTLEELVKKYA K	1622 LIEPSRTDGKMRLYSGRDMDKIKTILRL TRDMGVNLAGVDIILIRLKEKLDELDNLN KELQDALHKHSKNTKTPTKNLNTPTNF YELILFKK	1624 EDLNPLELARSYKEL ESYQMTGEELS KIVKKSRAHVANIMRI LTLSSKVQNALL EEKITSGHAKVLVGLIJGEKQELILNSIIG QKLSVRQTEDLARDI*KINANFDNKKHG FKQTQTLIAGDELERI_NQSLWDHYKLK AALKGNKIVL	1626 LGAPEIIVRNEKRML(JEAVDVLFDNGR STNAVKGANKRPLK;ILSEIIKGKQGRF RONLLGKRVDFSGR;SVIVVGPNLKMD ECGLPKNMALELFKFHLLSKLEERGYA TTLKQAKRMIEQKSNEVWECLQEITEG YPVLLNRAPTLHKQSIQAFHPKLIDGKA IQLHPLVCS
1619 TAAAGGCTCAAGAAGATTTCAAAAGAACGATCATCACTAAAAAGGATCGATC	1621 GTTTGATAGAGCCTAGCAGGACTGATGGGAAAATGCGCTTGTATTCCCAACGAGACATGGACAAAATCAAAACGATT TTACGCCTTACAAGGGATATGGGGGGTTAATCTTGCGGGGGTGGATATTATCTTGCGTTTAAAAGAAAG	1623 AGAAGATTTAAACCCCTTGGAATTGGCTAGATCTTATAAAGAATTGCTTGAAAGCTATCAAATGACCCAAGAGAGCTTGAAGAGCTTTAAAAATGACCCAAGAAGAGCTTGAAGAGCTTTAAAAAATCGTTAAAAAAATCCGAGCCCATGTGGCTAATATCATGGGTTTATTGACGCTCTTCTAAGGTTCAAAAACAAAAACAAAAACAAAAAACAAAAAAAA	1625 GCTTGGAGCGCCAGAAATCATTGTGCGCAATGAAAAAAGGATGTTGCAAGAAGCGTGGGATGTTTTGATAACG GCCGCAGCACTAATGCGGTTAAAGGGGCTAACAACGCCCTTTAAAATCGCTCAGTGAAATCATTAAAGGCAAGCAG GCGCAGCATTCAGGCAAAACCTTTTAGGTAAGGCGCGTGGATTTTTCAGGCAGAAGCGTGATTGTGGGCCTAATCT CAAAATGGATGAATGCGGGTTGCCTAAAAACATGGCGTTAGAACTCTTCAAACCCGATTTGTTATCCAAGCTTGAAGA GAGAGGCTATGCCACACGCTCAAAACGCATGATTGAGCAAAAAAGCAATGAAGTATGGGAGTGCTTG CAAGAAATCACAGGGGGTATCCGGTGCTACTCAACCGCGCTCCTACCTTGCAAAAAGCAATCAAT
HP1493	HP1493	HP1493	HP1493

HP1493	1627	1627 GCTGAGCATGAGCATTGATGCGATCAACCTCATGCGCGGCAAAAACCCTATTCAGGTCACCGTTGTAA GAAAAACGAGCCAAAACCTTTAGTGTTTAACATTCATTAAACTCCCCTCTGTCTATGTGAAAAGGT GAAAAACGAGCCAAAACCTTTAGTGTTTAACATCATTAGAACTCCCCTCTGTCTATGTGAAAAGGT TAAAGAAACCCCTTATCTGTATGTGAGGGTGGTTTTGACAAGAATGTTACCAAATCGGTTTTAGAAGGCTTAAA AGCTAACCCTAAGGGGATCGTGTTGGATTTAGGGGCAATCCTGGAGGGGCTATTAAACCAGCGGTGGG TTGTCTAACCCTTTCATTAAAGAGGGGTTTTAGTCTCTCAAAAAGGGGAAAATAAAGAAAATTAGAATACAAG GCTAACGCCAGGGGCCTTTAACCAATTTGCCGTGTTTAGCGGGGCGTGCA TGTCTGCCCCTTTCATTAACAAACGGGGCCGTGTTAAAATTATCCGGTGAAAAAAAA	1628 LSMS PVRV TVRV GVLV GVLV NLPIN NL NLPIN NLP	1628 LSMSIDDAINLMRGKPKTPIOITVVRKN EPKPLVFNIIRDIIKLPSVYVKKIKETPYL YVRVSGFDKNVTKSVLEGLKANPKAK GIVLDLRGNPGGLLNDAVGLSNLFIKE GVLVSQKGKNKEENLEYKANGRAPYT NLPIAVLVNGGSASASEIVAGALQDHK RAVIIGEKTFGKGSVQMLLPVNKDEAIK ITTARYYLPSGRTIOAKGITPDIVIYPGK VPENENKFSLKEADLKHHLEGELKKID DKTPNSKEADKDKKNEEEKEITPKMIN DDIQLKTAIDSLKTWSIVDEKMDEKAPK KK
HP1493	1629	1629 GGGAAGTGGCTCAAAATAAAACGAAGGGATTCGTTAAGGAGATCATTGGGAGCGGAGAAAGGCCTCTAAAAACTAAAAACCAAGGAGAGCCATTGAAAACTAAAAAAGCAAGGAAGCTTGAAGAAGCATTGAAGAGCGCCATTGAAAAAGGTAGCCATTGAAAAAGGTAGCCATTGAAAAAGGTATTTAAAAAAGGTAGTGAGAAAATCAAAAAGCTTTTAAAAAGGATCTTTAAAAGGATCTTTAAAAGGATCATCAATCA	1630 EVAQ EVSN KSALI KLLIG WQDI RRFC FMSS SYLEI LPNEE LPNEE LPNEE	1630 EVAQNKTKRFVKEIIGSEKASKTKNSAI EVSNTKASAMKNETIGSGDLKKVCEKI KSALPFGIISAFKPFKDAFYRDFNHNEQ KLLIGAAKSGCIGSSADKLAQLKTRLLY WQDKSVKVDWDKPILIKDFFKGNNYLY RRFCFLLGKHFMDRFLKNNAKASVKD FMSSKEFVAKYRYTPKQNTERAKKLQ SYLENKRDFIGFVQALNSLKDNPQDPF LPNEET SFLVFANEPTIVFNLRDNPQDPF LPNEET SFLVFANEPTIVFNLRDYLLVL AQIFNQAICYCESKCPIELINASPGKD
HP1493	1631	IB31 GGGAATTGAAAGAAGTGGAGAGCTTTTTACCCCTTAATGAAACGAATTTAGAAAAGAGCGAAAGAGTTTTTAGTTTTTG TGGATAATGAAAAAGTGGAGAGCTTTTTACCCCTTAATGAAACGAATTTAGAAAGAGCGAAAGAGTTTTTTG TGGATAATGAAAAAGTGAATGCAATGAGCGTTTTAGCTTTTGGAAAATCTAAGGATCTTATTGAGCGAGC	1632 ELKEY NEKYI AKYAI LRSSI QYLFE	1632 ELKEVESFLPLNETNLERAKEFLVFVD NEKVNAMSVLALENLRILLSEHNIKNDL AKYAMPESYKTHLAYSINARSLÖNFLT LRSSNKALKEMÖDLAKALFDALPGEH ÖYLFEDCLKH
нР0862	1633 2 4 4 6 4 5 F	1633 CGGTGGTTTTGGTGTTTGTGGGATCGCTTTTTGTGGCTTCAAGGATTGGTATGGAGTTCATGGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	1634 VVLVF FLVWI GLKPL RSLPE FOTEV PELKG ONANI	1634 VVLVFVĞSLFVAŠKIĞMEFMLKEDRĞR FLVWLKAKPGVSIDYMTÖKSKIFÖKAIE KHAEVEFTTLQVGYGTTQNPFKAKIFV GLKERKKEHÖLGÖFELMSVLRKEL RSLPEAKGLÖTINLSEVTLIGGGGDSSP FÖTFVFSHSÖEAVÖKSVENLKKFLLES PELKGKVESYHTSTSESOPÖLÖLKILR ÖNAMKXOKSA
HP0862	1635 6 7 A A D	1635 GATTGAAAAAGCGAAAACCTTCTATGGCGAAGATAAGGAAAATTGAATGTTTTGATATTGAAAATTCCAGCGCGCGC	1636 IEKAK LKOKN EKOKE VASKO EIPOIIT	1636 IERAKTTYGEDKEKLNVLIENSSALERE LKÖKNEHLENALKEÓEYLKNAWLLEM EKÖKEIFHNIKKLELEKSYÖDALNILKSE VASKÖTSSMHKEIHKASEILSKHKTNÖ EIPÖIITNFÖANEKARYKNESVLIVÖILÜ KGYYWIETEI GMRI

02/066501				PCT/EP01/
1638 GGVGAASRKGILMKGVHVLEVLTQAK SIAFDKTGTLTKGVFKYTDIVPQNGHSK EEVLHYASCSQLLSTHPIALSIQKACEE MLKDDKHQHDIKNYEEVSGMGVKAQC HTDLIIAGNEKMLDOFHIAHSPSKENGT NHVAFNQTYVGYIVISDEIKDDAIECLR DLKVQGIENFCILSGDRKSATESIAQTL GCEYHASLLPEEKTSVFKTFKERYKAP AIFVGDGINDAPTLASALVGIGMGKGS ELSKQSADIVITNDSLNSLVKVLAIAKKT KSIIWQNILFALGIKAVFIVLGLMGVASL WEAVFGDV	1640 LELNILLAI GOVLPANIILLUDAEGENGR LSIKSLDKIENOGIEKLL-HOOKLKTHAY ALQEKFGCEVLELDAKE SVKNI.HEKIA AFIKCAV	AIYLAUICKVYLIHRRÜSERCAPITEH AKNNDKIEFLTPYVYEEIKGDASGVSL SIKNTATNEKRELVYPG=FIFVGPVNN AVLKQEDNSMLCKCDEYGSIVVDFSM KTNVQGLFAAGDIRIFAFYKQVVCAASD GATAALSVISYLEHH	1644 KVYDLSVYVUMUVDILSSKK 1646 LGVALILCSGLLIALPALI.KELKKI	1648 FGLLFLRQHMNLLKRACDFSVLDSDEV KTLCKQLKISNFRASISCIKNGMMDLS MQDSECYKAYELYQNALKKDNLVDFD DLLFLSLKILQDNETIAKETSE
1637 TGGGGCGTGGGAGCAGCAGCAGAAGGGCATTTTAATGAAGGCCGTGCATGTTTTAGAGGTGCTTACCCCAAGCT AAAAGCATCGCTTTTGATAAAACCGGCACTTTGACTAAAGGCGTTTTAAAGTAACGGATATTGTGCCGCAAAATGGG CATTCTAAAGAAGAAGTTTTGCATTACGCTTCTTGTTCGCAGCTCTTATCCACGCACCCTATCGCTTTATCCATTCAAA AAAGCATGCGAAGAATGTTAAAGGACGATAAGCACCAACATTGAAAAATTACGAAGAAGTGAGCGGATGGG GGTTAAAGGGCCAATGCCGATTAATCATCGCAGGGAATGAAAAATTACGAAGAAGTGCCATATCGCGACA GGCCTTCCAAAGAAAAGGGCACGATTAATCATCGCAGGGAATGAAAAATTATGGGCATATTCGTCATTAGGGAT GCCCTTCCAAAGAAAAGGGCACGATCGCCATAGGGATTTAAAAGTGCAAGGGATAGTGGGATTTTGGGAT GGACAGAAAGAAAGGGCACGATCGCCTTAAGGGATTTAAAAGTGCAAGGAAATTTTTGGAATTTTTGGACTTTTTGAGGGAT AAAACGAAGAAAGAAGAGCGCATTAAAAGATTGGCATTAAAAGGCTTTTAAAAGGTGCCATTAAAAGGTGCCATTAAAAGGTGCCATTAAAAGGTGCAAAAGCAATGAGCGCATTAAAAGGTGCCTTAAAAGGTGCCTTAAAAGGTGCCTTAAAAGGTGCTTTAAAAGGTGCCTTAAAAGGTTTTAAAAGGTGCAATGGGGAATTTTTTGTAGGGATTTTTTTT	1639 CTTAGAATTAAACCTGCTTGCCCAAAGCGTCTTGCCTGCAAAATCATTCTTTTACTCATAGACAAAGAGGGCTT AAAACAGCGCTTAAAAGTTTAGATAAAATAGAAAAACCAAGGCATAGAAAAATTACTTCATATCCAGCAAAA GCTCAAAACCCACGCTTATGCGTTACAAGAAAATTTGGGTGCGAAGTTTTGGAATTAGAAGTTAAGAAAAGGAAAAGGAAAAAA	1641 CTTGCGCGACATGCGATGGCTTCTTTTATAAAATAAAGATAGCGGTGCTTGGTGGAGGCGATGCCCCGTAGAA GAGGCGATTTATTTGGCCAACATCTGCCAAAAAGTCTATCTCATCCACAGAAGAGGTGGTTTAGGTGCGCCCTAT GAGGCGATTTATTTGGCCAAAAACAACGATGGTTTTTAACCCCTTATGTGGTGGAAGAATCAAGGCGATG CACTTTAGAGGTGTCTTCTTTAAGCATTAAAAACACAGGCCTAACGAAAAAAGAGAATTGGTTGTGCCGGGGTTTTTA CTTCTGGAGTGTCTTCTTTAAGCATTAAAAACACAGCACTAACGAAAAAAAA	1643 CAAGGIGIATGATTTATCGGTTTATGTGCAGATGCAAGTGGATATTTTGTCTTCTAAAAAATAAAGCTTTTAAGGGGAT TTTATAAATACTTAAATAGGGAGTTAGGAGGTTTTTATGAATTACGATAACTATTGGGATGAGGACAAACCGGAACTC AATATCACGCCTTTAGTGGATGCTTGCTTCGTTTTGTTGGCATACGATAACTATTGGGACGACCCACTCTTATAAAG AAGAAATTGCTTTGCCTTCTGGCTCAAAAACTGCTAGAGCCACTCAAGAATAAAAATGCTTTGCCTTTGCCTTCTGGCTCAAAAAGCGCTCAAAAAATGCATTGATAAAAAATCTATTAAGATAGTCAAAAACCTATGATTAACAAACCTTAACAAAAATTTAAGGGGTGGCTTTGATTATAAAAAAATTTAAGGGGTTGCATTAAAAAAAA	ATTITAGGCCAAAACGATITGGCTITAAGATIGCCTITITGATCGCTCATCTCAT
HP0862	HP0862	HP0402	HP0402	HP0402

١	۷	5
¢	×	5
ŧ	•	i

104.01	7070	100011100011		٠
CCC 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,		ICAM MOLCAAAGGGAATT HICTATT TAATCAATGCGAATAGTTATAGCGTTGCGGATGTGGAAAAGATTCAAGTGG GTAATCATGTGCGTGTTGCCAAAAATTGCAAAAATTGAAAGCTTTTGCGAGCTTTTACGAGCTTTAAAG ACAAACCCGGTGTGATTTTAGAAATCCAAAAGATTGCGAGCGTTTTGGAAATCGTAGATAGGGTGTATGAA GCTTTAAAGCCGATTCAAGCCATTAGCCCTAACTATGAAATCAGACCCTTTTTAGACCCACGGGCTATATCCGCACC TCTATTGAAGCGCGATTCAAGCCTTAGCCCTAACTATGAAATCAGACCCTTTTTAGACCCCCCACGGCTATATCCGCACC TCTATTGAAGACGTGAAATTTGATCTAGTTTTAGGGGCGATTTTAGTGGGTTTTGCGTTCTTGCGTACC GGCACGATCACCTCGTTTCAGCGATCTCTATTCTAT	1650 NSQ VRL LEIC NYE ILAV FALI	1650 NSGREFSILINANSYSVADVEKIQVGNH VRLGDIAKIEIGLEEDNTFASFKDKPGVI LEIOKIAGANEIENDRVYEALKRIQAISP NYEIRPFLDTTGYIRTSIEDVKFDLVLGA ILAVLVVFAFLRNGTITLVSAISIPISIMGT FALIQWMGFSLNMLTM
HP1255	1651	1651 GAATTITGCCGGGGTTACCGTGGATAAAATGGAAGTGGGTTTGATCCCACAAAGAGGATCAATGATTTTAGAAAAGGGGCAATTGATTTTAGAAAAGGGGCAATTGATTTTAGAAAAGGGGCAATACGAACGA	1652 NFA WWD WPTS VPTS VPTS YGIF GFKG GVG SRW	1652 NFAGVTVDKMEVGLIHKEHQITIIDLPG TYALNDFTTEEKVTKDFLEKGYDLILN VVDSTNLERNLALSAGLDTNKKMLLA LNMWDEAQKEGIKINTEKLSKELGVVC VPTSARSKEDRLNTELLLDEIVRLYSQN TTNNENIKVPSQSFKESLKYSQSAGRI AQLVISENQQNASFEHTYKIDKILMHKR YGIFILGFMFIIFSLSFLIGGGVQKALET GFKFLSDGIKENVANEDLASLVGDGIIG GVGATVSFLPLIVVLYFGISLLETTGYM SRVAFLLDGILHKF
HP1255	1653	1853 CGAATTGAATTGAATTGAGTTTTCAAATCGCGCAAGCTCTAAAAGGGATTAAAGGATCTAGTGAAGTTTTAACCACGCT TAATGAGGGCGTGAATTATTGTATGAACCCCTAATAAAGAATCGATGGCGGATGTGGGGATCACTAGCGATGAAT TACCAAGTTTTAAAAATCCGCTTTAGAGGGCTTGGTTGTGATGGTGGTCCCTACAGGGATTTCACGCACG	1654 ELNE GVNY LKSA DFAS	1654 ELNEL SFÖJAGALKGIKGSSEVLTTLNE GVNYLYVTPNKESMADVGITSDEFSKF LKSALEGLVVDVIPTGISRTPVMIRQES DEASSITKIKSLALTSKYGVLVPITSIAKI
HP1255	1655	1655 GGGCGAGACCACAGAAGGCTTGGTGCTTTCTTTAAAAGACGCTAACAAGAAATCATCATCACTCAAGTGTATCAAAAAAAA	1656 GETT 1656 GETT ELKP VSKT	1656 GETTEGLYSK DANTKEIIT OV YOKLE ELKPFLPNGVSINVFYDRSEFT OKAIAT ELKPEL BY SILIEN FLEIGHT FILEN BASVANG
HP1255	1657	1657 TGCCGGTTTATAAAAAAGTCGGCGATAAAGTCTTTTCAGGGACATTCAATAGCCACAGGGTTTTTAATGAAAGGCCAACGCACTTTATAAAAAAAGGCCAAATTTCAGGGACATTTAATAACGCTCAAAGTTCAAAGGCCAGATTTCGCAAAACAAAAAAAA	1658 PVYK ONNY ADKV OFWN ATPIN KARL KARL	WILL LSL.SVAT. ONNKNSTLSOIIEMIYNAOSSKAEISRL ADKVSSVFVPSVIAISILAFV/WLIIAPKP OFWWINFGIALEVFSVLVISCPCALGL ATPMSILVANDKASSLGLFKDAKSLE KARLVNTIVFDKTGTLTNGKPVVKSVH SKIELLELLSLALSIEKSSEHVIAKGI

0 0 > 0 1 4 4 - V -	la S	PCT/EP0	1/15428
1660 SFYAAASMAYMLGAKHAFDADHIACID NTIRKLTQQGKNAYGVGFYFSMGHSS VVILMTIISAFAIAWAKEHTPMLEEIGGV VGTLVSGLFLLIIGLLNAIILLDLKIFKKS HSNESLSQQNEEIERLLTSRGLLNRF FKPLFNFVSKSWHIYFIGFLFGLGFDTA SEIALLALSSSAIKVSMVGMLSLPILFAA GMSLFDTLDGAFMLKAYDWAFKTPLR KIYYNISITALSVFIALF GLIELFQVVSEK LHÜKFENRLLRALQSLEFTDLGYVVSEK	1662 RLKÖRTEHDLEMISATGVCKGIENYAR HFTGKAPNETPFCL.FUYLGIFEREFLVI VDESHVSLPOFGGMYAGDMSRKSVLV EYGFRLPSALDNRPLKFDEFIHKNCQF LFVSATPNKLELELSKKNVAEQIIRPTG LLDPKFEVRDSDKQVCIDLFDEIKLVVA RGERVLITTTKKMAEELCKYYAEWGL KARYMHSEIDAIERNHIIRSLRLKEFDILI GINLLREGLDLPEVSLVAIMDADKEGFL RSETSLIQTMGRAARNANGKVLLYAKK ITQSMQKAFEITSYRRAKGEEFNKIHNI TPKTVTRALEEELKLRIDEIRIAKALKK DKMPKSEREKIIKELDKKMREGTKNIN	FEEAMRL RDEIAOLRTI 1664 NIVSIIVWFCIFOISTESL VOLFTTILYLFI GLYYFNRWNKSCKO	1666 AVDĚEHNKĎAMKMTDL EAGKLGSVIL SDVEMGGKILLKAIPILDGEMLTDAKVV YDGNNQPVVSFTLDAGGAKIFGDFSG ANVGKRMAIVLDNKVYSAPVIRERIGG GSGOISGNFSVAOASDI AIAI RSG
CATCGCTTGC CTATGGGGCA CCGATGCTAG TGCGATTATTC SAGATCGAGC TGGCATATTT AGCATTTAGAT TCTCTATCACG CCATTTAAAAT			
1659 TTCGTTITATGCGGCGGCGTCTATGGCCTACATGCTAGGGGCAAAGCATGCGTTTGATGCGGATCACCATCGCTTGC ATAGATAACACCATTAGAAAGCTCACCCAACAAGGCCAAAAAGCCTATGGTGTGGGGTTTTACTTTTCTATGGGGCA ATAGATAACACCATTAGAATTACACCCATCATCACGCGTTTGCGATTGGTTTGGGCTAAGAACACGCCGATGCTTAG AAGAAATAGGGGGGGTATTAAAAATATTCAAAAATTGCACTTTTTTTT	1661 CCGCCTCAAACAACGCACCGAGCATGATTTAGAAATGATTAGCGGGGGTGTGTGAAGGGGCATTGAAAATTACGGCGCTCAAACAACAACGCACCGAGCATTTAGGAAATTACGGGGGATTTAGGGGGGATTTTGAGGGGGGATTTTTGAGGGGGG	GGAATATCGTATCCATTATCGTGTGTTTTGTATTTTTCAAATTTCTACAGAGAGCTTGGTGCAACTCTTCACAACGAT GGAATATCCTATTTTTTTTTT	TGTCTGATGTGGAAGACACAATAAAGATGCGATGAAAATGACGGATTTAGAGGCTCAAAAATTAGGCGCGTGTTGT TGTCTGATGTGGAAATGGGGGGGTAAAATCTTGCTCAAAGCGATCCCCATTTTAGATGGCGAAATGCTTACAGATGCG AAAGTGGTGTATGACCAAAACAACCAGCCGGTGGTGAGCTTCACGCTGGATGCGCAAGGGGCTAAGATTTTGGGG ATTTCTCAGGTGCGAATGTGGGCAAACGCATGGCGATTGTTTAGACAATAAGGTCTATTCAGCCCGGTGATTAGG GAGCGTATCGGTGGGGGGGGGG
GCTAGGGCAAAGCATIGGGGCTTIGGGCTTIGGGATCGCTTIGGGATCGCTTIGCGATCGCTTIATITITIGCGTTAATGAAAGCCTTGTTIAAGGGTTAAGGGTTAAGGGGTTAAGGGGTTAAGGGGTTAAGGGGTTAAGGGGTTTTGCAAAGCCTTTAAGGGTTTAAGAATTACAAGATTAAGAATTACAAGAGTTTAGAAGATTAAGAATTACAAGATTAAGAATTACAAGATTAAGAATTACAAGATTAAGAATTACAAGATTAAGAATTACAAGACTTGG	AATGATTAGCGCGACCG CGCCTTTTGCTTGTTT CGCCCTTTTGCTGTTT CGCCTTTTGCTTGGGGG CGATAAGCTAGAATAG ATTGAAGTGCGAGACA ATTGAAGTGCGAGACA AGGGTGCTCATCACAC AGGGTTTTAAGGA TTAATAGGGATCAAAAA TGAAATTAGAAAAAAAAAA	TITCAAATTICTACAGA 3GTGGAATAAGTCATGO AACGCTCCTTTTAAT ATTGTCCAAGCCTTTT ATTGTCCAAGCCTTTT AGTCACGCTTTAGGGA 3GTCTTTTAGGGTGTTA AACATCAGTTTCACAAA GCGGGTTTGTTCGCTTT CAATGAAGCTACAAAAAAAAAAAAAAAAAAAAAAAAAAA	AAAATGACGGATTTAGA SAAAGCGATCCCCATTT TGAGCTTCACGCTGGAT GATTGTTTAGACAATAA GGGAATTTTAGCGTGGC
GCGTCTATGGCCTACAT AAAGCTCACCCACACAA TAATGACCATCATCAG AGTTCAAAAATCGCA ATATTCAAAAATCGCA TITGGGCTGGGTTTTA GGGCATGCTCTTTA GGGCATGCTCTTTA GGCGTATGACTGGGC CGCGCTTACAAAAACCI TTTTATGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ACCGAGCATGATTAGA AAAGCCCTAACGAAA SAAAGCCATGTGAGTT TGGTTTAGATTGCCTA TTGTGTCCGCTACGCC GGGCTTTAGACCCTA GGGCTTTAGACCCTA AATGGGGCTTGAGGC CTTAAAGAATTTGACAT ATCATGGCAAGA ACGCTAATGGCAAGA ACGCTAATGGCAAGA	VICGTGTGGTTTTGTATT CTTGTATTTTTAAC GCTTAGACCTTTTAAA AACCCAGCGTTGTTATA AACCCAGCGTTGTTATA SAACAAACAGCAACGA GAATGGCAACGAGA GCATTAGCCTGGATC CTCTTTTGGCTGGATC CTCTTTTTAGCCTGCT ATCAAAAATTCTTATAA GCAAGAAATTCTTATAA GCAAGTAGAAAAATAGAAC AAAATCCAAAGAACA	ACAATAAAGATGCGATGGGGTGGGGTGGGGTGAGGGTGGGT
TTCGTTTTATGCGGCGGCGTCTATGGCCTACATGCTAGG ATAGATAACACCATTAGAAAGCTCACCCAACAAGGCTAAA TTCAAGCGTGGTGATTTAATGACCCATCATCAGCGCGTTT AAGAATAGGGGGGTTTTAATGGGCGACTTTCTAGTTCTAAT TCTTGGATTTATAAAATATTCAAAAAATGCCGCTTTTTTAA ATCCTATCGGTTTTCTTTTTAAAAATATTCAGCGGTTTTTTTT	CCGCCTCAACAGGC CGCGCCATTTCACCGGI TTTTAGTCATTGTGGATA AGTGTTTTAGTGGAATA AAATCATCCCGTTCCTT AAATCATCCAGTTCCTT GATGAAATCAGTTAGTG TGACAATATTATGTAGG TGACCCTTTTAGTAGGC GGGCGAGCCGCTAGAA TGAGATCACTAGAA GGGCGAGCCGCTAGAA TGAGATCACTAGTACAG GGGCGAGCCGCTAGAA	GGAATATCGTATCCATTATCGTGTGGTGTTTTTTTTTTT	Geces i Galigaagaac TGTCTGATGTGGAAATGG AAAGTGGTGTATGACCAA ATTCTCAGGTGCGAATG GAGCGTATCGCTGGGGG
1659	1861 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1663 0 1 1 1 4 4 4 4 4 7 1 1 1 1 1 1 1 1 1 1 1	2001 2014 2014 2014 2014 2014 2014 2014
HP1255	HP1255	HP1255	6621

HP0978	1667 CA	1667 CAGGACTIGGAGGAGGGACTGGGACTGGAGCCACCCCTACTATAAAATCGCAAAAGAAGAAGAGGGGGCGCTCA	1668	1668 GLGGGTGTGATPTIVKIAKEVGALTIAIV
_	E	TTGGAGCATCTAGCGATTCTATTTGGTTATCCCTAATGACAAAATCCTTCTCACCATGAAAAAAAA		I RPFKY EGNOKKKKAEEGLKELEGSS DSILVIPNDKILLTMKKNASTTECYREV
	14	AUGGAGTETTTCTACTATCATCATGATGATGATGATGATTTAGGGCTGTGAGTGGCATTTCTACTATCACTAAAACGGGTTTAAAATGCGGGTTTAAAAGAGGGGTCTTGGTTTTAAAGGGGTTTAAAAGAGGGGGTGTTTAAAAGAGGGTTTAAAAGAGGGTTTAAAAGAGGGTTTAAAAGAGGGTTTAAAAGAGGGTTTAAAAGAGGGTTTAAAAGAGGGTTTAAAAGAGGGTTTAAAAGAGGGTTTAAAAAGAGGGTTTAAAAGAGGGTTTAAAAGAGGGTTTAAAAGAGGGTTTAAAAAGAGGGTTTAAAAAGAGGGTTTAAAAAGAGGGTTTAAAAAGAGGGTTTAAAAAGAGGGTTTAAAAAGAGGGTTTAAAAAGAGGGTTTAAAAAGAGGGTTTAAAAAGAGGGTTTAAAAAGAGGGTTTAAAAAGAGGGTTTAAAAAA		DDVLVRAVSGISTIITKPGNINVDFADLK
	CA	CACTGGCGAAGATCCGCTAAATTAGCGGTGCAAATGCGATCCAATCGCCTCTTCTTGATGACGCTTCTATTGAAG		NAIOSPILDDASIEGAKSIIVEFEHHPDY
	9 1	GGGCTAAGAGGCATTATTGTGTCTTTTTTGAGCACCACCCTGATTATCCTATGATGGCTTATTCTCAAGCGTGCGATTTTA		PMMAYSQACDFIQDQAHQDVDVKFG
		CAAGA CAAGCCCATTGCAAGCGGTGTTGAAAGAAGAAGAAGGGGAAGAGGGGGGTTAGGAAGATTGCTATTGATGATGTGC		CHTSDNIPIDHVRVTIIATGAERNSGGA
	<u> </u>	GCCTGTGGTGAAACAAACGAGAAAAGTGGGTAATGGCGAGTATTTAAAGATCCCTACTGAAGAAGAGAGCTATCCATAC		SLESIA I PSQPVVKQTRKVGNGEYLKIP TEFFI SIPTTMRIOOD
	<u>3</u>	CCACAACCATGAGAATCCAGCAAGACTGATTGCAGATCTTGTTTTCTCCCCTATTTTTACAGGGCTATAATAAAGCG		
HP0978	1669 660	1669 GGGGTTTCTCAACTCATTCAAGTGGGAGCGTTAGTCAAGTTTTTGTTAGCGTTTTCAAAAAAAGCAACTCAAAAA	1670	Charles and a second of the se
	70,	TCGTTCAAGTGTGTGTTTTAACCCCCATGCGGGCGAAGAGGGCTTATTTGGGGAAGAGATGAAAGGATTTTAAAA	200	AVSGENPHAGEEGLEGEDERILKAIOK
	<u> </u>	GCCATTCAAAAGAGCAACCAAACGCTAGGCTTTGAATGCTTTTTGGGGCCACTGCCGGCTGATAGTGCTTTTGCCCC		SNOTLGFECFLGPLPADSAFAPNKRKI
	30	CAMIAAACGAAAAAIAAAGCCCIIIIIAIGIGAGCATGAGCCATGATGTGGGGGCTAGCCCCTTTAAAAGCGCTCTATTT IGATGAAAGCATTAATGTGAGTTTGAACG		TPFYVSMSHDVGLAPLKALYFDESINV
HP0753	1671 AAA	1671 AAAAGCGACTTGTATGCCCTATGATTACTCTAAATTGGGTATAGAGACTATTGGCGAGGACATTAGAAGCAATATTAA	1672	1672 KATCMPYDYSKI GIFTIGEDIRSNIKAI
	AGC	<u>AGCATTACAGAAAATGTCTCGTGGGTATGGACACCCTAAAGAGTTCTTTTTGGACGCAATGATAAAAAAAA</u>		OKMSRGYGHPKEFFLDAMIKKGENAIK
		IGCGATTAAACGCATAGAAGCACGAAAATGTGCGGTAAGCGATGACTTCAAACAAGGTATGAAACGAAACATTAAAG	-	RIEARKCAVSDDFKQGMKRNIKVNNLV
	W-1	IAA MACCI GI AAAGC AIGCGACAAGGCAAAAAGTGAGTAGGACATTGATTGATTGCTAAAGTGCTTGCT		KAMROGKKVSRTLIAKVLANTIDTDAĞ
	151	TOTAGAGGETAGTTACCGCCATAGAGCAGAGGGGGCGCTGAGTTATGAGTTGAGTTGATTGA		YCFISPTDLATOLGNISPRLSKSIVTAIE
	TAA	TAACTCCACCACAATATCTTAAGTTTCATTTTTTGATAACCCTTTAAGCGACCAAGTGTTTGAGAGTATAGTC		CAEGOVENI ALIUNI I INSCHINILSTIFUI DINPI SOOVEERI VIEVEREAI KNIVKI P
	ATT	ATTGAAGTCCCAAGAGAAGCACTTAAAAATGTGAAGTTGCCACAAAATCAAAAATGTATTGACTTCTCAAATCTTTGACT		QIKNVLTSQIFDGAYHFKS
	ပ္ပင္ပ	GGGCTTACCACTTTAAAAGTTAAAACCATGCTCTTTATCAGCGCAACTAACACGGAATGCCGGAAAAACCACATGCGCTA		
1	225	GECLATTAGECCEAGIALI GEAACGETTGTGGCGTTAAAACTATCTTGTTAAAACCCATTGAAACGGGCGTTAATGAC GCCATTA		
HP0753	1673 TGC	SAACGCTTTGACATGAGCGAA	1674	1674 HFERFDMSEYKEAHSVAKLIGSPSGYV
	- K-	A LE LEGE GENTI GAACAA GGGGGGTTATT GGT GAAT GCGATT AAAAAA CACCCGCATT GTTGCTGCTTTT AGATGA		GFEOGGLLVNAIKKHPHCLLLLDEIEKA
	4 S	GATAGAAAAGCCCATTTAAACGTGTATGATTTGTTGCAAGTGATGATAGCGCCACTTTGAGCGATAATTTAGG		HSNVYDLLLQVMDNATLSDNLGNGAS
		CANTCAGGGCTAAAAACACCATGGCTATGATAAAACCCTTAAAAAAAA		FKHVILIMTSNVGSKDKDTLGFFSAKNT
	ÇGA	CGATCGTGCCCTTTAACGCGCTCAGTTTGGAGGATTTTGAACGCATTGTTTGT		KYDKAVKELLI PELKSKIDAIVPFNALS
	TAG	TAGCGCTAGAGCAAGACATAACCTTAAAATTCCATAAAGAAGTTGTGAAATTCATCGCGCAAAAAAGCTACCGAACGA		KEVVKFIAOKSYOTTI GARFIKKIIHNEI
	E (CTTTAGGAGGGAGGAAATTAAAAAATCATTCATAATGAAATCAAAACTAAATTAAGCGATATACTGCTCTTGCAATC		KTKLSDILLLÖSFKKPCKIACLLEKNÖLV
	5 0	GITTAAAAACCTTGTAAGATCGCTTGCTTGCTAGAAAAAACCAATTGGTTTTAAAAGAAATCAAGCGCGCGC		LKEIKRAQKVKENDF
	146.	BGTGAAAAATGACGTAATGAAGGATTTAAGCAAAATCCATAAGGGGGGGG		
	TGT	TGTCAATAATGGCGAACGCTTCAGCACCTATGTGATTTTAGGGAAAAAAGGGGGCGAAATTTGCGTCAATGGTGCAAA		
	CAG	CAGCCAGAAAGGTGGCCATAGGCGATGTAGTGATTTTAGCTTATGCGAGCATGAATGA		
	ICAC	CACAGCCGAGCATCG		

HP0753	1675	1675 TIGATTGTGATGGATATGGCAGATTCAGCGCGCACTTGGACAAGATCCGCTCGGATATGGGTTCGGTGCAAAT	1676	1676 IVMDMADSARTOLDKIRSDMGSVOME
·		GGAATTGGTTACAACCATTAATAATATTCTGTAACCCAAGTGAATGTTAAAGCGGCTGAATCTCAAATCAGAGATGT GGATTTTGCTGAAGAGGGCGCAACTTTCTAAATACAATATTTTGGCGCAAGGCGGGGAGTTTTGCTATGGCGCAAG GGATTTTGCTGAAGAGAGCGCGAACTTTTGTAAATACAATAACAGCCCTTTTAATTCAAAGGGGCGTTAGCCCTTTTTA TCAGATTATTATAAAGTTAGAATGATGAATGTATATACAAAAACTTGCAAGGCTCTTTTCAAAAAAGGCCCTTTTGT TGGCAAAACTCAAAGACACATTAAAGAAAAAAATATCGAAGTGTTTTTAAGGGAATGATTGCGCAATTTCAACAAAAACTTCAAAAAACTTAAAAAAAA		LVTTINNISVTQVNVKAAESQIRDVDFA EESANFSKYNILAQSGSFANIAQANAV QQNVLRLLQ
		ATTACATGCTTTATCCTTATTTGTATTATTTTGGCTAGGCTGTTTTATCGCTTTTAGGTATTGAGAATTTATAGGTATTGAGAATTTTATGGTATTGAGAATTTTTAGGTATTGAGAATTTTTT		·
HP0753	1677	1677 CCGTGCAGCTTGCTTATGCGATTGGGGTGATAGAGCCAGTGTCTATTTATGTGAACGCCATAACACGAGCAAGTAT TCAAGCGCTGAGTTGGAAAAATGCGTGAAAATCGGTTTTCAAACTCACGCCAAAAGGCATTATTGAAAGCTTGGATTTA TTAAGACCCATTTATTCGCTCACTTCAGCTTATGGGCATTTTGGGCGCGGAATTAGAGGAATTCACTTGGGAAAAAACC AACAAAGCTGAGGAGATTAAAGCGTTCTTTAAGCGTTAAAAAAATTTTTAAGGGTAATATTTAAAAAAATTTTGTATA ATCAACAATTCACAAGGGTTTAAATTGAAACGAAGGCTGTCTTATTAAAAAAATTTTTGATA	1678	1678 VOLAYAIGVIEPVSIYVNTHNTSKYSSA ELEKCVKSVFKLTPKGIIESLDLLRPIYS LTSAYGHFGRELEEFTWEKTNKAEEIK AFFKR
HP0753	1679	1679 GGATTIGAAAGGGTGGGTAGGAATCTTAGAAGATTTAAAAGGATCCCAATAATCCTAATTTAGACAC GCTAGTGGAATCCTAATTTTAGAAAGCAATCCTAATTTTGC GCTAGTGGATCCTAAATCCTTACAAACACCAATCATTTTGCAAACAGCAATCGTGTAGTCCTAATTCTTCAAACAG GCTAGTGGAAGTAGGCCATTTCAGGCCATGCTTACTTACAACAGAATCTTGCAATGTTCTTCAAACAG CATTATCCATGAAAAGAAAA	1680	1680 DLKGWVGILEDLKMNLKDPNINPNLDTL VDGSSGSVWFNFYEPESNRVVHDFAV VDGSSGSVWFNFYFHNNSGGLNSSNSII HEYLEKNKEDAIHKILNRMYAVVMKKA VTELTKENIDKYREAIDRMKGFKSSMP QKK
HP0753	1681	1881 TATTGCAAAAATCAGGCGAGCGAATGATTTTTAATCAAAAGCGAAAAAGCAACGCCTTTAAAAAAGGTTTTAA AACAAGCTTTAAGGATTTATTCGCAATCTTTTGAGGGTCATTTCGCATAATTTGCAAGAATTCTAAACATGCGAGCG GAAAAAAAACCCTTGATTTAGGAACTTTTGAAGACTTTTCAAAAAAATCAAGCCCCTATTTTAATAGAAATTGGTTTT GGGAGCGGGAGGCATTTGATAGAATTAGCCAAAAACCACCCCCACTAAAACATTAGGGATTCACCCCCC GTCTATCGCGCAAGCGTTAAAGCAAATTGAGTTTAAGAACTCTGCATTAGGGATTGCGTTT GGTTTTAGAGAGCATGCCAAATTGAGTTATTGGATTTAAAAATTTGCCTTGTGCCATGGCAATGGCGTTT ACCGCCGGGTGCTAAGCCAAATTGAGTTATTGGATTTTTTAAAAATTTGCCTTGTGCCATGGCAATGAGAAAAAC ACCGCCGGGTGCTAAGCGAAAAAAAAAA	1682	1682 LOKIRRANDFLIKSEKATPLKIŘEVLKOA LRIYSOSFEVISHNLOENSKHASGKKTL DLGTFEDFIOKNOAPILIEIGFSSGRHLI ELAKNNPTKTCLGIEIHTPSIAQALKOIE LLDLKNLHILOGOGRLVLESWIPNHRCE KIFVHFPVPWNEKKHRRVLSIEKFLNEA LRVLKPRGFLELRTDD
HP0753	1683	1683 AGAGGCTAATAAGCAAGACGCTTTATTGCAAGCTTTAAAAGATGAAGCCATAAAAAAAA	1684	1684 EANKODALLOALKDEANHKKEREKRE VKQEEEIKDINLOLSKIRDSLK-LICNNF WDEKNPNSINIPGEFAEIYKL-AKQSGM KPSHLDEIMQLSLELMPLRMIKENSVTI KRYFREVLRKMILCCPEDLNI.RÖKRIL MLVGPTGVGKTTTLAKLAARYSRMLAK KYKV

۱
á

02/066501			PCT/EP01/15428
1686 GALCLGGLMAEQDPKELVGLGAKSYK EKDFTQAKKYFEKACDLKENSGCFNL GVLYYGGGGVEKNLKKAASFYAKACD LNYSNGCHLLGNLYYSGGGSSGNTNK ALQYYSKACDLKYAEGCASLGGIYHDG KVYTRDFKKAVEYFTKACDLNDGDGC TILGSLYDAGRGTPKDLKKALASYDKA CDLKDSPGCFNAGNMYHHGEGATKN FKEALARYSKACELENGGGCFNLGAM QYNGEGVTRNEKQAIENFKKGCKLGA KGACDILKQLKIKV	1688 THSESALDLLKLLKKNOMNASAIEIÄH LLNÖDDDLKAKEQALYDLGALYARIKD FKNAHLYNLOYLQDHAELDKASVARIKD FKNAHLYNLOYLQDHAELDKASVARIKD RDEKALESMEGNTÖEKIAHYDKIIONF NSNEALKALELKAQLLFENKRYAEVLS MOKNLPKDSPLIÖKTLNVLAKTPLENH RCEEALKYLSOITTFEFSPKEEIÖAFDC LYFASLKEKAQIIALNAFKTAKAPSEKLI WLYRLGRNYYRLGDFKNSTLASKDALI LAĞSLNIKKEFYDIAFVLFSDYMÖNNEK ELALHLYAFLEKHFKGDKRMALVYFKL LENEKDPKSVKIYATSLLKLQDAYKDYS	1690 LQĞSKSMĞDLLAKAMPIERILKAYSVP VGSLENYEKIYYQNAFKPKVÜTFÜNN GDAEIKSALISAYARVLTPSDEEKLYĞI KNEVFTDSANGITRIRVVVSASÜCĞGT PVLNRSLEVDEKNKNFAITRLĞSLLYKE LKDYANKEGĞĞNTĞL	1692 PFDDFEKTLLQLKKEHFKAAHFVTAFR YSLEGKITEGFSDDGEPKGSSGMPML SVLRREDLINIGLYSVRYFGGTLLGVG GLMKAYAKSALLCVENAGKEDALKDFV ELETLSAHYSYKELDALGREIKKFSLQL SKKNFSNGSVEVEISGTRENLGAFLQO NKIN
1685 GGGTGCGTTGTGTTTAGGGGGGGCCAATGGCAGGAGCCTAAAAGAGCTTGTGGGGTTTGGGGGGCAAAGAGGGTA CAAAGAAAATTTGACAGAAGAAATATTTGAGAAAGCGTGCGATTTGAAAGAAA	1687 CTACGCATAGCGAATCAGCCCTAGACTTACTGAAAAAAAA	1889 ITTACAGCAATCCAAGAGCATGGGGGGATTTATTGGCTAAAGCGATGCCTATAGAAAGGGATTTTAAAAGCGTATTGTGT TCCGGTGGGTTCGTTAGAAAATCTATTATGGCTAAAGCGATGCCTATAGAAAGGGATTTTTGAT AACAACGGCGATGCGGAATCAAAAGCGCTCTCATAACGATTGCCAGAGCGCTAGTGCTAACGCCTAGTGATGAAAAAAAA	1891 GCCTTTTAAAAAACCCTTTTGCAATTGAAAAAAGCCTTTTTAAAGCCGCGCATTTTGTAACGGCGTT CCCTATTCTTTAGGGTAAAATCACGGGGGTTTTAGCGATGCGCGGGCCTAAAGGGGAGTTCAGGCCTTGCTTTAGGGGTGCTTTAGGGGTGCTTTTAGGGGTGCTTTTAGGGGTGCTTTTAGGGCGAGGGTTTTAGGGGTTTTAGGGGTGGGGGGTTTTAGGGGTGGGGGG
HP0753	нР0753	HP0753	HPU/53

•		-
¢	2	١
i		4

02/066501	T	Pe
1694 RLSVMVILAPERLGLATLHQLRGRVSR NGLKGYCFLCTIQEENE:RLEKFADELD GFKIAELDLEYRKSGDLLQGGEQSGNS FEYIDLAKDENIIAEVKRDFLKAASVSR GTFEN	1696 LYQITEQNFNHSFSAEE SQYMQRLVN NTKTDFFDKALIEELKKIYYKIVKYIQ	1698 DPAYKGAKIVVIGVGGGGSNMIKHLVE YGVHQDVTPIATNTDGCHLKNNPAPV KILLGKESTGGLGAGGIPDIGRKAAEES ANEIKEAIKDAKLVIISTGLGGGTGTGAT PTIVKIAKEVGALTIAIVTIKPFKYEGNQK RKRAEEGLKELEGSSDISILVIPNDKILLT MKKNASTTECYREVDVLVRAVSGIST IITKPGNINVDFADLKSALGFKGFALMGI GEATGEESAKLAVQNAIQSPLLDDASIE GAKSIIVFFEHHPDYPMIAAYSQACDFI QDQAHQDVDVKFGQHTSDNIPIDHVR VTIIATGAERNSGGASLE:SIATPSQPVV
1693 ACGATTGAGCGTGATGTGATTTTAGCGCCCGAAAGGTTAGCGACTTTACACCAGTTAAGGGGGCCCGTT TCTCGTAACGGCTTGAAAGGCTATTGTTTTTTATGCACGATCCAAGAAAACGAACG	16995 TGCTCTATCAAATCACAGAACAAAATTTCAACCACTCATTTAGTGCAGAAGAAGGCGTATATGCAGTTTAGTCA ATAACACTAAAACGGATTTTTTGATAAAGCTTGATAGAAGAATTGAAAAAACGCTATAAGATAGTCAAATACATTCA ATAAATGCAAGGGGAAATCATGGAAATCGTTATAGGGGTTGATCTAGGCCTATAGAAAGAA	1697 CGATCCAGCTTATAAAGGGGCTAAGATTGTCGTCATCGGTGTTGGAGGTGGGGGGGTCTAACATCAAAACAACTTG GTTGAATATGGCGTGCATCAAGATGTTACCCCTATTGCGACCAACACTGTGGCCAACACTCTCAAAAACAACAATCCCGC TCCGGTTAAAATCCTTTTAGGCAAGAAGACCCTGGAGGTTTGGGCGCTGGGGGGATTCCTGATTTGGTAGAAAG TCCGGTTAAAAATCCTATTAAGGAATTAAAGAGCGATTAAAATTAGTCATTATCTCTACAGGACTTGGA GGAGGGACTGGGACTGCAATGAAATTAAAGAGGCATTAAAATGCCAAAAAGAAAG
HP0753	HP0979	HP0979

¢	V
C	ת
-	N

HP0979	1699 AGGCGTAGAGCCGGCGGGGTTTTAGGAAAAAAAAAAAAA	I DAGONIA ITACHNIA IO IOAGENOIGE
) } =	TTTGCATGGGAATAAAACCTATCTTTACAAGATGAAGGCCAGATTGCAGAAAGCCATAGCATTAGCGCCGGGC TTGATTATCCAGGAGTGGGGCCAGAACACAGCTATTAAAAGAAAG	GNKTYLLQDDEGQIAESHSISAGLDYP GNKTYLLQDDEGQIAESHSISAGLDYP GVGPEHSYLKESGRAVYESASDAEAL
	TGCTGAAGCGCTAGAAGCCTTCAAGTTGTTGTGCCAAAAAGAAGGCATTATCCCAGCGCTAGAAAGCTCACACGCCT TAGCGTATGCCTTAAAGCTCGCTCAAAAATGCGAAGAAGAAGCATCATCGTAGTGAATTTAAGCGGCAGAGGGTT	EAFKLLCOKEGIIPALESSHALAYALKL AOKCEEESIIVVNLSGRGDKDLSTVYN
	ACACGAAAAAATTGAAAAATCATTATCCCGTTTATAACCTTGGCGATCCTAAATTATGAATTGAGATTTTGAAAATCATTAAAAACC	ALKGGLK
	CTAATTATTAGGGGGGTGAGCGCTTTAGAATTGGGTCTTGCTTTTTCTGATCCTGTGGCGGATGGCGTTTACCATACAAA GCGAGCGTTTAAGAGAGCGCTAGCATGCCTAGAAAATTTCCAGCTTTAAAAAAAA	•
	CACAATATICCCATAGGCTTTTAGCGTATGCGAATITAATIT	
	AACACCCAAATCAAACCTTTATCGCCAGCCCCAATGCGAGGATTTAGAACAATCGCTTCG	
,	CARGECIAITITAGAGATGATTCGAGTGGGGTTACAGGGGCGAGCCGTATTTAGAGAATGATTCGAGTGCTAT TATTAAAACCTTAAAAG	
HP0614	1701 GTTTTGCTCTCGCCCAGTTTTATGGCTAAAGTGGATGAATACATGAAAG	1702 VLLSPSFMAKVDEYMK
HP0739	1703 TTTTATGGCTGAACGCTAAGTCTTATTTGATTTCTGTTTTTGCGCCTTTTATCTTGCTGCTTGGATTGATT	1704 LWLNAKSYLISVFAPFILLPWIDLLSAFL LYLGFLALFSVLEFFDEDIADIIVAKSKIK TKTKCYRA
	ACAAAAGGTTTCAAACTATTTTTAGGGGTTTTGCCTAAAAGCTATTCTATGAGCGAAGAAAAAACAACTTTTAGGCTTG TATGATGAGCATTTCTTGCTCACTAAAAACGAAAACTTAGTGGGCATCCTCCGTTTAGAAGGGGGTTAGCTACACAA	
	TFAAGCACAGAGAGCAATTGCAAGAGTCTTTTCACCGAGCGCCCAGATGGCGTTGGATTCTTTAGAAAAAGTCGTGGCGCG	
	CAATTTGAAAACAAAGGTGTATGAAAATCAGTATTTTTTAGAAAGGACACTCACT	
	AGAAACTTTAAAAAGCTTAGAAATCCAGCTCAAAAATTATGCCCCCAAACTCTTAAGCTCCAAAGAGGGTTTTGAATTTT	
	INTECTATION FOR THE SECOND FOR THE SECOND SAFET SECOND FOR SECOND FOR THE SECON	
	AAGCTTATGAGAGCGAAAGGATCACTTCTATAGCGATCGGAGCGCTTTTATACCAAGAAACGCCTTTAGATATTATCT	
HP0739	1705 TCAAATAČCTGCACACACCAAACGCTTATTTAGACATCCTATCAAAACAACCCTTTAAAACACAAAACAAAAAA	47AC IVVI UTLUDRIAVI AMI VERIOI METI ACIA
3	CTTACTTTTACCAAGATTTGAGTTTTAAAAAAATCCTAGATTTTTTAAAAACGATTTTAGAAAACGATACGATTTTATCAC	FYQDLSFKKILDFFKTILENDTIYHKFST
	AAATTCTCAACATCTTTCATGTGGGAGTACGATCTGCATAAGCCGTTAGTATGATTGAT	SFMWEYDLHKPLVSIDDLRVNYDDLRV
	AAATCTATCGCAAAGCTTATCAAAAATCCTTGCCTTGTTGCGCGGGGGGGG	OKSLPLLRAVRKLGL
	AAAATTGGGG	

~	1
0	١
ā	à

		PCT/EP01/15428
1710 KIDKDVAETAKNISEIALKNIKKEKSGEF VDENGNPIDDKKKAEKQDETSPVKQA FIGKSDPTFVLAQYTPIEITLTSKVDATL TGIVSGVVAKDVWNIMIGTMILLDKGTK VYGNYQSVKGGTPIMTRLMIVFTKAITP DGVIIPLANAQAAGMI.GEAGVDGYVNN HFMKRIGFAVIASVVNSFLQTAPIIALDK LIGLGKGRSERTPEF NYALGQAINGSM QSSAQMSNQILGOLINII	1712 KTLVGNGLSGIEATA AKNFSDIKKELN EKFKNFNNNNNGLKIJSTEPIYAKVNKK KTGQVASPEEPIYTQVAKKVNAKIDRL NQIASGLGGVGQAA(3FPLKRHDKVDD LSKVGLSASPEPIYATIDDLGGPFPLKR HDKVDDLSKVGRSRINGELAQKIDNLN QAVSEAKAGFFGNLEQTIDKLKDSTKK NVMNLYVESAKKVPASLSAKLDNYAIN SHTRINSNIQNGAINEKATGMLTQKNP	1714 RSANGYFYLLPESAGKIAQKIAQIGNEI DCCIVEMCQTLSHSLJKHLLFLKFLFKE FDFLDSLQARLNFAKAYNLEFVMPSFT QKKMILENFSHPILKEPKPLNLKFEKSM LAVTGVNAGGKTMLLKSLLSAAFLSKH LIPMKINAHHSIIPYFKEIHAIINDPQN 1716 SSLMDLLVSVEEGRTGQLGFGLGYGS YGGLMLNGSVSERNLFGTGQSMSLYA NATGGGRSYPGMPKGAGRMFAGNLS LTNPRIFDSWYSSTINLYADYRISYQYI QQGGGFGVNVGRMLGNRTHVSLGYN
1709 TAAGATAGACAAAGATGTGCCAAGAATATCAGTGAAATCGCTCTTAAGAACAAAAAAGAAAAGGAGTG GGGAATTTGTAGATGAAATGGTAATCCCATTGATGACAAAAAGAAAAGCAAGACAAAAAGAAAG	1711 ATAAAACCCTAGTCGGTAATGGGTTATCTGGAATAGAGGCCACAGCTCTCGCCAAAAATTTTTCGGATATCAAGAAA GAATTGAATGAAGAAA GAATTGAAAAATTTTAAAAAATTTCAATAACAATAATAATGGACTCTCGAAAAACACACAGAACCCATTTATGCTAAAG GAATTGAAAAAAGAAATTTAAAAAGTTGCTAACAAAAGGTAAAGGCAAAGGCAAAAGGCAAAAGGCAAAATTGACCAATTGAAAAAGGCAAATTGAAAAAGGCAAATTGACCGAATTGACCAATTGAAAAAGGCAATTGAAAAGGCAATTGACAATTGACAATTGAAAAGGCATTTCCCTTTGAAAAGGCATTGAAGGTTGATGATGGCTTCCGGGCTTCCCTTTGAAAGGGAATTGAGGTTAGAAGAATTGGCAAATTGACAAAAAAGAATTGACAAAAGAATTGACAAAAAAAGAATTGACAAAAAAAA	1713 AAGGAGCGCTAATGGCTATTTCTATCTTTTTGCCTGAAAGCGCCCAAAAAATCGCCCAAAAAATCGCCCCAAATTGGTAA TGAAATAGATTGTTTTTTAAAATTGCCTAAGCCGTAATTTCGCTAAAGCCTTTTATTTTTAAAATTC TGAAATAGATTGATTTTTTTAGACAGCTTGCAAACTCTAAGCCTTAATTTCGCTAAAGCCTTTAATTTTTAAAATTT GCCAAGCTTTACACAAAAAAAAATGATTTTAGAAAACTTTTCACACCCCATTTTAAAAGCCTTAAATTT GAAGTTTGAAAAAAAAAA
4P0739		HP0739
	CCAAGAATATCAGTGAAATCGCTCTTAAGAACAAAAAGAAAG	1709 TAGGATAGACAAAGATGTGGCAAGAATATCAGTGAAATGGCTCTTAAGAACAAAAGGAAAAGGAAAGGAAAGGTG GGGAATTTGTAGACAAAAGGTGACTGCATTGATGAAAAAGGAAAAAGGAAAAAGGAAAAGGAAAAGGTGT AAAGAGCCTTATAGGCAAGAGTGGGGTTTGTTTAGCGCAATACACCCCCATTGAAGCTGCTGTTGT AAAGAGGCATTATGGCAAGGTGGGGTTGGTGGGAAGTGTGGAACGTGAACGGTGAATGTGGAACGTGTGATTGTATGGAACGGTGATGTTGAACGGCCATTATGGACGCCTTTGATGGAAAGGTGGAAGGTGGAAGGTGTGATGGAAGGTGGAAGGTGGAAGGTGTGATGGAAAGGTGGAAAGGTGGAAAGGTGAAAGGGTGAAGGGGAACTTAAGAAGGGTGAAGGGGAAGGGAACTTAAGAAAGGGTGAAGGGAAATTATGAAAGGGTGAAAGGGTGAAGGGAAGGGAAGGGAACTTAGGAAAGGGTGAAAGGGTGAAAGGGTGAAGGGAAGGGAACTTAGGAAAGGGTGAATAATACGCTTAGGAAAGGGTGAAAGGGGAAATTAGAAAGGGAAATTATAGGTAAAAGGGAAATTAGGTAAAAGGGAAATTAGAAAGGGAAATTAGAAAAGGGAAATTAGAAAAGGGAAATTAAAAAA

-	
_	
·	

02/066501			PCT/EP01/15428
1718 LGVVCVPTSARSKEDRLNTELLLDEIVR LYSQNTTNNENIKVPSQSFKESLKYSQ SAQRIAQLVISENQQNASFEHTYKIDKI LMHKRYGIFIFLGFMFIIFSLSFLIGGGV QKALETGFKFLSDGIKENVANEDLASL VGDGIIGGVGATVSFLPLIVVLYFGISLL ETTGYMSRVAFLLDGILHKFGLHGKSFI PLITGFGCSVPAYMATRTLQNYNERLIT LFVIGFMSCSARLPIVVLFVGSFFPSSS AGFVLFCIYILGAVVALVMAKLLKLSVF KGQTESFIMEMPKYRFPSWRMVYFSIY TKSLSYLKKAGTYILVGAILWFMSQYP KSDAAMKAYKGESLLVINKDTTLSSEAK EEKLKELKTELDKKNLKNSIVGFGGAY LEKVFSPMDFDWRLSVSLVTGFMAKE VVVSTLGVLFSGÖNEKSDAFRGILR KEVSVPSGIAFIVFVMFYIPCFAATITFG REAGGIKFVAYLFITTVVAYAFSLIAFY ATGIL	1720 ESFFYTLOÄEINGAHFIEVFSGSÄSMG LEALSRGRSAVFFECHKSAYKTLLENI SLFKNRLKKEMEIQTFLDDAFKLLPTLC LKNGVLNIIYLDPPFETSGFLGIYEKGF CALERLKRFNPKNLLVYFEHESMHEM PKSLVTLAIIKOKKFGKTTLTYFQ	1722 RAĞTLEFKEEKEAKKNIDEKSLLEEIHK KKRĞLYMLKGELHEKNESLLFGRMAK NKSGFFIGVILGDIGVSAHSYEKFELLS NIĞASPLLYGLRSGYĞKYFANGISALRF YGEYLGGAMKGFKSDSLASYĞTASLNI ÖLLMÜKPIDKEKRFALGIFGGVGWN GMYĞNLKEVKGYSÖPNAFGLVINLGV SMTI NII KH	1724 NGVSÖTTNILINLLTEFIKTAGFIGNINDS SVSTSLTSAFGAITSAISGGFÖALGNDI SPNAILTILOEITSNITTIÖSFSOTLRÖL LGÖKTFFMAQOKLIDAMINARNOVONA ONOANNYGSOPVLSÖYAAAKSTOHG MSNGLGVGLGYKYFFGKARKLGLRHY FFFDYGFSEIGLANDSVKANIFAYGVG TÖFLWNLFRRTYNTKALNFGLFAGVOL GGATWLSSLRÖQIIDNW
1717 ATTAGGGGTTGTGCGTGCCAACAAGTGCAAAGAAGATCGCTTGAATACCGAGGTTTTATTAGAGAACTTTAAA TTGTCAGGCTTTATTCTCAAAATACTACAAATAATGAAAACATAAAAGTCCCGTCTCAAAGCTTTAAGGAGTCTTTAAA TTGTCAGGCTTTATTCTCAAAATACTACAAATAGGAAACATAAAAACCCGTCTCAAAACCGAGGTTTTTGAAATTTTGAACACTTT ATAGATTCATAAGATTTTAATGCAAAGAGGTTAAGGGGTTTAAATTTTTAAGGGTTTTAATTTCCTTG AGCTTTTTAATGGGGGGGGGG	1719 AGAGTCGTTTTTAACACCTTGCAAGCAGAATTAATGGAGCGCATTTTATAGAAGTGTTTTCAGGCCAGCGCTTTTATAGAAGAGAGGCGTTTTATAGAAGAGGCGTTTTTATAGAAGAGGGCGTTTTTATAGAAGAGAGGCGTTTTTATAGAAGAGAGGCGTTTTTAAAAGGAGGCTTTTTAAAAGGGGGGGG	1721 ACGCGCCCAAACGCTAGAATTTAAAGAAAAGGCAAGCTAAAAAGAATATTGATGAAGAAAAGCCTTGAAGAAA TCCATAAGAAAAAACGCCAACTTTACATGCTCAAAGGGGAATTGCATGAAAAAATGGAATCTCTCTTGTTCCAACGAA TCCATAAGAAAAAAAAAA	1723 CCAATGGGGGTTTTACGAATTATTTAATCTGCTCACTGAATTCATTAAAACCGCCGGGTTTATCCAAATA ATGATAGTGGTGAGCGATTACGAAGCGCTTTTCAAGCCTTTACGAGCGCTCATTTCTCAAGGGTTTCAAGCCT TACAAAACGATATTAGCCCTAATGCGATTTTAACCTTGCTCCAAGAGATTACTTCTAACACCCACC
HP0739	HP0739	HP0739	HP0739

יייייייייייייייייייייייייייייייייייייי	2/066501		·		PCT/EP01/15428
	1726 GINNRDLHTLKTDINHTLKLRPLLPKDA LIISESGIYSHAQIKALAPYVNIGFLVGSS LMKEKDLKKACIKLILGENKVCGLTRIK DAKAVYKNHFIYGGLIFEKSSPRYIKPK EALKITKAVKKLDFVGVFVKI)SIKKIQKI VKKLDLKAVQLYGYSQKEIA	1728 SRVFGSLAGYKFPSFIOKGIIVALYVKIF KIDL SEFEPLENYRSLNALFTRSLKKER PFDKSPNICIAPCDALITECAFLDNDSA LQIKGMPYKAHELVGEINPLSPSFFYAN FYLSPKDYHHYHAPCDLEILEARYFAG KLLPVNKPSLHKNNNLFVGNIERVTLVA KDIQGNRLYFVAVGALNVGKMRFNFD KNIQTNAKARFTQTYSYNPPIKVKKGD NLGNFEMGSTIVLFIQNTAFKDLKEKNV KFGESIGEFHAN	1730 SGVTNSVNKKISOLKAEGTKIDKKLINN EFVCKIIGTHKGLAKODLIVLAEKNKED HNLONQYDTAPSORAINFCKSINTSKNI KDSFETIMECYDEELKKKSFICNLK 1732 QRDMDKIKTILRLTRDMGVN AGVDIIL RLKEKLDELDNLNKELODALI-KHSKNT	KTPTKNLNTPTNFYELILFKK 1734 SKKNVAEQIIRPTGLLDPKFEVRDSDK QVQDLFDEIKLVVARGERVLITTLTKKM AEELCKYYAEWGLKARYMHSEIDAIER NHIIRSLRLKEFDILIGINLLREGLDLPEV SLVAIMD	1736 ANGFSELNDPLDQLERFKNÇVAEKEK GDEEAQYMDEDYYWALAHGMPPTAG QGIGIDRLVMLLTGAKSIKDVILFPAMR PVKNDFNVESEE
	1725 AGGCA CAALAACAGGGALITACACACCITAAAAACGGATATTAACCACACGCTCAAATTACGCCCCCTGTTGCCTAA AGATGCGCTCATTATCAGGGATTTATTATTCGCATGCACAAATCAAAGCCCTAGCCCCTGTTGCTAA AGATGCGCTCATTATCAGGAAAAGGAATTTGAAAAAAGCGTGTATTAAAATTGATTTTAGGCGAAAATAAAGT TTTAGTGGGTTACAAGGATTAAAAGGCTTAAAAAAGCGTGTATTTATT	1727 ITCAAGGGTTTTTGGCTCTCTCGCTGGTTATAAATTCCCTTGTTTTATCCAAAAAGGCCATCTAACGCCCTTTATGTTAAGAAAAGGCATCAAGGCGCTTTTTTGGCGCCCTTTTAAAAAAGAAGTTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAATTGAAAAAGAATTGAAAATTAAAAGCGCTTTTTTTT	1729 TAAGCGGCGTTACTAACAGCGTGAATAAAAAGATCAGCCAGC	CTAAAATACCAAAACCCCAACGAAAATTTAAACACCCCTACGAATTTTTACGAATTGATTTTAAAAAATGAGC CTGACTTCGCTTTTAAACCCCAAAA CTGACTTCGCTTTTAAACCCCAAAA T733 TTTCCAAAAAGAATGTCGCTGAGCAATCATTCGCCCTACAGGCTTTTAGACCCTAAATTTGAAGTGCGAGACAGC GATAAGCAAGTCCAGGATTTGTTTGATGAAATCAAGTTAGTGGTGGCTAGAGGGTGAAAGGGTGAAAGGGTCATCACCACGCT CACTAAAAAAAAGGAATTGTTGATGAAATTATGCTGAATGGGGGCTTGAAGGGGTGCTTAAAGGGATCAATGTGAAA TTGATGCGATTGAAAAAAGGAATCATCCGCTCTTTAAGGGCTTTAAGGGGATCAATCTTTT AAGAGAAGGCGTGGAATTGCCGCTCTTTAGTAGCGATCATGCTGATGCT	1735 CGCTAACGGCTTTAGCGAGTTGAACGATCCTTTAGATTAGAACGCTTTAAAAACCAAGTGGCTGAAAAAGAAAAAAAA
	HP0739	HP0739	HP1025 HP1025	HP1025	HP1145

١	2)
C	5	١
¢	`	1

02/066501			PCT/EP01/15428
1738 TGHYEAQKIYITGSIESGNRISSGGGAS LNFGLQGILLTNATLYNRAAGTQSSS MNFISNSANIQAQNSYFIDDTAQNGGN PNFSFNALNLDFSNSSFRGYVGKTQS VFKFNAKNAISFTNSTNLSSGLYQMQA KSVLFDNSNLSVSVGTSSIKANAINLSG NASINASNHSTLELQGDLNVNDTSSLN LNQSTINVSNNATINDYASLIANSSIVFKGAV SLGGQFNLSNNSSLDFGGSSATTSNTA FNFYDNAFSQSPITFHQALDIKAPLSLG GNLLNPNNSSVLDLKNSQLVFGDQGS LNIANIDLLSDLNDNKNRYVNIIQADMN SNWYERISFFGMHINDGYDAKNQTYS	FTNPLNNALKITESFKDNQLSVTLSQIP GIKNTLYNIGSEIFNYGKVYNNANGVYS YSDDAGGVFYLTSNYKGYYNPNGSYQ ASGSNNTTKNNNLTSESSIISGTYNAQ GNPISALHIYNKGYNFNNIKALGQMALK LYPEIKKVLGNDFSPSSLNALNSNALN QLTKLITPNDWKNINELIDNANNSVVQN FNNGTLIVGATQIGQTDTNSAVVFGGL	1740 EYLKNKGVKITDATCPYVIKPQQIVESM SKEGYQIVLFGDINHPEVKGVISYATNO ALVVNSLEELQEKKLQRKVALVSQTTK QTPKLLQIASYLVERCTEVRIFNTICNAT SYNGKAALDLSKEVDIMIVVGGKTSSN TKQLLSIAKGHCKDSYLVEDENELELA WFKDKKLCGITAGASTPDWIIENVKQKI STI 1742 DNLTPLFPDEQIKLEYEPTKVTGRMLD LFSPVGKGĞRALIVAPPRTGKTELMKE LAGGISVACOVIESS	
12	,	127	1744
1737 TACAGGGCATTATGAAGCGCAAAAGATTTACATCACCGGTAGCATTGAAAGCGGGAATCGCATTTCTAGCGGTGGGGGGGAATCGCATTTCTAGCGGGTGGGGGGGAATCGCATTTCTAGCGGCGCGCGC		1739 GAATACTTGAAAAATAGGGGGTCAAAATCACTGATGCGACTTGCCCGTATGTGATCAAGCCCCAACAAATTGTGGA ATCCATGAAAAATTGTGGA ATCCATGAAGGGCTATCAATCGTACTTTTTGGGGATATTAACCACCCTGAAGTCGAAGGGCGTGATAAGCT ATGCCACTAACCAGGCTTTAGTCGTTAGAATTGGTTGCAAGAAAAAGTGGCTTTAG ATGCCACTAACCACAAACACACACAAAACTCTTGCAAATTGGTTTTATTTTAGACTCCAAACACACAAAACTCTTGCAAAAATGGTTTTTAACACGCAAAAGTGCGTA ATTTTAACACGCATTTGTAACGCCATTTCTTACAACACCAAAAAGGCTTTTGGATTTGGATTGCAAAGACTGCTACT AGTCGTGGGCGGTAAGACTTCTTCTAACACACAAAAAGGTTTGGAAAATGGTTAAGCATTGCAAACACGCTTTCTTCAAACACCACAAAATGGTTTAAGCATTAAGCATTGCAAACACGCTTTCTTCAAACACGCTTTAACACACCAAACAGGCTTTCTTAACACACAAAATGTTAAGCATTAAGCATTAAGCATTGCAAAAATGTTAAAGCAAAATGTTAAAAATGTAAAAATGTAAAAATGTAAAAAATGTAAAAAA	1743 TCCAĞCGCĞTAĞAAĞGGĞATTĞAAAÇAAAĞAĞAĞTĞAAÇATTTAĞAAĞCĞTTTAAAĞĞĞGCAĞAAĞATTTTĞAAA AACGCATGGCTTTTAGAAATGGAAAAAGAAAAGAAA
HP1145		HP1145 HP1145	HP1145

HP1145	1745 GCGCACTTCTGGGGAAGTGTCAAAAAAAGAG	1745 GCGCACTTCTGGGGAAGTGTCAAAAAAAAGGGAGGGAAAATCTTTGATAGCGGATCGAGGCGACGGTAGCGATT	1746 RTSGEVSKKE	1746 RTSGEVSKKEGGKIFDSGSRATVAIIFF
	ATCTTTTTGTGAAAGATAAGAGCACTCCTGA;	ATCTTTTTGTGAAAGATAAGAGCACTCCTGATAATACGATTTTTTATTATGAAGTGGAAGATTACTTGAAAAGAGAAG	VKDKSTPDNTI	VKDKSTPDNTIFYYEVE:DYLKREAKLN
	CCAAACTCAACTGGCTCGCCAATTTTGAAAAT	CCAAACTCAACTGGCTCGCCAATTTTGAAAATTTGGATTTTGTGCCTTTTGAGAAAATCACCCCGAATGATAAAGGCG	WLANFENLDF	WLANFENLDFVPFEKITPNDKGDWINQ
	ATTGGATCAACCAAAGGAATGACGCTTTTGAA	GAAAAACTCATCCCTTTAAAAAGAGACAAAACACTCCAAAACGACAGCG	RNDAFEKLIPL	RNDAFEKLIPLKRDKTLQNDSVFDINSL
	TTTTGACATCAATTCTCTTGGCG		၅	
HP1145	1747 TGGGCGCGATGAGATGGTGGTGTGCGGTGG	1747 TGGGCGCGCATGAGATGGTGGTGTGTGTGTGGGTGGAGAACATGAGCGCAGCACCCTATTTGTCGTTTTGACATGCG	1748 GRDEMVCGC	1748 GRDEMV/CGGVENMSAAPYLSFDMR
	AGATGGGAAAAGAATGGGGAATGCGAACATG	AGATGGGAAAAGAATGGGGAATGCGAACATGATAGATTCCATGATACATGGTTGTGGGATGCGTTCAATAATT	DGKRMGNAN	DGKRMGNANMIDSMIFIDGLWDAFNNY
	ACCACATGGGGATCACCGCTGATAATGTCGC	CGCTCAAGCATACCACATAAGCCGAGAAGATCAAGATAATTTCGCGCTC	HMGITADNVAC	HMGITADNVAQAYHISIREDQDNFALQS
	CAGTCGCAACTCAAAGCAAGAGCCGCCATTA	CAGTGGCAACTCAAAGCAAGAGCGCCGCATTAATGCAGGGAAATTCCAAGAAGAAATCACGCCTATTGAAATAGCGAA	OLKARAAINAG	OLKARAAINAGKFOEEITPIEIANKKGV
	TAAAAAGGCGTGGTGTTTTAAAGAAGACG	ACGAATACCCTAGAGAAACGACGCTAGAATCCCTTGCAAAGCTCAAAC	WFKEDEYPRE	VVFKEDEYPRETTLESI AKLKPAFKKD
	CCGCTTTCAAAAAGACGGATCGGTAACGGC	CCGCTTTCAAAAAGACGGATCGGTAACGGCGGGAAATTCATCAGGGATCAATGATGGCGCGAGTATTATCATTTTA	GSVTAGNSSG	GSVTAGNSSGINDGASIIILCSTKKAQT
	TGCAGCACTAAAAAAGCGCAAACATTGGGGTT	TGCAGCACTAAAAAAGCGCAAACATTGGGGTTAAAAGCCATGGCGACTATCAAGGGGTTTGGTTTGGGTTGGGTTGCA	LGLKAMATIKG	LGLKAMATIKGFGLGGCSPDIMGICPSI
	GTCCGGATATAATGGGTATATGCCCTAGCATCGCGATTA	SGCGATTA	AI	
HP1145	1749 AAAGTGATTTATTTAGATCAAGCCCCCATAGG	1749 AAAGTGATTTATTTAGATCAAGCCCCCATAGGCAAAACCCCAGGAAGCAACCCTGCCACTTACACGGGAGTGATGGA	1750 KVIYLDQAPIGI	1750 KVIYLDQAPIGKTPRSNPATYTGVMDEI
	TGAAATCAGGATTTTATTTGCCGAGCAAAAG	TGAAATCAGGATTTTATTTGCCGAGCAAAAGAAGCTAAAATTTTAGGCTATAGTGCGAGCCGTTTTAGCTTTAATGTT	RILFAEOKEAK	RILFAEQKEAKILGYSA:SRFSFNVKGG
	JAAAGGAGGCCGTGCGAGAAATGCCAAGGCC	AAAGGAGGGGGGTGCGAGAAATGCCAAGGCGATGGGGACATTAAAATAGAAATGCACTTTTTGCCTGATGTGTTAG	RCEKCOGDG	RCEKCQGDGDIKIEMHFLPDVLVQCDS
	TCCAATGCGATAGCTGTAAGGGCGCTAAATAC	TCCAATGCGATAGCTGTAAGGGCGCTAAATACAACCCCCAAACTTTAGAAATCAAGGTGAAAGGCAAATCCATTGCC	CKGAKYNPQT	CKGAKYNPQTLEIKVKGKSIADVLNMS
	GATGTGTTGAACATGAGCGTGGAAGAGGGCTT/	GATGTGTTGAACATGAGCGTGGAAGAGGCTTATGAATTTTTTGCTAAATTCCCTAAAATCGCCGTGAAGTTAAAAACG	VEEAYEFFAKF	VEEAYEFFAKFPKIAVKLKTLMDVGLG
	CTTATGGATGTGGGCTTAGGCTATATCACTTT/	CTTATGGATGTGGGCTTAGGCTATATCACTTTAGGGCAAAACGCTACGACTTTAAGTGGGGGGGG	YITLGQNATTL	YITLGQNATTLSGGEA()RIKLAKELSKK
	TCAAATTAGCTAAAGAATTGAGTAAAAAAGACA	TCAAATTAGCTAAAGAATTGAGTAAAAAAGACACGGCAAAACCCTTTATATTTTAGATGAGCCTACTACCGGTTTGC	DTGKTLYILDE	DTGKTLYILDEPTTGLHFEDVNHLLQVL
	ATTTTGAAGACGTGAATCATCTTTTACAAGTCT	ATTTGAAGACGTGAATCATCTTTTACAAGTCTTGCATTCTTTAGTGGCGTTAGGCGAATTCTATGCTAGTGATTGAGCA	HSLVALGNSMI	HSLVALGNSMLVIEHNI.DIIKNADYIIDM
İ	TAATTTAGACATTATCAAAAAGGCTGACTACAT	TAATTTAGACATTATCAAAAACGCTGACTACATTATAGACATGGGGCCCTGATGGGGGGGG	GPDGGDKGGK	
HP1145	1751 GTT AGAATT CCAAAAAAT CCAAGCCCTACTOT	1751 GTTAGAATTCCAAAAAATCCAAGCCCTACTCTTAAAAAGGGCTTTGTATCACCCCCCTATAATGAATTGAATTTAGAG	1752 LEFOKIOALLFK	LEFOKIOALLFKKGLCITPYNELNLEOK
	CAAAAGCGAAGGCTAAAACCTATTTTAAAGA	CAAAAAGGGAAGGCTAAAACCTATTTTAAAGAGCAGCTTTACGCGTTAGTTTTGCCTTTTAAATTGGATTCTTCACACA	AKAKTYFKEOL	AKAKTYFKEQLYALVLPFKLDSSHTFP
	CTTTCCCGCCTTTAGCGAATTTGACTTTCGCG	CTTCCCGCCTTTAGCGAATTTGACTTTCGCGCTTTTTGCCCGCATCAAAGAAAAAAAA	PLANLTFALFA	PLANLTFALFARIKDKETQIISYALIKLPS
	CGCTCATCAAACTCCCCTCTTTATCTTCCGTT	CGCTCATCAAACTCCCCTCTTTTATCTTCCGTTTTGTAGAGGCTAGAAAAAGGCTTGTTGTGTTTGTGTTAGCTGAAGAAATCG	FIFRFVELEKGL	FIFRFVELEKGLFVLAEE:IVEAHLEELFL
	TGGAAGCGCATTTAGAAGAATTGTTTTAGAG	TGGAAGCGCATTTAGAAGAATTGTTTTAGAGCATGAGATTTTAGATTGCATGGCGTTTAGGGTAACTTGCGATGCG	EHEILDCMAFR	EHEILDCMAFRVTCDADIAITEDEAHDY
	GATATTGCTATCACTGAAGATGAAGCGCATGA	GATATTECTATCACTEAAGATGAAGCGCATGATTATGCAGATTTGATGAGTAAGAGTTTGAGGAAACGCAATCAAGG	ADLMSKSLRKF	ADLMSKSLRKRNQGEI/RLQTQKGSQ
	CGAAATCGTGCGCTTGCAAACCCAAAAAGGG	CGAAATCGTGCGCTTGCAAACCCAAAAAGGAGTCAAGAGCTTTTAAAAACCCTCTTAGGGTCTTTAAGGAGTTTTCA	ELLKTLLASLRS	ELLKTLLASLRSFQTHSYKKHKLTGMHI
	AACCCACTCTTACAAAAGCACAAACTCACCG	AACCCACTCTTACAAAAAGCACAAAACTCACCGGCATGCAT	YKSAIMLNLGD	YKSAIMLNLGDLWELVNHSDFKALKSP
	GIGGGAATTAGTCAATCATAGCGATTTTAAAGC	GI GGGAATI AGTCAATUATAGCGGATTITAAAGCGCTCAAATCGCCCAATTI CACACAAAATCCACCTCATTICAA	NETPKITPTEN	NFTPKIHPHFNENDLFKSIEKODLLLFH
	IGAAAACGATCTTTICAAATCTATAGAAAAACA	16AAAACGATCTTTTCAAATCTATGAAAAACAGGATCTGTTTCATCCTTATGAAGTTTTGAGCCTGTGATT	PYESFEPVIDLI	PYESFEPVIDLIEQAASI)PATLSIKMTLY
	GALLIAALAGAGCAAGCCGCLAGCGALCCAGC	GALLIAA I AGAGCCGC LAGCGA I CCAGCCC I I CLA I CAAAA I GACGC I I I AGAGC I I I AGAGC I I I A I CG I G I G G G CA	RVG	
HP0177	1/53 GCAAAAAGACGCI GCGGG CA CIA GAG	1753 GCAAAAAAGACGC1 GCGGG ICA C1A1GAGA CAGCGAGT CATGAAAGAGCC1ATACGGCATTGCATGAAAAAAAAAAAA	1754 KKDACGFIYEIS	1754 KKDACGFIYEISEFMKAYTALLKKODRY
	0717171004444611711171717171717171717171717171717	SANCOROLANDE OLIVERITATION OF A SANCOROLANDE OF A SANCOROLAND OF A SANCOROLANDE OF A	VILLATLPSKY 01 222 1 225250	VICLET LESET WASILI I ALTORI PUFU
	2	SOLGICI I AL I AL I ACCARACI I GGALI GCAGGAGGCACGAI CACG	ALKKLLVST TT	ALKALLVST TTUI WIAGGIII KIKUI SIN
	CGCA CAAGCAAACCAG	CAAAAACGIIAAAAGCAAIAAGAGCGIIGAAACCAICAAAGAGCIIAIA	IIKNVKSNKSVE XI XIII XIDOGO	IKNVKSNKSVETIKELILNSIDSYNTFDQ
		GATICANTACICICIATACITIATEGECATAGCICITICICATACCA	TLYNLWDSSS	TLYNLWDSSSVINSKWIVKFVLALANI
	COMPAND	COGAAACCCAAGTGGAGCATTTTGCCACAAAACCACATCAATATTTAATAAAAAAAA		FMADEENFIFTAMDAE JUVETILPUTE
	AAAAAGAAGAATGGGTAAATAATATCGCGA	AAAAAGAAGAATGGGTAAATAATATCGCGAATTTAACCCTTTTAAAAGGCGTAAAAAGAACGCGCATCCTTTAAAACG	I KDKKNADA	I KEKNALAI NGRENETEWININGKET
	GGATTTGATGAAAAAGAAAATTTATGGAGG	GGATTTTGATGAAAAAAAAAATTTATGGAGGCAAAGACACACGAGCAAAGTGATTAGCTGTTATGACATCACTAAAAGA	SKVISCYDITKE	SKVISCYDITKEI YSNYBKWNEKSI OF
	ATTGTATAGCAATTATAGGAAGTGGAATGAGA	ATT GTATAGCAATTATAGGAAGTGGGAATGGGAAGTCCCCCCCC	BYKSI VNTITEV	RYKSI VNTITRVI HIEGOEDDEDDED
	TGTTTTACACATAGAGGGGCAAGAAGATGATTTTGAAGATGATTTTGATCT	TIGAAGATGATTTTGATCT		יבי וובטעבטטרבטטרט
			-	

٥	0
C	Ň
Ċ	ч

02/066501	<u></u>		PCT/EP01/15428
1756 YVDNDYVFLFHNTDNKDHEFYFKVLG QKDIQIKKPLNPIAIKAGQKIKAVVILRKP LKSNATEYKNAKDALIPITIQAYSADDK NITIERESVFIAPSED	1758 SLIASVILYAYGTGAIKGFALTTGIGILA SIITAIVGTQGIYQALLPKLTQTKSLYFW FGVNKRA	1760 NKPKILFILETSKINKTYPIERFKELALILE NFQICLLWHADEYKATTLYHALKHQRD VLLLPKLTLNEVKALLFKMDLIIGGDTGI THLAWALQKPSITLYGNTPMERFKLES PINVSLTGNSNANYHKKDFSIQNIEPKK IKECVLNILKEKE	1762 ALDNÉLSDLLDKRLEIALKIALIKÒESPIY CPKRECEILKRLSORDFKHLNGEILTGF YTEVFKISRKFČENALKELKK
1755 GTATGTGGATAACGATTACGTGTTTTTATTCCACAACAGACGATAAAAGACCATGAGTTTTATTTCAAAGTTTTAGGG CAAAAAGGCATTCAGATCAAAAAGCCTTTAATTCCACAACGATTAAAGCCGGGCAAAAGGTTTTAGGGTTTTAGGGTTTTAGGGTTTTAGGGTTTTAGGGTTAGCGTTGATTCCAAAGGGGTTGATTCCAAAGGGGTTGATTACCATTACCATTACCATTACCATTACCATTACCATTACCATTACCATTACCATTACCATTACCATTACCATTACCATTACCATTACTATTAGCCCTAAAAAGGGATTCAAAAAGGGATCGGTGTTTAATTCTTCTATACCACCTCCAAAAGGGATCCAAAAAGGGATCGGTGTTTAATTCTTCTATACCACCACCACCACCACCACCACCAC	1757 ITICITTGATCGCTICAGTGTTATTATACGCTTATGGCACAGGAGCGATTAAAGGCTTTGCCCTAACTACAGGCATTGG GATTITAGCCTCTATTATCACCGCTATTGTTGGCAGCAGGCATTATCAAGCCCTTTTACCTAAACTCCAAAC AAAAAGCCTTTACTTTTGGTTTGG	1759 AGANTAAGCCAAAAATCTTTTATTTTAGAAACTTCTAAAATCAATAAAACTTTACCCCATAGAGCGTTTTTAAAGAATTA GCGTTAAATTTTAGAAAATTTTCAAATTTGCTTGTTATGGCATGCTGATGAATAAAAGGCACTACGCTTTATCACGCTT TAAAACACCCAACGCGATGTGTTATTGCTCCCCAAACTCACTTTAAACGAGGTTAAAGGCGTTGCTTTAAAAATGGATT TGATTATTGGGGGCGATACGGGCATCACGCATTTAGCACTGCAAAAAACCCCAGCATCACCCTTTATGGCAAC ACGCCCATGGAGCGTTTTAAATTAGAAAGCCCGATCAAAAAATGTTCGCTCACCGGTAATTCAAACGCCCAACTACCATAAA AAGGATTTTTCTATCCAAAATATAGAAAAAATTTAAAAGAAAAAGGCGTTTTAAAAGGAAAAAAGAATGAC TTACAAAGAACACCCCATTTTGAAAAAAATTTGAAAAAAAA	1781 ATGCGTTGGATAATGAATTAAGCGATCTTTAGACGAGCGTTAGAAATCGCTTTAAAATCGCTTTAAAATCGCAAAGCAACAAGAAGGAAG
HP0177	HP0177	нР0291	HP0291

02/066501		PCT/EP01/
	17 DO ELEVTRSHAGFETT SUGENGIALISTOUS SSHRVMDRLLSGOVGFGKTEVAMHAI FCAFLNGFGSALUVPTILLAHGHFETL RAFFENFGVKORRLDRYASEKNKLLKA VELGOVDALIGTHAILGAKFKNLGLVVV DEEHKFGVKORFALLSKSVHFLSMS ATPIPRTLNIMALSQIKGISSLKTPPTOR KPSRTFLKEKNDELLKEIIYRELRRNGQ IFYIHNHIASILKVKTKLEDLIPKLKIAILH SQINANESEEIMLEFAKGNYQVLLCTSI VESGIHLPNANTIIIDNAQNFGLADLHQL RGRVGRKKEGFCYFLIEDQKSLNEQ ALKRLLALEKNSYLGSGESVAYHDLEIR GGGNLLGQDQSGHIKNIGYALYTRMLE DAIYELSGGK	1768 SLIASVLLYAYGTGAIK'GFALTTGIGILA SIITAIVGTQGIYQALLI'KLTQTKSLYFW FGVNKRA
1783 AGGGATTAAAAAAGGTGTTCCAAAGACAGCAAAAAAGACGCTTGCGGGTTCCATCTATGAGATCAGCGGAGTTCATGAAAACAAAAACAAAAAAAA	1765 GGAGTTGGAAGTCTTTAAATCGCATGCGGGGTTTGAATACACCAGGGATCAAGAAAAGGCTACGTGGGAATTTAAGCGCTGTGAATTTTTGGGGAAAACGGGATTTGGGGAAAACGGGATTTAAGGGCTGTTTTTGGGGAAAACGGGATTTTGGGGAAAACGGGATTTTGGGGAAAACGGGATTTTGGGGAAAACGGGATTTTTGGGGAAAACAGGATTTTTTGCGCTTTTTTTT	1767 ITCTTTGATCGCTTCAGTGTTATAGCCTTATGGCACAGGGGATTAAAGGCTTTGCCCTAACTACAGGGCATTGG GATTTTAGCCTAAACTGCCTTTGTTGGCAGGGATTTATCAAGGCCTTTTACCTAAACTGAACTCAAAC GATTTTAGCCTTTTTGGTTTGG
HP0291	HP0291	HP0291

ς	-	
ć	-	5
	3	5
ŗ	7)

HP0874	1769 TTTGACAGAAAGAATCCCTGAAAGGGTGGTGCATGCTAAAGGAAGCGGAGCTTATGGCACTTTCACTGTGACTAA	1770 FDRERIPERVYHAKGSGAYGTFTVTKD
	AGACATCACTAAATACACTAAAAGGAAAATTTTCTCTAAAAGTGGGCAAAAAAAA	ITKYTKAKIFSKVGKKTECFFRFSTVAG 9
	GTAACTGGGATTTAGTGGGGAACAACAACGCGGIGAGGACCCTAGAGGGTTTTGCGATGAGGTATTACACTGAAGAAG	
	CTCARAMACGATCATA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	_
	TATACOAACTAAACAATCAACAATAAAAAAAAAAAAAAA	PO NEW POWD WORK STACK
	ACTION CONTROLL AND CONTROLL AN	TWVMSDRGIPKSFRHMDGFGSHTFSLI
	ACTITICACIONICA CONTRACTOR AND ACTION OF THE CONTRACT OF THE CANADA	NAKGERFWVKFHFHTMQGVKHLTNEE
	TITICACIONAL CANAGAGECECAGAAGII AGGAAGIA I GAITCCGGATTCCAATCAAAGGGATTTATTCAATGCGATCG	AAEVRKYDPDSNQRDLFNAIARGDFPK
	CIASAGGGGAI I CCCAAAAI GGAAA I TAAGCATTCAAGTGATGCCAGAAGAAGAAGAAGTATCGATTCCAT	WKLSIQVMPEEDAKKYRFHPFDVTKIW
	CCG I GAI GI AACTAAAA I I I GGTA I CTCCAAGA T TA T CCAT GGAAGT GGAAGT GGAAGT GGAAGAT GAAGAAAT	YLQDYPLMEVGIVELNKNPENYFAEVE
	CC1GAAAACTATTCGCAGAAGTGGAACAAGGGGCATTCAGTCGGGCTAATGTCGTTCCTGGAATTGGCTATAGCCC	QAAFSPANVVPGIGYSPDRMLQGRLF
	IGA I AGGA I GITACA A GGG CGC TT GIT CITAT GGA GA CA CA CA CA CA CA CA CA CA CA CA CA CA	SYGDTHRYRLGVNYPQIPVNKPRCPF
	ACCESTI A TAVIA A CONTROCCATION OF THE CONTROL AND A SECTION OF THE CONTRO	HSSSRDGYMQNGYYGSLQNYTPSSLP
-	ACAAACTATACGCCTA	GYKEDKSARDPKFNLAHIEKEFEVWN
_		WDYRADDSDYYTQPGDYYRSLPADEK
		ERLHDTIGESLAHVTHKEIVDKOLE
HP1382	1771 CGGGCAAGATATTCCTGCCTTAAGCGACACCAAAGAACTTAATTTTGAAATTAAAGGGAAAAAAATGATAGCGTCCA	1772 GODIPALSDTKELNFEIKGKKNDSVQP
	GCCAGGAGAAAGGAAATTCCCATGGACTAATGGAAAATTTGTTTCAGTCAAGTGGGTGAATGGGAAGTATGAAG	GERWKFPWTNGKFVSVKWVNGKYEEI
	AAATTAAAGAAGACATCAAAGTGTCAAATAACGCTCAAGAGCTTTTAAAACAGGCTAGCACTATTTTAACCACTCTTAA	KEDIKVSNNAQELLKQASTILTTLNEAC
		PWLSNGGAGNVAGGNSLWAGIDKGD
	AAAGGCGAACGCGGAGCGCATTTTAAAAATGAAATCAGCGCGATTCAAGACGTGATCAAAACGCTGAAAT	GSACGIFKNEISAIQDMIKNAEIAVEQS
	AGCUGI AGAGCAAI CCAAAAT CGT TACCGCCAACGCGCAAAACCAGCAACCTGGGAAAGCATTCAAC	KIVTANAQNQHNLDTGKAFNPYKDANF
	CCCIAIAAAGACGCCCAAAGCATGTTCGCCTAACGCTAGAGCGCAAGCGGAGATTTTAAACCGCGCTC	AQSMFANARAQAEILNRAQAVVKDFE
	AAGCAGTGGTGAAGGACTTTGAAAAGAATCCCTGCAGCGTTCGTGAAAGACTCTTTAGGAGTATGCCATGAAAAGGGT	RIPAAFVKDSLGVCHEKGSDGNLRGTP
	AGGACGCCATCTCCGTGGCACGCCATCTGGCACGGTTACTTCTAACACTTGGGGAGCCGGCTGCGCGTATGTG	SGTYTSNTWGAGCAYVGETYTNLKNS
101282	1955GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	
700	GCTTATGTTAAGGGTTTAGAAGAGCCTAAAGAGAAGAAGAAAATGCGAAGAGTATTGTAAGAGAGAG	I 74 TREGENAL TONGENTO I NAMERENTA I
	TTTAATGGGTAAGGCATGTTTAATAAAGTTGAAGATGAAGCACGATTTTGCAAGTTTCGCAAAATGAATTG	GKACFIKVEDESTILOVYVSONEI NDFF
	AATGATGAGTTTAAAAGCTTTGAAAAGCATTTAGAAGTGGGCGATATTGTGTTGGTGAAAGGCTTCCCTTTTGCTACC	KSI KKHI EVGDIVI VKGEPEATKTGEI S
	AAAACCGGTGAATTAAGCATTCATGCCCTAGAATTTCATATTTTAAGCAAAACCATTGTGCCTTTACCTGAAAAGTTTC	IMALEFHILSKTIVPLPEKFHGLSDIELRY)
	ATGGACTGAGCGATATAGAATTGCGTTACCGCCAGCGCTATTTGGATTTGATCGTCAATCCTAGCGTTAAAGATGTG	RORYLDLIVNPSVKDVFKKRSLIVSSVR
	ITTAAAAAGCGCAGTITGATJGTCTCTAGCGTGCGGAAATTCTTTGAAATGGAAGGGTTTTTAGAAGTGGAAAC	KFFEMEGFLEVE
	1775 CTT GGCCTT GCACATGATGATGTTTT AGAGCCTTTT GCCAAAAACCCTAAAGTGTGCAAGAGTATCC	1776 SPHPLHMNDGFLERFAKNPKVCKSIH
	ACATGCCTTTATAGGGGGATCTAGCGCGGTGTTAAAGATGATGCGAAGGGGGTTATAGGAAGGGGAGTGGTTTTTAAAT	
	JAGGETAGGATTTTGAAGACACAATGGAGGTG ICGATAAGGATTTTGAAGACACAATGGAGGTG	RVERLKALVPEVGISTDIIVGFPNESDK 2

HP1382	1111	1777 CCAGCAAGCTTTAAAAAATCAAAGTGGGTTTCCTGAATTAGGCGGGAACGGCACAAAAGTGAGTG	1778 QQALKNQSGFPELGGNGTKVSVNYNY ECRQTADINGGVYQFCKAKNGSSSSS NGGNGSSTQTTATTQDGVTITTTYNN NKATVKFDTTNNAEQLLNQAANIMQVL NTQCPLVRSTNNENTPGGGQPWGLS TSGNACSIFQQEFSQVTSMIKNAQEIIA QSKIVSENAQNQNNLDTGKI?FNPYTD ASFAQSMLKNAQAQAEMFNLSEQVKK NLEVMKNNNNVNEKLAGFGKEEVMTN FVSAFLASCKDGGTLPNAGYTSNTWG
HP1382	1779		1780 LLNHAKKTÖSLNGVEIVGLEI-LDKVIYL DQAPIGKTPRSNPATYTGVNIDEIRILFA EQKEAKILGYSASRFSFNVKGGRCEKC QGDGDIKIEMHFLPDVLVQCDSCKGAK YNPQTLEIKVKGKSIADVLNMSVEEAY EFFAKFPKIAVKLKTLMDVGI.GYITLGQ NATTLSGGEAQRIKLAKELSIKKDTGKT LYILDEPTTGLHFEDVNHLLGNLHSLVA LGNSMLVIEHNLDIIKNADYIIDMGPDG GDKGGKVIASGTPL
HP1382	1781	AGCAACACTACAAAACTTGATTTCACTATCAATGGAGACAAAAGAA GTTCCCATGGAGTGGTGGGAAATATATTCACACCCCAATGGATTAACACA CACAGAAAATAACGCTCAAGAGCTTTTAAAACAAGCGAGCATCATTATC TCCAAAATGGTGGTAGAAGTTATTGGCAAGGGATAAGCGCCAATGGGA SAGCGCGATCCAAGGCATGATCGCTAACGCTCAAGAGCTGTCGCCCA	1782 ANGDGVPVLSNTTTKLDFTII/GDKRTG GKPNTPEKFPWSDGKYIHT(?WINTIVT PTETNIINTENNAQELLKQASIITTLNEA CPNFQNGGRSYWQGISGN(3TMCGMF KNEISAIQGMIANAQEAVAQ;3KIVS
HP1382	1783	1783 GATGGAAGACTACGCAAGCAGCAGGAGCACTGGAGAGATTGTTGATAGATTGTTGAAACGGAACAGAAT CAACAACTACACTAC	1784 MEDYASRTAGALERLDKIVETEOKNO QTKLDTENLKIIETLRSKINGNOOKMLD KSKEMSRNFKLDSTKNEIDAIKDLIKKA NEQIANYNEMIKDIEKOKKSCKEOTWK FLVNEFKSDIOEYNKYGGLEKGINNLE KAISENOEEVKKLENEIKELEKTMYSIK PIVNEINTLLKGYGETLSEGEVTFITFLYY YRIQREDGQLVGETLSEGEVTFITFLYY YRIQREDGQLVGETLSEGEVTFITFLYY YHLAKGSLEENDISKNIKLVIDDPIISSL DSNILTHNTYFYKEITLECDLKRYGGKYSF WIIKKDNNYSKIKDYKENPIKNSYELLW QEVKQAKENNASWYSLQNYMRRIIEY YFRILGGFKHNDSLSECFENIEEKRVC NSFISWFNDGSHGISDDLFWQSQDTSI ETYLKVFEKIFKETGHEAHYKMMMRM

	_	
	r	٠,
4	ŕ	_
	٠	
4	۰	•

02/066501	
1786 KVAIAHHLDDAVESFFMNFTYNGSLRS MPPIYRAENGLLVIRPLIKVREASSIHFV TSQNIPVADCNCPAKQPTSDKPPIAR LATKNFLKE 1788 SNGPGDPLSLQQEIGEIKQLINAKIPML GICLGHQLLSIAQGYPTYKLKFGHHGS NHPVKNLKTNAVEITAQNHNYCVPEDI EEIAIITHRNLFDNTIEGVRYKNAPIISVQ HHPESSPGPKESHYIFKEFVELLKDF	1790 YTCSGQGNNINCSPSVNGTKTTTQTID GKSVTTTISSKVVGSIASGNTSHVITNK LDGVPDSAQALLAQASTLINTINEACPY FHATNSSEANAPKFSTTTGKICGAFSE EISAIQKMITDAQELVNQTSVINSNEQS TPVGNNNGKPFNPFTDASFAQGMLAN ASAQAKMI.NLAHQVGQAINPENLSENF KNFVTGFLATCNNKSTAGTGGTQGSA PGTVTTQTFASGCAYVEQTLTNLGNSI AHFGTQE 1792 TTTQNNIIEHYYTENGKEIPVSYSGGSS FSPTIQLTYHNNAENLLQQAATIMQVLI TQKPHVQTSNGGKAWGLSSTPGNVM DIFGPSFNAINEMIKNAQTALAKTQQLN ANENAAQITQPNNFHSIQG MLNRAEAQAEILNIAKQVANNFHSIQG PIQGGDLEECKAGSAGVITNNTWGSGC AFVKETLNSLEQHTAYYGNQVNQDRA
	1789 CTACACATGCTCAGGGGATTAATAACTGGTCGCCAAGTGTCAACGGAACCAAAACCCAGAGCCAAACCATAG ACGCCAAAACCGTGTCAGTCAGTTCAAAAGTGGTTGGTAGTGGCAACACATCACTGTCATCACTGTCATCACTGTCATCATCATCATCATCATCATCATCATCATCATCATCAT
HP1382 HP1382	HP1382

500	ž	3
•	•)

02/066501		PCT/EP01/15
1794 EPGIYIPGFFGVRIEDLVVIKIVSRSELL	1796 DTKVLITDWNMPEMNGLDLVKKVRSD SRFKEIPIIMITTEGGKAEVITALKAGVN NYIVKPFTPQVLKEKLEVVLGTND	1798 MDILLNRHLAEPVMVGKEVLLDMLTQL DKNKLEKIHDLGVQEFVIINDI ALGHDA SIIQSFSADSESLKLLKQTEKIDDENALA AIRIHKVMKPGDPVTTEVAKGIFVKRLFF DPERYDLTMVGRMKMNHKLGLHVPDY ITTLTHEDIITTVKYLMKIKNNQGKIDDR DHLGNRRIRAVGELLANELHSGLVKMQ KTIKDKLTTMSGAFDSLMPHIJLVNSKM ITSTIMEFFMGGQLSQFMDQTNPLSEV THKRRLSALGEGGLVKDRVGFEARDV HPTHYGRICPIETPEGQNIGLINTLSTFT RVNDLGFIEAPYKKVVDGKVVGETIYLT AIQEDSHIIAPASTPIDEEGNII.GDLIETR VEGE
1793 AGAGCCTGGGATTTATATCCCTGGGTTTTTGGGGTGCCCATTGAAGATTTAGTGGTCAAAAATTCTAGGTCTGA GCTTTTGTGATGCGAGGATCTTACTAGCGGCTTTTTCCCTAGCCTTTTTAAAAAAATTGTTTTTTGTTTTTTTT	1795 GGGACACTAAGGATTGGAACATGCCTGAAATGAACGGCTTAGATCTCGTTAAAAAGGTGCCTCT GATAGCCGTTTTAAAGAAATCCCTATTATCATGATCACCACAGGGGGGGG	1797 TATGGATATTTACTCCAATCGCCATTTAGCTGAGCCTGTTATGGTAGGGAAAGAAGTCTTATTGGACATGCCCCCCCC
HP0150	HP0150	HP0150

HP0150	1799 AAAGCGAGAGCGATTTTTTGGAGGTTGTTAAAGATTACAGAAACGCTGCAAGAAAACTATGATTTTTGGGCGTTCA GCAAGATTGATGATTGACAATTTGTTTATCCCTTATTTCAACAACACGCTGCAGAAAGGAATTTTTCCCTGATTT TATCTTTTGGCTAGAAAAAGGCGGCCACGATCATTTGCTTCATTGATCCTAAAGGGAGCAACACACTGATTACG TATCTTTTGGCTAGAAAAAGGCGGCCACGATCATTTTTTAACCCCAAAGGGAGCAACACAACAACAACAAGATCAAAGTTACG AGCATAAGGCAGATGCGTATCAACTTTTTAAAGATTAAAAAGATCCCAAAGGCAATCTCAAAATCCAAAGTCAAAGT GGTTTTAAAAATTTTATGGGGATAAAGATGAGGGGGGGG	1800 SE DE EK	1800 SESDFLEELLKITETLQENYDFWAFSKI DEHLDNLFIPYFNNAAERKFFPDFIFWL EKGGTQIICFIDPKGSKHTDYEHKADAY QLFKDKIFNPKDNPNLKIKYVLKFYGDK DEVADGYRDYWIKKGKLEDFFLKQLA
HP0150	1801 GGGATAGCTCTTCTGTTTATCATAGCAAATGGGTGCGTCCTGTCTTAGCCCTAGCTAATTATTTCATGGCAGATGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	1802 DS KPI NAP DTT	1802 DSSSVYHSKWVRPVLALANYFMADEE KPHFIAMDAETQVEHILPQTPKRGSQW NADFDKEKREEWVNNIANLTLLKRKKN AHALNGDFDEKRKIYGGKDTSKVISCY DITKELYSNYRKWNEKSLQERYKSLYN TITPVLHIEGQEDDFEDDFDLE
HP0150	1803 CAAACTTAAACGCACCCAAACCCTTATITGAATGTTTTGTAGGAGTTAATCTGGCCAAAGCCAAATATTATTCTAAAAA AGAAGAAAAGAA	1804 NERE PERE SYR	NLNAPKPLFECFVGVNLAKAKYYSKKË EREKEKMILNFCKIFEIILFEAIGKOPKP DFKNKDELLGDYPNLKNLDSLREVRED FLKRAFKNDEASLGAYVLVLLSCKYFE SVFEKYQEWLDFIARLALRGHVHKITK ELERLEEEDLEKLEKQALEYFNKIAN
HP0294	1805 ITITITAGCCCAAAAAACGATCGCAACTTACCGCTTATTAAATGGAGGCGTGTGGGTTTCTAAAATTCAAAACCCCTTG AATTGCTGCATTTTAGCGCGCGCCCTTAAAAGTTAAAGTTAGGATTTAGAACTTTTAGAATTCAAAACCCCTTG AATTGCTGCTGCTGCGCGCTCTAAAAGTAAGGTGAAAGCTTGTATTAGAAGGCCTTAATAGCC TTTAAGCGTGCTAGTGGGTTATAGCCAAAGAGAGAGACCTTAAATTATGAAGAAGACCTTTATGGC GAAAAACTACGATAATTAAAAAGGTTATATCGTGCTTAAATTATGAAAAAGAAAAGAAAAAGGCGTTTATTAAAAGCCGTTATTATCGTGCTTAAAAGAAAAGGTTATTATAAAAAAAGCTAAAAAAAGTTAAAAAAAA	1806 CCI VLV SIN SIN FYL	1806 FLAQKTIATYRILINGGVWLSKNSNPLN CCILARSKSKAKVRINDLRWVFSQRLS VLVGYSQRDETLFLTLEGLNTLMAKNY DNLKELNLNPLNYEEELSLRALVSGSE SINPIIVLEERTEKTLFVEIKSVFQEEKV FYLL
HP0294	1807 TTAATGGGGTAGATAGTATCGGTAACGCTACCGTCACGCAACATAACGCCGGGAATCTATTCAATGCTATGA CTTTTCCACGAAAGCATGGATAATTCGCAGAATTTCAATGGTCTAAATTCTAACGCCGGAACTTTCGGTGTATGGCA CCTTTTCACTAACGAAGCTAAAGATGGGAAATTTCAATGCAGGCGAAGCGTTTTTTGAAACCCCAACTTTA CCACTTTCACTAACGAAGCTAAAGGTTGGATTGAATTTTTCAAACACAGGTCAATTCGAACTTTGAAA ATGGAGGGAGTTTCAATTCAA	1808 NGVDS TQSME TNEAK SYGFS NASFN CGPTIV GPTIV GDGTI GDGTI SEKLV SEKLV SEKLV SEKLV SEKLV	1808 INGVÖSINIANÄTITOHNAGIYSSSMTFS TÖSMÖNSÖNLNGLNSNGKLSVYGTTF TNEAKDGKFIFNAGOAVFENTNFNGG SYÖFSGDSLNFSNNNOFNSGSFEISAK NASFNNANFNNSASFNFNNSNATTSF VGDFTNANSNLQIAGNAVFGNSTNGS ÖNTANFNNTGSVNISGNATFDNVVFN GPTNTSVKGOVTLNNITLKNLNAPLSF GÖGTITFNAHSVNINAESITNGNPITLVS SSKEIEYNNAFSKNLWQLINYÖGHGAS SEKLVSSAGNGYYDVVYSFNNOTYNF ÖGEVFSQNSISIRRLGVNMVFDYVDMEK SDHLY

02/066501		101/2	
1810 NDKYMLLVFGRNGCSYCERFKKDLKN VKELRDYIKEHFSAYYVNISYSKEHDFK VGDKNNEKEIKMSTEELAQIYAVQSTP TIVLSDKTGKTIYELPGYMPSTGFLAVL EFIGDGKYQDTKDDEDLTKKLKAYIKYK TNLSKSKSN	1812 YKKAISQQKIQAKIEELEEN YENAHEUN INGKNIKGGYIVESQGVE YELSRSHSSL INGKNIKGGYIVESQGVE YELSRSHSSL KNDANHIGKRYKACIIRVDKENHSINIS RKRFFEVNDKRQLEVSKELLEATEPVL GVYRQTPFGIPPAEAKGIEGLVHYSEIS HKGPVNIPERYKEGDEVYVKAIAYDAE KRRLSLSIKATIEDPWEIIQDKLKPGYAI KVVVSNIEHYGVFVDIGNDIEGFLHVSE IS	1814 JAEVSGGGKKPWAUNG GONANG ON THE SPAFFERADAWILFVVEKINKK SPVFVGGGVSHGATNNIRNYNLKINKK GOVEDNKRKHLTKEANOMFGALEGRD TLFV KODRYVYLLRYLDSRYNASILTTALIV KYDPFDALKKLLVSYYYOTWIAGGTITR KYPDFDALKKLLVSYYYOTWIAGGTITR IKATSINIIKNVKSNKSVETIKELILNSIDS YNTFDQYLYNIWDSSSYYHSKWVRPV LALANYFMADEEKPHFIAMDAETQVEH ILPOTPKRGSQWNADFDKEKREEWVN NIANLTLLKRKKNAHALNGDFDEKRKIY GGKDTSKVISCYDITKELYSNYRKWNEKSLQSKOTSKVISTYNITITPVLHIEGQ	1818 MLYENPLNTLDGKAYFYQDLSFKŘILD FFKTILENDTIYHNNPFIFYRDLHEPLISI DDLRVNYDDLRVNYDIJLRVNYDDLRV NYDDLR
<u>8</u>	18,	±	81
1809 CTAACGATAAATACATGCTITTAGTITTTGGCCGTAATGGTTGCTCTATTGCGAAAGGGTTTAAAAAAGATCCAAAAAAAA	AACGG 1811 CTACAAAAGGCCATTTCCCAACAAAGGTTCAAGCTAAAATTGAAGAATTAGGCGAAAACTATGAAAACGCCCATTAT 1811 CTACAAAAAGGCCAATTTCCCAAGAAAGGGGGTTATATCGTGGAGTTTAAAGGCGTGGAGTATTTCCTCCCCGCT TGAAGGCAAGATTGTAAAGAAAAAACCATATCGGCAAACGCGTTAAAGCGTGCATCATTCGTGTGGATAAGGAA CGCACTCTTCTTTAAAGAATGACGAAACCATTTTGAAGAACGACAACGACAACTTGAGGTTTCTAAAGGAATTGT AACCATTCTATCAATATTTCTCGCAAACGATTCTTGAAGACACCCCTTTTTGCAATTTTTGTAAAGGGGATT TAGAAGCCACAGAGCCGGTGTTAGGGGTTGTGCGCCATAAGGGACCAGTCCTGAAAATACTACAAAGGGGCGATG TGAGGGCACAGAGCCATTATTCTGAAATCAGCAAAAAAATCCTGAAAAATACTACAAAGAGCCATTATGGGG AAGTCTATGTCAAAAGCCATATTATGAAACCCGGATACGCCCTTTTCACTCCATAAAAGCCAATTATGGGC CATGGGAAGAACAACTAAAACCCCGGATACGCCCTTTTCACTCCATAAAAGCCAACTTATGGGC CATGGGAAGAACTAAACCTAAAACCCCGGATACCATGTTTCTGAAATCTTTCTT	GTGTTTGTGGATATTGGTAATGGTAATGATTGGTGGGGGG	TGACATCACTAAAGAATTGTATAGCAATTATAGGAAGI GGAATTGTAGAAGI CAATTTACCAAGATTTTAAAAAAAAAAAAAAAAAAAAAA
HP0294	HP0294	HP0294 HP0294	HP0822

1819 GAAGTTCAGACGATTAAAAACAATGTGAGT
ITTEGCGAAAGCAAAAGATGGGGGTTATAGGGTATTCTTGATTACAACCACGGCTACAACAAAGAAGCACGGCTACAAATCCAGCTT CTTTAACTCTTCTTCTGATATAGGACTTATGGCGGGGGGGG
ACGTGAATTTAACCGCGTTCAATAACCCTTACAGCGCGAAAGTCAATGCTACCAATTTCCAATTCTTGTTCAATCTCG GCTTGAGGACGAATCTCGCTACAGCTAGGAAAAAAGACGGCGAACATTCCGCGCAACATGGCTTGAATTGGGTATT
AAAATGCCCACCATTACCAGGAATTACTATTCTTTTTTTAGGCACTCAATTGCAATACAGAAGGCTCTATAGCGTGTAT CTCAATTATGTGTTCGCTTACTGAGTGATTCAAGCTCTCTTTTAAGGGGGGTTTAGAAAAATCGCAACGCCAAGCTT TTTATCGTTGGTGATAAAATCTACAAAACTAACGGCGGCGACAAAAACCCTAACGCTACGCTCAAAGACAAAAAAAA
1821 GGATAÁGGTGGGCGAGACTTTGTATTATGGGGCTGGGGCTÓGGGGAGAGACCTACCGCAAGCGCGGTCATTAGCGA TATTATAGAAATCGCAAGGAAAAAAAGCTCTCTAATGCTGGGCTTTGAAACCCCTCAAAAACTCCCCTAAAACCCCTAAAACCCCTAAAACT
AGAAGAAATCCAATGCGCTTATTATGCGCGCTTGTTAGTGAGCGATGAAAAGGGGGTTTTTTCTCAAATCAGCGGA
ACCCACACACCACCAAAAGTCTA SCAAGATGATTGGAAAATTGA
1823 AATACGCTAAAAATTTGAGCGCTTTAGCCCAAGACACGCTTTAGATCCAGTCATTGGCAGAGAAGAAGAGATTTTAA
GAGTGATAGAAATTTTAGGGCGCAGAAAAAGAATAACCCGCTTTTAATTGGCGAAGCGGGCGTAGGGAAAACCTC CATCGCTGAAGCTTTTGGCTTTAAAAATCGCTCAAAAAGAAGTGCCGGAGTTTTGCAAGAATATGAAGTCTATTCTTT
GGATTTAGCCTTAATGGTGGCTGGGGCAAAATACAGAGGGGGATTTTGAAAAACGCTTGAAAAAAAA
AGCTTGGATGCGGCGAATATATAAAACCGGTTTAAAACGGATGGGAGCTTGAAATGTTTAGGAGCGACCACTTTGA
AGAATACCGCAGCGTGTTTGAAAAAGACAAGGCTTTTAATAGGCGTTTTTCAGTCATAAAAGTTGAAGAGCCTTCTAA AGAGGCGTGTTACTTGATTTTAAAAAAGATCGCTCCCCTTTATGAAGAACACCACCAGGTGCGTTATGATGAGAGCG
TGTTTAAGGCATGCGTGGATTTAACGAGTGATTACATGCATG
CGCTCTAAAGCTTAAAATCCCTAAAATGCGTTTGAGCGAGC
I MANAMA I MAGA I I I I I GCCCAMGCAGAMGCGATCAGTCTTGTCAGCAMTGCGATTAMAMTCCAGCATTGCGGGCTTTC TGCAMAMATAMGCCTGTGGGGAGCTTTTTATTCGTGGGGCCTAGTGGGGGGGG
1825 CAGCGGATAAATACGACTCCGGTTGCGGGTGGCCCAAGCTTTCTAAGCCTATCAATAAAGATGTGGTGAAATACGAA
GACGA GAGAGATTAGGGGGGCTTAAGGTATTGCATCAACAGCGCGCGC
TGGAAAAAGAGGGTTATGGCGAGTTTATCCCTTATATCAAAAAGGGTGAATTGAAAAAATACATCAATGATAAAAAGT CGCATTAAGGGGTAATGACTAAGCCCCCCTAAGGGGGGGTTAAAATGAGGGGGTTTAAGCGTTTGGGGTTTGGGGTTTGGG
THATCHTANAAAACGCCTAAAAAACGCCCTTAAATGATTATTITTTAATACCCTTACTTTAAAAACGCTCCTTTAAGCTTT
AAACTTATTTTTTAAGGGGGTGGGGGGTTATCCCATTACAACCCCCAAACTAAACCCCCCTAAAGTGC
TITITTAGAGATTATCGCTTGCTGGTGAAAGCTCTTTGATATTAAAAAATGCCCTAGAAGCGTTTTTAGATTTAC CCCATAATGAGCTTGTGTAAAGTCGCTAAAATGCTTAAAGCATAAATAA
1 ŢAG¢¢AĄAG¢GATAAG¢TTGATĠ¢¢AATGĘ¢¢A¢G¢¢¢TAAĄAAÇG¢T¢ČĄATG¢¢GGGTAATCĄ¢¢¢¢G¢TT

4 1827 TCAACACGCACAGIATGATGATGCAGTAAAAGGGTTAAAAGGGTTAAGGAGAAGAACCGATGTCAAAGGAA GGGCCAAGTGGTTACCCAGTGCCAAGAACTCCATTAAAAGGGTTAAGGAAAAGAAAG	1	2/000301	12					PC'
4 1827 TCAACACGACAAGTATGATGATGATCCCGTGATTCCTTTAAAAGGGATTAGAGGGGTTACAGAAGAAGAGTGAAAGG GGGAAGTGATTCCCAGTATCCCAGATGATGATGATGATGATGATGATGATGATGAGGAGTGAAAGG GCGAAGTGATTCCTTGGAATCTCCAGTAAAAAGGGGTTAAAGTAGGGTTAAAGAAGAGGGTGAAAGGA CCGACACGACA		628 N I HKYDDPLIPLKRIRGVTERTDVKGG VVIPVROEEVKVAVKELLEAGAKAIVIC LLOSHKNAESERIVKDIALKIIEKLGKNI PVFASVDYYPQRKESHRMNTTILEAYA AEPSRQTLSKVSNRFKEHGAKFDLRV MATHGGTISWKAKELARTIVSGPIGGVI GSKLLGETLGYDAIAGSONGGT	330 LGIDVSTGEFKGADIHSQTTJSMENIKA ILKEAGLGMDSVVKTTILLKSLDDFAVV NGIYGSYFTEPYPARATFQVAKLPKDA LVEIEAIAIK	32 ALEYALEEKAQANKLFVVEKIAIKGVVE DNKRKHLTKEANQMFQALEQRDTLFV CMNMDEYTELAFSNLKKCLIVDVSELN AYLLAAFSSVVMEEAAFQHVVQDKTEE	NO OF A PERSON SERVICES OF A CO.	34 RKLVVYFARLYTPNPTLSLAG 36 FVVFRNDNFEHFKSELDLNLGALAREN ELYRONYCGCGFALKIGKESONRSPF ELYSPLKRGILPASIEERTGVFRTLDMA KKDANKPFLAGKTIATYRLLNGGVWLS KNSNPLNCGILARSKSKAKVFINDLRW VFSQRLSVLVGYSGRDETLFI.TLEGLN TLMAKNYDNLKELNLNPLNYEIEELSLR ALVSGSESINPIIVLEERTEKTI.FVEIKS	8 PFPSEDTTPMGDHLRTKGAEFGTTTK RPRRCGWLDLVALKYACALN3CTQLA	DIDELSMSEKIAILLIQVGEDTTGEILRHL DIDSITEISKQIVQLNGTDKQIGAAVLEE FFAIFQSNQYINTGGLEAKTATLG
1827 TCCACGCACAGGTATGATGATCCCGCTG GGGCAAGTGGTTATCCCAGTGCCTCATA TCGAAAATTGGGTAACATCCTGTAT TTGAAAATTGGGTAACTTTGCGGCT CATGGCGCTCATTGGAGCCTTATGCGGCT CATGGCGCTCATTTGGAGCCTTATGGAGCC CATGGCGTTGATTGGTGCACGAG 1829 ATTAGGCATTTTAAAAGAACACGGGGGTTA AATTGCGGTTTAAAAGAACACGGGGTTAA ATTGCGGTTTAGAACCCTTTAGAAATTGCGAATT AAAGAGGCTTTAGAACCCTTTAGAAAATTGCGAATACGAATAAAAAAAGAAATTGCGGTGTCAAAAAAAGGAAAATTGCGCTTTAGAAAAAAGGAAAATTGCGGAATACGAATAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAA				181	102	8 8	1838	1840
4 4 4 6 8 8	1827 TCAACACGCACAAGTATGATGATCGCTGATTCCTTTAAAAAGGATTAGAGGGTTACAGAAAGAA	GGGCGAGTGGTTATCCCAGTGCGTCAAGAAGAGGTTAAAGTTGCTGTTAAGGAGCTTTTAGAAGCAGGTGCAAGAGCAGCAGTGCAAGAGCAGCAGTGCAAGGCAGCAGCAGCAGCAGCAGCAGCAGAGCAGCAGCA	1829 ATTAGGCATTGATGTAGGCGCGGGGGGGGTTTAAAGGCCGCAGACATTCATT	1831 GGCTTTAGAATACGCTTTAGAAGAAAAGCGCAATAAGCATTAGCTTTTTGTGGTGGAAAAAATCGCTATAAAAGGCGGTTTGTGTTTTTGTTTTTGTTTTTGTTTTTGTTTTTGTTTT	1833 GAGGAAATTAGTCGTGTATTTCGCCAGGCTTTATACCCCTAACCCCACGCTCTCGCTCG	1835 ATTIGICGIGITIAGAAACGATAATTITGAACATTITAAGAGCGAGTTGGATTIAAACTIGCCAGAGTITGGCGAGAGA AAACGAGCTTTACCGGCAAAATTATTGAACATTCGCTTTAAAAATCCAAAAAGAACGAGACTTTGGCGAGAGA CTTGAGCTTTACTCGGCAAAATTATTTACCCGCAAGTATTGAAGAAAGA	1837 GCCTTTCCCTAGCGAAGACACTACACCCATGGGCGATCATTTAAGGACTAAGGGTGCGGAGTTTGGCACGACAACC AAGCGCCCAAGGCGTTGCGGGTGGCTTGGATTTGGTTGAAATACGCTTGCGCTTTGAATGGTTGCACGCAAT TAGCGTTA	1839 ATTAGACGAACTCTCCATGAGTGAAAAATCGCTATTTTACTCATTCAAGTGGGCGAAGACACCACGGGCGAAATTTT AAGGCATTAGACATTGACTCTATTACAGAGATTCTAAGCAAATCGTGCAATTAAACGGCACAGACAAGCAAATTGG TGCGGCGGTTTTAGAGGAATTTTTTTTTT
90 00 00 00 00 00 00 00 00 00 00 00 00 0	HP0944		HP0944	HP0944	HP0944	HP0823	HP0823	HP0823

307

٦,		u
e	-	٦
3		•
t	۰	ח
۰	7	•

2/066501		PCT/EP01
1842 DLDYAIVKAKDI.KPSFTTGGTQKRTDM NEEQIKSIAENFDPKKIFGSGGFEDLPII LHDGQVIAGNHRIQGMLNFTPKSRFSY ERAIKEYYHIDLKPDELLVRVPHKRLNN TEINNLAASSNQGRFNSESDHAIAVLS HYGAKLKELDQKLDADSIYSLKNIVAKN LNFDKATHPNVTDSNLALLMFNMPRTK TQGIELLNRWKKEFSNDIKSYEKVKKM FVDNAGSFHNLIHDLNFPKVSLNAYLS DIMDRSFANLKNYQSTSESLKDLSEKF YKTSSLEMFEKS	1844 DTLYFEPIHFECVKSIIGRERVDGIIVHF GGGTPLKLAKDLAKMQAPIIGTPFKVIDI AEDREKFSLFLKELDIKQPKNGMAKSV DEAYSIANVIGFPIIVRPSYVLGGQHMQ ILENIEELRHYLESVTHALEISPKNPLLID KFLEKAVELDVDAICDKKEVYIAGILÜHI EEAGIHSGDSACFIPSTLSPEILDEIERV SAKIALHLGVVGLLNIQFAVHÜNSLYLIE VNPRASRTVPFLSKALGVPLAKVATRV MVLEDLKEALKFYÜKKNINGYSKGVYK PKMPHFVALKEAVFPFNKLYGSDLILG PEMKSTGEVMGIARSLGLAF	1846 DISPTÓVKIILKLPGSSPEEMENNIVRPL ELELLGLKGÓKSLRSVSKYSISÖTTIDFD DSVDIYLARNIVNERLSSVMKDLPVGV EGGMAPIVTPLSDIFMFTIDGNITEIEKR QLLÓFVIRPQLRMISGVAĎVNSIGGFSR AFVIVPĎFNÚ 1848 MFGGÓNFSĎFSPORSEDLŐĎILSŠI FGKGGFSQRFSÓNSQGFSGFNFSNFA PENLÖITAALNVSVLDTLGNKKQVSIN NETFSLKPIGVEEGEKIRVRNKGKTGR TTRAMQKFRIKEKGIKINRKTSHVGDLYL ÓARLILPKTETLSNELKALLE
1841 CGATCTAGACTATGCGATCGTCAAAGCGAAAGATTTTAAAACCAAGGCTTTACCACAGGCGGGCG	1843 GACACGCTCTATTTTGAACCCATTCATTTTGAGTGCGTGAAAAGCATCCCAAAGGGAGCGAGTGGATGGCATTAT CGTGCATTTTGAGGCAAAACCTCCTTAAAACTCGCTAAAAGGCATCAACTCCAAAATGCAAGCCCCCTTATTGGCACCCC CTTTTAAAGTGATTGATATTGCAGAAGACAGGGAAAAATTTCCCTCTTTTTAAAAGGCTTGACATCAAGCAGCCCCA AAAACGGCATGGCTAAGAGCGTTGATGAAGAATTTTAGAAAATGCATTGGTTTCCCTATTGTGCGCCCA AAAACGGCATGGCTAAGAGCGTTGATGAAGCTTTAGAAAACTTGAGGATTTCCCTATTTTTGGAAAGCCCCTTATTTGGCACCCTTATTTTTAGAAAAAGCGCCTTTATTTA	1845 GATÁTITIC GCCCACTCAAGITA AAATCATTITA AAACTCCCCGGCTCTAGGCCTGAAGAAATGGAAAACACATCGTG CGCCCTTA GAATTGGAGCTTTA AGGCTTGAAAGGCCAAAAATCTTA AGGAGTGTTTCAAAATTTTCAGATA TTACCATAGAATTGGAGCTTTTA AGGCTTGAAAGGGCAAAAATCTTTA AGGAGTGTTTCAAAATTTTTTTTTT
HP0823	HP0823	HP0823 HP0823

HP0823	24 0 0 0 0 ≤ 0 0 0 0 0	1849 CTAGACTATGCGATCGTCAAAGCGAAAGATTTAAAACCAAGCTTTACCACAGGCGGGACGCAAAAGAACGGACAT GAACGAAGAGAGATTAAAAGCATTGCTGAAAATTTTGATCCTAAAAAGATATTTGGTAGCGGAGGGTTTGAAGATTT ACCGATCATTCTACATGACGGGCAAGTGATCGCAGGAACCCACAGAATCCAAGGAATCCAAGAAATCTAACATAGAAACCGAAGAGAGAG	1850 LDYANKAKDLKPSFTTG EEGIKSIAENFOPKKIF3S HDGOVIAGNHRIGGMI.NI RAIKEYYHIDLKPDELLVF EINNLAASSNOGRFNSES YEAKLKELDOKLDADSIY	1850 LDYAIVKAKDI KPSFTT GGTQKRTDMN EEQIKSIAENFDPKKIFGSGGFEDLPIIL HDGQVIAGNHRIQGMI.NFTPKSRFSYE RAIKEYYHIDLKPDELLVRVPHKRLNNT EINNLAASSNQGRFNSESDHAIAVLSH YEAKLKELDQKLDADSIY
HP0823	1851 144 144 144 144 144 144 144 144 144 1		1852 LEYADPSTSH ACGFIYEISEI LLRYLPSRYW KLLVSYYYGI VKSNKSVETI NLWDSSSYY DEEKPHFIAM SQWNADFDK SQWNADFDK KSLYNTITPVI	1852 LEYADPSTSKKRADKG-LKKVFKDSKKD ACGFIYEISEFMKAYTP-LLKKQDRYYYL LRYLPSRYWASILTTAI.YVKYPDFDALK KLLVSYYQTWIAGGTITRIKQTSINIIKN VKSNKSVETIKELILNSIDSYNTFDQYLY NLWDSSSYYHSKWVRPVLALANYFMA DEEKPHFIAMDAETQVEHILPQTPKRG SQWNADFDKEKREWVNNIANLTLLK RKKNAHALNGDFDEKFKIYGGKDTSK VISCYDITKELYSNYRKANEKSLQERY KSLYNTITPVLHIEGQEIDFEDDFDLE
HP0947	1853 6 6 7 7 7 1 1 1	1853 GCGGGGAATACAGTCAAAGCGATCTTTTTACGCACATTAGCGATATTAAAATGGGGCTTATTAAAGGGAGTCAATGG GGGGTTATTGGTTTAGGGACTATCGGTAAAAGAGTCGCCCAAGCTCGCTC	1854 GEYSQSDLFTI GLGTIGKRVAK KKEEYERLSLK TRDLIALKELQS EKDLAEILETK HAFLNPKIQNK LVEKTKENIQD	GEYSQSDLFTHISDIKMIGLIKGSQWGVI GLGTIGKRVAKLAQAFGAKVVYYSPKD KKEEYERLSLKDLLATSIDIISIHAPLNES TRDLIALKELQSLKDGAILINVGRGGIVN EKDLAEILETKDLYYASDVFVKEPFEKD HAFLNPKIQNKLLLTPHIAWAYSDSLKT LVEKTKENIQD
HP0947	1855 C7 66 67 77 77 77 77 70 70 70	CTTACATGAGGACCGATAGCTTGAATATCGCTAAAGAGGCTTTAGAAGAGCGAGGAATAAGATTTTAAAAGACTATG GCAAAGACTATTTACCCCCTAAAGCCAAAGTCTATTCCAGCAAGAATAAAAACGCCCAAGAAGACCCATGAAGCGATC AGGCCCACTTCTATTATTTTAGAGCCAAACGCTTTAAAAGACTTAAAGCCTGAAGAATTAAGGCTCTATACCTTAA TTTACAAACGCTTTTTAGCTTCTCAAATGCAAGACGCTCTTTTTGAAAGCCAAAGCGTGGTTGTGGCTTGCGAAAAAG GCGAGTTTAAAGCGAGGGGAGAAAGCTCCTTTTTGAAAGCCAAAATTTAGGCAATGACGATAAGGACAAAT TGCTCCCCAATTTGAAAGAAAGCTCCTTTTTGATGGCTATTAAAAATTAGGCAATGACGATAAGGACAAAT TGCTCCCCAATTTGAAAGAAAAGGTTTAAGAAAGTTTAGAAAGGCACGCATGTTACAGAACCTCCAG	1856 YMRTÖSLNIAKEALE DYLPPKAKVYSSKNI- SIILEPNALKÖYLKPE ASÖMÖDALFESÖSV GRKLLFDGYYKILGN NDPIKLEKLESNAHV KVLESLGIGRPSTYA	1856 YMRTDSLNIAKEALEE/RNKILKDYGK DYLPPKAKVYSSKNKNAQEAHEAIRPT SIILEPNALKDYLKPEEL RLYTLIYKRFL ASQMQDALFESQSVVVACEKGEFKAS GRKLLFDGYYKILGNDÜKÜKLLPNLKE NDPIKLEKLESNAHVTEPPARYSEASLI KVLESLGIGRPSTYA
HP0947	1857 G. T. 7. A.A.	IBS7 GAGCAAGGGGGAGGGTTTAGGCAATCAGTTTTTAGCCAATATCAAGGAATGCGAAGTGATCTTGCAAGTGGTGCGT TGTTTTGAAGATGATAATATCACGCATGTGAACGACAAGATTGATCCTTTGAATGATATAGAAACTATTGAATTGGAGT TGATTTTAGCGGATATTGCCGCTTTAGACAAAAGGATCGATC	1858 SKGEGLGNO EDDNITHVND AALDKRIDRL(SLKTHLEELK	1858 SKGEGLGNQFLANIKECEVILQVVRCF EDDNITHVNDKIDPLNDIETIELELILADI AALDKRIDRLQKALKSSKDAKNLLECAL SLKTHLEELKPAKTFPLNTSEAF
HP0947	1859 74 17 17 17 17 17	1859 CGAAGI CGCI I CAAAAGAI ACI ACAI GCAI GC	OEIPOITNEOA DESAMIETEL PPKINKEKPPKT ORSEEALDLLD	CYASAD I SSMITKEINVASELSKIK IN GEIPQITINFQANEKARYKNESVLIKQIL DKGYYWIETELGMRLKAHGSLLKKIQK PPKNKFKPPKTTIPKPKEASLRLDLRG QRSEEALDLLD

•	-
_	_
_	-
	^
•	

02/066501		Pe
1862 FHSL YYQPKNAIVI.VYGDVNSGKVFEL SKKHFESLKNLDEKAIPTPYMKEPKOD GARTAVVHKDGVHLEWVALGYKVPAF KHKDQVALDALSRLLGEGKSSWLQSE LVDKKRLASQAFSHNMQLQDESVFLFI AGGNPWYKAEALQKEIVALLEKLKKGEI TQAELDKLKINQKADFISNLESSSDVAG LFADYLVQNDIQGLTDYQRGFLDLKVS DLVRVANEYFKDTQSTTVFLKP	1864 SHIEYETENRHYAHYDCPGHADYYKN MITGAAQMDGALVVSAADGPMPOTR EHILLSRQVGVPHIVYFLNKQDMVDDQ ELLELVEMEVRELLSAYEFPGDDTPIVA GSALRALEEAKAGNVGEWGEKVLKLM AEVDAYIPTPERDTEKTFLMPVEDVFSI AGRGTVYTGRIERGVVKVGDEVEIVGI RPTQKTVTGVEMFRKELEKGEAGDN VGVLLR	1866 DQVSGLLHTIELSSDDVFEAIKDQVREI SSALRSVLEEVKPDLAKDIVQNGNVLT GGGALIKGLDKYLSDMVKLPVYVGDEP LLAVAKGTGEAIQDLDLLSRVGFSE
1861 AATTCCATTCGCTCTATTATCAGCCTAAAAACGCTATCGTTTTGGTGGTAGGCGATGTCCAATTCCCAAAAAGGTTTTG AATTGAGTAAAAAGCATTTTGAATCCTTAAAAAACGCTATCGTTGATGAAAAAGCTATTAGAAAAGGCTATAAAGT AGCAAGATGGAGCCAGAACGGCAGTCGTGCATAAAGATGGGTCCCTTTAGAATGGGTGCCTTTGGGTATAAAGT AGCAAGCGAATTCAAGGATCAAAAAAGGTCGCCTTAGAGCATTTTAGGCGAAGGCCAAAAGCTCGTGGT TGCAAAGCGAATTAGTGGAATAAAAAAGGCTTGGCCTTTCAAGCTTTTTTAGGCGAAATGAATTAGAAAAGCTGTTAAAAAAGGCGAAATTAGTGGGGGGGTAATCCTAAAGCTTTTTTTT	1883 ITCTCACATTGAGACTGAAAACAGACACTATGCGCATGTGGATTGCCCAGGACACGCTGACTATGTAAAAA ACATGATCACCGGTGCGGCGCAAATGGACGAGTTTTGGTTGTTTCTGCAGCTGATGGCTTATGTAAACAAAC	1865 GGATCAAGTGGCCTGTTGCACGGTTGAATTGAGCTCTGATGATGTGTTTGAAGCCATTAAAGATCAGGTGAGGTTAAATTGCCTGTGTGCGAAAATGGCTTAAAAGGCGATGAGGCGATGAGGCGATGAGGCGTGTGAGGCGTGTGAGGCGTGTGAGGCGTTTAATTGCCCTGTGTAATTGCCGTGGCGATGAGGCGATGAGGCGATGAGGCGTTAATTGCCGAGGCGATGAGGCGATTAATTGCCGGGGGTTTTAATTGCCGTGGTTTAATTGCCGTGGTTTAATTGCCGGGGATTTTAAGGGAATTTCAAAAGGGCGATTTTAGGGATTTTAATTGCCGTGGTTTAAAAATTCCTTTGGGAATTTCAAAAGGGGGTTTTAGGAGCGTTTAAAACGGGATTTAAGAGGAAAATTGAAAAAGAAGGAGCGTTTAAAAACGCCGAGTTTTAAAAAGAAGAAAATTAAAAAAAA
HP0947	нР0947	HP0947

2/066501	PC1/EP01/1
1868 LRVNYDDLRVNYDDLRVNY DRLLQNASPLLELSQNT FKIYRKAYQ KSLPLLRTIRRWVKK	1870 NVDKIEGLTPAIAIDQKTT SKNPRSTVG TITEIYDYLRLLFARVGECGFCPTCLEPIS SMSTSDIISQICHLEENSKIIILAPIIKDKK GSFNDKLESLRLKGYVRAFVDGVMVR LDEEIHLHKTKKHTIEAV/DRVVVNNEN ASRIASAIEKALKESYGELEVEILQDNA PSIRKHYSEHKACFKCKINSFEELEPLS FSFNSPKGACESCLGGTKFSLDISKIL DPNTPLNQGAIKVIFGYNIRSYYAQMFE GFCEYNGDSALCFNELIKEQGDALLY GNGTEISFHFKNSPLKRIWKGQDALLY GNGTEISFHFKNSPLKRIWKGGQDALLY GNGTEISFHFKNSPLKRIWKGGQDALLY GNGTEISFHFKNSPLKRIWKGGQDALLY GNGTEISFHFKNSPLKRIWKGGQDALLY GNGTEISFHFKNSPLKRIWKGGQDALLY GNGTEISFHFKNSPLKRIWKGGQDALLY GNGTEISFHFKNSPLKRIWKGGQDALLY GNGTEISFHFKNSPLKRIWKGGQDALLY GNGTESTHROPHYGGNTLIYVEHDKETTK HADPVVDIGPKAGRHGGEVVFSGSVK ELLQNNHSTALYLUGTKIRRPKFELPK EKHFLEIKVNINNIKNLSVQIPLKQLVC ITGVSGSGKSSLILQTLLITAQTLLINHA KKTQSLNGVEIVGLEHLINKVIYLDQAPI GKTPRSNPATYTGVMDIERIRLFAGKE AKILGYSASRFSFNVKGGRCCQGD GDIKIEMHFLPDVLVQCUSCKGAKYNP QTLEIKVKGKSIADVLNMSVEEAYEFFA KFPKIAVKLK
STTAATIATGATGATGATTAATTATGATGATTTGAGGGTTAATTATGATG	1869 TANTIGREGATAMANTIGANGECCTACCEGATICGCTATTGAAAAACCCTTCTAAAAACCCCAGATTCCCAATTTTGCCCCCAGATTTTTAAGGTTGTTTGT
HP1114	HP1114

_	-
~	٦

02/066501		PCT/EP01/1
1872 IIVHFGGOTPLKLAKDLAKMQAPIIGTPF KVIDIAEDREKFSLLKELDIKOPKNGM AKSVDEAYSIANNIGFPIIVRPSYVLGG OHMOILENIEELRHYLESVTHALEISPK NPLLIDKFLEKAVELDVDAICDKKEVYIA GILQHIEEAGIHSGDSACFIPSTLSPEIL DEIERVSAKIALHLGVVGLINIOFAVHQ NSLYLIEVNPRASRTVPFLSKALGVPLA KVATRVMVLEDLKEALKFYDKKNIVGY SKGYYKPKMPHCALKEALKFYDKKNIVGY SKGYYKPKMPHCALKEALKFYDKKNIVGY SKGYYKPKMPHCHGLKGLINGFPRIKLYG SDLILGPEMKSTGEVMGIARSLGLAFF KAQTACFNPIKNIKGLIFVSIKDKDKEEA CVLMKRLVQLGFELCATEGTHKALEKA GVKSLKVLKISEGRPNIMDLMMNGEIS MAINTSDHKSQDDAKLIRASVLKNHVS YFTTLSTIEVLLLALEESSKEDELLALQD	1874 EENCACYACKRYSKAYLHHLFRAKELT YARLASLHNLHFYLELVKNARNAILEKR FLSFKKEFLEKYNSRSH	1876 GESYVATGNIYÖTLVÖFRYGTTEVEPA LATSWDISPDGLVYTFHLRKGVYFHQT KYWNKKVEFSAKDVLFSFERGMDKAK RYYSPGAKSYKYWEGMGMSHIIKSIEA LDDYTIRFTLNGPEAPFLANLGMDFLSI LSKDYADYLAQNNKKDELAKKPIGTGP FKFFLWNKDEKIILLKNQDYWGPKAYL DKVVVRTIPNSSTRALALRTGEIMLMT GPNLNEVEGLEKVPNIVVDKSAGLLAS WLSLNTQKKYFDNPLVRLAINHAINAD DYIKYLYEGFAQKMVNPFPPTIWGYNY NIKPYEYDLKKAKELLKQAGYPNGF
1871 CATTATCGTGCATTITGGGGGACAAACCCCTTITAAAACTTCGCTAAAGATTTGGCTAAAAAGGCCCCCATTATTGG CACGCCTTTTAAAGTGATTGCAGAAGACGGGAAAAATTTTCCCTCTTTTTAAAAAGAGCCTTCATTGTGC GCCCAAAAACGGCACTGGCTAAGAGCGTTGATGAGGCATTGTGGCTTCCCTTTGTTGGAAGC GCCCTAGTTATGTGCTAAGGCGTTGATGAAGCCTTCTCATTGATGAGTTGGCCCCATTATTTGGAAAGC GCCCTAGTTTGGCATAAAAAACCCGCTTCTCATTGATAAGTTTTAGAAAAAAAA	1873 TGAAGAAATTGCGCATGTTATGCTTGCAAACGCTATTCTAAAGCCCTATTTGCATTTTAGGGCCTAAAGAACT CACTTACGCTCGTTTGGCCAGCTTGCACATTTGCATTTTATTTA	1875 ATGGCGAAAGCTATGGAACGGGCAATÁITTATGACACGGCTCGTGCAATÍCAGATACGGCACCACAGAAGTTGAACGGCACACAGAAAGTTGAACGCCACAGAAAGTTGAACGCCACAAGGGGTTTATTTCCCCCACAAGGGGTTTATTTCCCCAAACGCAAAGGGGTTTATTTCCCCAAACGAACG
HP1111	HP0481	HP0481

ı		•	7
0	۰	-	-
1		۲	7

02/066501		PCT/EP0
1878 WASECDFHLLMAESLRIHYAKTLDIWR NNFNHNLDQVKRLSYCERFIRMWDLY LRTCASAFRVGSADLFQLLLTNSVDNT FPLTKEYIYQ	1880 VKIAREMQVPYIGSFHLQPEHISYNIMKL GWFSWFNIMLFSWFKSSHYRYIHIH CPSKFIVEELEKYNYGGKKYAISNGFD PMFRFEHPQKSLFDTIPFKIAMVGRYS NEKNGSVLIKAVALSKYKQDIVLLLKGK GPDEKKIKLLAQKLGVKAEFGFVNSNE LLEILKTCTLYVHAANVE:SEAIACLEAIS VGIVPVIANSPLSATRQFALDERSLFEP NNAKDLSAKIDWWLENIKLERERMQNE YAKSALNYTLENSVIQIEKVYEEAIRDF KNNPHLFKTLS	1882 EADHLTWHCNFENYLNÄKLKVLTLMPK TSLAILPLKFKEHPIIQNSQAQKIFFDKS EEVLERLKIPSNALFFKGAFILDAALAL LVYEQFLKINSNALFFKGAFILDAALAL LVYEGSHKMEEFRDKGGRLWVDDSKAT NIDATLQALKTFKNQKIHLILGGDIKGVN LTPLFEEFKNYKISLYAIGSSAFIIQALAL EFNVSCQVCLELEKAVCIEIKSVLSQNEI ALLSPSAASLDQFSSYKIERGEKFKAFV LKD
1877 CG I GATGAGCGAATGCGACTTCCACTTGCTCATGGCTGAAAGCTTACGCATTACGCTAAGACTTTAGACATTTAGACATTTAGACATTTAGACAATGCGAATGCTTTAGACCATTTAGACAATGCTTTAGACAATGCTTTAGACAATGCTTTAGACAATGCTTTAACCAATGCTTTAACCAATGCTTTAACCAATGCTTTTAACCAATGCTTTTAACCAATGCTTTTAACCAATGCTTTTAACCAATGCTTTTAACCAATGCTTTTTAACCAATGCTTTTTTTT	1879 CCGTAAAAATGCGGGGAAATGCAAGTGCCTIATATTGGCTCTTTTCCATTTACAGGCCAGAGCATATTTCTTATAACA TGAAATTGGGGTGCTTTTCTTGGTTCAACATGATGCTTTTTTCGTGGTTTAAATCTTCGCATTACCACTTACCACCA TGAAATTGGGGTGCTTTTCTTGGTTCAACATGAAGAAATTACAAAATTCCACCA TATCCATTGCCCGTCAAAATTCATTGTAGAAGAAGAATTAGAAAAATTCCACCATTACCACTTTAAATCCATTGGTA GGCTTTGATCCCATGTTTTAGATTTGAACAACCCGCAAAAAGCCGTTTTTTGCTCAACAAATTCGCTATTGTA TATTGCTCAAAGGGCCTGATGAAAAAAATCAAAAAAATTAGAAAAAACTTTAGCCCAAAAACTAGGCGTTTTTTTT	TCATTTGACTTGGCATTGCAATTTTGAAAATTGAACGCTAAACTCCAAGGTTCTAACATTGATGCC STCGCTATCCTCCCTTTAAAAATTCAAAGAACACCCCATTATTCAAAACTCGCAAGCGCGAAAAATTTTTGAACATTCAAAACTTCAAAACTCGCAAGAACTCGCCAAAAAATTAAGGGAACCGCTTTTTAAGGGAACGCGTTTTTAGGGAAACTCCTTTTAAGGGAATTTAAGGGAAAACGCCTTTTAAGTTTATTAGGCAAAATTGGCAAGATTTTAAGGAAAAACGCCTTTTAAAATTGGCAAAAAAAA
	HP0481	HP0481

٩	Ç	j	į
٠	•	-	
¢	1	1	

02/066501			PCT/EP01/1542
1884 YAYNAGPGFLRRWLESSKRFKEKNHF EPWLSMELMPYSETRMYGFRVMLNYL IYQEIFGNFIPIDGFLEQTLNSKDKP	1886 PILHTLGLQRYFELVÖNLGGFEALÝRE TKKAALATOKAVLALGLKIFPKSPSLSM TTIVNEHAKELRNLLKEKYQVÓFAGGÓ EPYKDALIRINHMGIPVYKSAYALNALE LALNDLDLREFDGVANATFLKQYYGI	1888 AYPYNPGHLIIPHVHQASVÉLLĎLŇTW LNMNALAPKVLKALYAYGAĠGINLGLN LHRNAGAGIPEHLHMHLVPRFLGDSNF MSVIAQTRVCGMDLNETYLTLKNLLEK ELG	1890 APPSQARLWYVPPSKMDEGELINEGY YAIFGAAGARTEVPGCSLCMGNQARV RDNAVVFSTSTRNFDNRMGRGAKVYL GSAELGAACALLGRIPTKEFYMNLVSE KLESQKOKIYRYMNFNLMENFRL
1883 CCTACGCTTATAACGCTGGGCTTGGGTTTTTAAGGAGGTGGTTAGAAAGTTCCAAACGATTTAAAGGAAAAAATCATT TGAGCCATGGCTTAGCATGGAGCTTATGCCTTATAGCGACTGGCTTTAGGGCTCATGCTCAATTAC TTGATTAACAGAAATTTTGGGAATTTCATCCCTATTGATGGATTTTAGAACAACTCAAAGGACAAAC TTGATTAACAAAATTTTTGGGAATTTCATCCCTATTGGAGGATTTTTAGAACAACTCAAAACCATTCCTAAAGA CATGATTAAAAAATGCCTTTTACCGGGGCTATGGCAGCGCTTTTTTTT	1885 TCCTATTITACACACITTAGGGTTGCAACGCTATTITGAATTGGTGCAAAATTTAGGGGGGCTTTGAAGCGCTCTATAG AGAGACTAAAAAAAGCCGCTTTGGCCACTCAAAAAGCCGTTTTAGCTTTTAGGTTTTAAAAGAAAATTCCCTAAAAGCCCCAAG GCTTGAGCATGACAACGATTGTTAATGAGCAAGGCGTTCGTATCAACCACTTTTAAAAGAAAATACCAGGTGCAATT TGCGGGCGGTCAAGAGCCTTATAAAGGCTTAGCGCTCATTCGTATCAACCACTTGTGGGATTATTAAAAGCG CTTACGCTTTAAACGCCCTAGAGTTAGCGCTCAATGCGCTTTGATTAAGGGAATTAGCGAACGCAACT TTTTTAAAGCAATATTATGGAATTTAAGGAAACCAACGACTTGTGTGCGTGATCCCAAGCAACGCAACGCAACGCAACGCAACGCAACGCAACGCCTTAGGGAATTAAGGGAAGTTAAGGGAAGCCCTTGTGTGCGTATTATGAACCACCAAGCAACAAAAACAAGCGGTGCAAATTTAAGGGAAGTTAGGAAGCCCTTGTGTGCGTTTTTAAAAGCAACAAGCAAAAAACAAGCGGGGCATTAAAGGAAGAATTTAAGGGAAGTTAGAAGAAAAAAAA		1889 ACGCTCCTCCCAGTCAAGCACGCCTTTGGGTAGTGCCACGTAAATGGACGAACAAGAGGCTTATTAATGAGGG CTATTATGCGATTTTTGGGGCTGCCGGGGCAAGGACTGAAGTCCCAGGCTTGTGCATGGGCAATCAAGCG CTATTATGCGATTTTTGGGGCTGCTCTTTTCCACTTCCACGCCTGTAATCGCATGGGTAGAGGATCCAGCG AGGGTTAGGGATAATGCGGAGCTTGGGGCGCGCTTCCCACGCCTAAAGAAGAATACATGAAT GTATTTAGGCATGAAAAGCGTCGTCTTTTCCACTTACTAGGGCGAATCCCCACTAAAGAAGAATACATGAAT TTAGTGAAAAGCGTGAAAAGGGGCGATCCCTTTTTAATTTAATTAGGCGACTTAATGGAAAAAAAA
HP0481	HP0481	HP0481	HP0481

2/066501					PC1/EP01/15428
1892 QKEAJANKKRI.MEMGRIAYEAQKIGLF EYLIYQNSYMDALITLAEAKIEYIDISALL EETLGESLTRLGELH	1894 KGEHSKESUKAMILISD WYLP I IPSUL DTAYLLDMLERIRDIQAI.NENLKACIVM NRIPTIPTLKEKKALIDFINQNNANESVF LMDNLLSERIAYKRSVSEGMGVMEYN DNKAKNEWSQFYDELNGYLRIKK	1896 LYSQKUMUKKI ILKU FUMGVNLAGV DIILRLKEKLDELDNLNK =LQDALHKHS KNTKTPTKNLNTPTNFYELILFKK	1898 SIKTENPLVRYAINNALKLNKASCIAMH PIKDNALANLCRSSFCITHEVGAEEILL GMILKMLNIESAALK 4001 AKT AKAINGEEI GI HI IACCGRADI EGI	EFILDAGIHSYNHNLETSONFFPKICST EFILDAGIHSYNHNLETSONFFPKICST HTWEERFITCENALRAGILGLCSGGIFG LNESWEDRIEMLRALSCALLAKEFL IKNPVLPIDAETLSADEALECVLLAKEFL PNARLMYAGGR	EVDKILKTPSIKGVLLLIDSPGGAVSASV ELSEKIADLKQKMPVLAYARGVMASGS YYAGMQASEVYASKASLIGSIGVIFSGA NVENLLNKVGVATQGVHAGEYKEIGTF TRAWKPNEKDFLQNLVNEQYQMFVND VAKARKLDAKDYKDFAIGGVFSAQKAL KLKLIDKISTIKQAQDRLMELSKVKKAY WLEKSPMERFIEKATQSATNIITQAFGY
	GGGCTATGCTATTGAGCGATTGGGTGCTAATACCCACCACGCCAGG GCTAGAAAGGATTAGAGACATCCAAGGGTTGAATGAAAACTTGAAAG CCCCACTCTTAAAGAGAAAAAAGCTCTCATTGATTTTATCAACCAAAA AATCTATTAAGCGAAAGGATAGCTTATAAAGCGTTCAGTGAGTG	TCAAAACGATTTTACGCCTTACAAGGGATATGGGGGGTTAATCTTGCG AGCTTGATGAATTAGACAACCTGAATAAAGAGTTGCAAGACGCTCTG CGAAAAATTTAAACACCCCTACGAATTTTTACGAATTTGATTTTATTA AAAAGCCTAGAAGATTTTTAGGCCAAGAGCATTTAGTAGGGAAAGA CACTTCCCCCATGCCTTTTTTAGGCCAAGAGCATTTAGTAGGGTAAAA CACTTCCCCCATGCTTTTTTATGCCCTCCTGGCGTGGGTAAAA AGAGCGCCCATTCTTTTATTCAATGCGACGGATTTTAAATTAGAGG		1899 TCGCTAAATTAGCTAAAGCCATCAATGGAATTGGGCTTGCATCTAATCGCATGCTGCGGGGGGGG	1901 TAAAGAAAGCGCCCAAGCGCCCCGCCTAATCTCGCTAATCTCGCTTTTGATTGA
HP0481	HP0481	HP0481	HP0481	HP0481	HP0481

١	ć	3
,	Ē	٠
ť	٠	١

02/066501		
1904 DVDLSNRVALEEILALKPSLLSFSADKF FNSAQAGIIMGQKERVEALKNHPLYRV LRVGKITLTLFCSLKAWINHQEDITIHA ILNGTKDALLQKALKLYALLKPLELNVS IASSFSKIGNLFGRELESFCVKIQPKNT RALNSEKLYLKLFQKGVIARISCEFVCF EVFSLNEKDFEKIALVLEEILNKA	1906 ISĎIĴĒIARKKSSĹMĽGFETPQKLPLKPK EEIQCAYYARLLVSDEKGVFSQISAILA QNDISLNNVLQKEILHSNKAKILFSTHTT NEKSMLNALKELENLQSVLĎTPKMIRL EN	1908 EYYKNFDNATARKMALDYFKRINDDKG MIYMVVDKNGVVLFDPVNPKTVGQS GLDAQSVDGVYYVRGYLEAKKGGGY TYYKMPKYDGGVPEKKFAYSHYDEVS OMVJATTSYYDINTENKAIKEGVNKVF DENTTKLFLWILTATALVVLTLIYAKLRI VKRIDELVLKINAFSRGDKDLRAKIDVG DRNDEISQVGRGINLFVENARLIMEEIK GISTLNKTSMDKLVQITQETQKSMKDS STTLNSVKNKATDIASMMNASIEQSQG LRKRLIETQGLVKESKDAIGDLFSQITE SAHTEEELSSKVEQLSRNADDVKSILDI INDIADQTNILLALNAAIE
190	190	1900
	8 1905 I CATTAGCGATATTATAGAAATGGCAAGGAAAAAAGGCTCTCTAATGCTGGGGCTTTGAAGCCCCTCAAAAACTCCCCCCTCAAAAACTCCCCCCCTTAAAAAA	1807
HP0481	HP1118	HP0149

2/066501		
1910 PHLAFAKASHAFKIPFFKNPESVNEPK HFERVTIMPNVVIGEGVEIGENSLIYPG VVIADGVKIGKNCILYPRVTLYQNTILED NVTIHAGSVIGGDGFGYAHTALGEHVK IEHVGIVRIQKNVEIGAITAIDRAVFGET LIKEGVKIDNLVQIGHNCVLGEHSIVVS QVGLSGSTTTGRNVVI:GGQVGIGGHL HVGEFTQIGGKSAVGKDLPPNTNFAG AIPAMEIHEWHHFLAHI.RTNFRKQQKT SLLQKAKGFFKS	KWVAVDFDIGLENLD HIGGENRIVYD WAS AS GENERAL TO KTENLE AS GENERAL TO KTENLE AS GENERAL TO KTENLE AS GENERAL TO KTENLE AS GENERAL HADMAL WVT PEVSSLRDSDRVGIIDAKSNRAKKGM EVHKHLINRLKPELVANGEMISIEEVLK ILCLPLIGIIPEDHHIISATNKGEPVIRTD CESAKAYQRITRRILGIEVEYVEFKAK RGFFSALKGIFS	1914 GULEGUSDSENALIUS NIVANDENDU SOLRNRKTFONMARKGYPLLPMDFKN GGOJATINATNVDADKIASDNPIYASIEP DIAKQYETEKTIKOKNI. EAKLAKALGGN KKDDDKEKSKTAEAAKAENNKIDKDV AETAKNISEJALKNKKE KSGEFVDENG NPIDDKKKAEKQDETSIPVKQAFIGKSD PTFVLAQYTPIETILTSIVVDATLTGIVSG VVAKDVWNIMNGTMILLDKGTKYYGNY QSVKGGTPIMTRLMIVFTKAITPDGVIIP LANAQAAGMLGAGVDGYVNNHFMK RIGFAVIASTOTATATATATATATATATATATATATATATATATATA
1909 CCCGCATTTAGCCTTTGCTAAAGCTTCGCATGCCTTTAAGATCCCTTTTTTAAAAACCCAGAAAGCGTGAATGAGCCTTTTTTAAAAAGCCCAGAAAGCGTGAATGAGCCTTTGATTTTTTTT	1911 AGTAGTTACTATCACTTCAGGTAAGGGGGGGTGAAAAGCACCACGGGCTAATTTAGCTTACTATCACTATCACTTCAGGTAAAAGGTTCAGGGGTGAAAAGCTTAGGAACTTGGACTTTAGGTTATTAGGCTTAGGAAAAAAAA	1913 CAATGITTAGAGGGCTTGAGCGATAGTGAAAGGCCTAATTCTAGGAATTAAACGACAAGCTGATGATGAGGTGAGGTGAGTGA
HP0149	HP0149	HP0149

02/066501		PC
1922 SFFDNKGNTKFIAITSGKGGVGKSNISA NLAYSLYKKGYKVGVFDADIGLANLDVI FGVKTHKNILHALKGEAKLQI;IICEIEPG LCLIPGDSGEEILKYISGAEAI.DGFVDE EGVLSSLDYIVVDTGAGIGATTQAFLNA SDCVVIVTTPDPSATTDAYACIKINSKNK DELFLIANIMVAQPKEGRATY FRLFKVA KNNIASLELHYLGAIENSSLLIKYVRER KILKKIAPNDLFSQSIDQIAGLLVSKLET GALEIPKEGLKSFFKRLLKYLG	1924 IGAISFNTNNQLKLKVKDIKEKVPLSVF GDGLKKYLHIVSAFMADNAKTIYIDEVE NGLHFSRMRLLLKNTIDFINNINKDGNL QVFMTTHSQEFIEILDQVIREKDFAHQT KLFCLKQDDQYVIPRTYYGENLEYYFE NEENLFG	1926 IEWLNNAGESLKTKMKEYEGFFSDFNT SMRTNEQEVSATLNANTENII:(SEIKKLE NQLIETTTRLLTSYOIFLNNARDSANNQ ITANKTESLEALNQAKTSANNEITANQT QALTNINEAKENANNQITENKTQAITNI NEAKNQSLSKH
1921 AGITITITIGATAATAAAAGGGAATACCAAATTCATCGCTATCACAAGCGGGTGGGGAGGCGTGGGGGAATTCCAACAT TAGTGCTAATTTAGCCTACTCTCTATACAAGATGCTAAAAGGTGGGGGTGTTTGATGCGGATATTGGTTTAGCGAA TAGTGCTAATTTAGCCTACTCTCTAAAAAGGTTATAGCGGGGTGTTTGATGCGGATATTGCAAGAAT TTTAGATGTGAACCCGGGGTTATATATTTTGCGGGGGTGTTTTAGAATTTTAGAATTGCAAGAAT CATTTGTGAGATTGAACCCGGGGTTTTAGATACCTGGGGGGAAATTTTTAAAATTAGCATTAGCGTG CAAAGCTTTAGAACCTACTACGGAAGGGGGGGTTTTAAGACTCTTTTGGATTATTTGGGTTGATACGGGTGCT GAATTGGGATGCAATGCA	1923 ATCCAAGCCATTAGCTTTAATACCAACCAACTCAAATTAAAAGTGAAAGATATCAAAGAAAAAGTCCCATTATCTG TATTTGGCGATGGTTTGGAAGAAATATTTGCATATTGTAAGCGCTTTTATGGATAACGCCAAAAAGGTCCCATTATTGA TATTTGGCGATGGTTTGAAGAATATTTGCATATTGTAAGCGCTTTTATGGATATTGAATATATGA TGAAGTGGAATGCTTACCACTTTTCTCGCATGAGGTTATTGTTAAAAAACGATTATCAACAAAAAAAA	1925 ATTGAATGGCTTAACAACGCGGCGAGAGCTTAAAAACGAAAATGAAAGGAGGGGGCTTTTTAGCGATTTCAAT ACGAGCATGCGCACCAACGAGCAGAGTAAGTGCTACTTTAAACGAGACTCAAAAGCGAAAAGCGATTAA AAGCTAGAAAATCAATTGATAGAAACCAAAGCGCTTTAACGAGCTATCAAATCTTTTTAAACAACGAGGAA TAGCGCTAACAATCAACAACACAAAACCGAAAGCGCTTGAAGCGCTAAACAAGAACAATTGAAATAACGAAATCAATTAACGAAAGCGCTAACAAATAACGAAATGCGAAAACCCAAACGCGAAACCAAACCAAACGAAAAAACCAAACGAAACGAAACGAAACAATAACTAAATAACTAAACTAAACTAAATAAA
HP0149	HP0149	HP0149

HP0149	1927 AA	1927 AAAGACGCTAAAGATTTTGACGATGCGATTTTTTATGACCAAGAAAAAAGGGGTTTTGTTGTGGGGGTTGCTGATGTG	1928 KDAKDEDDAIFYBOFKRVI FVAVADVŠ
 !	AG		EFVPKHSSLDKEARVRGFSVYFPNSVY
	<u> </u>	CGTCTATCAAATCCCATGCTGCCTTTGAGATAAATTGCTCTCAAGGGGCATGCTCATTAAAAGGGTTTGAAAAAGGCCTGGCTTTAGT	PMLPLSLSQGACSLKAFEKRLALVYEIP
<u></u>	88	GAAGAAATCAATTITITAAGCGCTAATCAAAGCTCTTTAGATAAAGGTTTTGCAACAAGAGCCTTTTAGGGTTTTAG	LUNLKNAKLSGGVIEVKANCI YEEINH FI SANOSSI DKDI OOSI I GEI EMAI KI
	¥	AAATGGCTTTAAAGTTAAAAAAGGAGCGTTTAAAAAAAGGGGTTTAATTTCAATTCCTTTGAAACAAGCTGTATTTGAA	KERLKKGFNFNSFENKLYLNKEGRIE
-	¥ +	TAAAGAAGGGCGTATAGAAAAAATTGAAACAGAAAAGGAAGCGATGCGCACACCCCTCATAGAAGAAGCCATGCTCT	KIETEKESDAHTLIEEAMLLANGSSARL
	¥ (2	AGCCAACCAALCIAGI GCGAGGI AI I I GGA I GAGCA I I I CACAA I AAGGGGGATATACCGCACCCATAAAGAGCCC	LDEHFHNKGIYRTHKEPSLEQQKRLYD
	2 5	AGITTITAGAGCATGCCTTAAAAATAGCCAAAAAAAAAAA	KLFDYEIVRPKNMGFFPFLEHALKIAKE
	S S	CAMPATTI AGCCCTT TATA AGCCCCT COA AGCCCATT TO CATT TO	CI DEACYTHETCOLODOXON ALGOLIVE
_	8	CCCATTAGACGATACAGCGATCTAGCCTTACACAGGCTTTTAAAAGAATTGTTGTTTTATCAAGCTAAAGGCTGCTCG	ILFYOAKGCSYLLEETPELCAEINALO
	TAT		KKAALIERDFIKRKFARLALELLEKEFLG
	E	TTATCAAGC	WILEVKDWWWGLKEFIGLKYL
HP0149	1929 AAA	1929 AAAACCCCCATGCCAAGCGTGCAAGGGTAAAACCTATATCCTTAAAGATGAAGAAATTGATGCGATAATCCCTGAGGG	1930 KTPCQACKGKTYILKDEEIDAIIPEGIDD
	TAG	CATTEATEATEATEAAACCECATEETECTTGAAATAAAGGCAATGAATGAATACGAAGGGAAAAAGAGGGGGGATTTGTATT TAGAAGCGCAAGTCAAAGAAGATGAGCATTTCAAGCGCGAAGACTGCGATTTATTCATTAAAGGGGGGGG	QNRMVLKNKGNEYEKGKRGDLYLEAQ
	ACC	ACCACTATCGCTTTAGGGCATACGATTAAAGTGCCGTCTTTAAAAGGGGACGAACTGGAATTAAAAATCCCTAGAAA	HTIKVPSI KGDELELKIPRNARDKOTFA
	<u>ფ</u>	CGCCAGAGACAAGCAGACTTTTGCGTTTAGAAACGAGGGCGTGAACACCCTGAAAGCTCTTATAGAGGGAGTTTG	FRNEGVKHPESSYRGSLIVELQVIYPK
	ATC	ATCGTGGAATTGCAAGTGATTTACCCTAAAAGTTTGAATAAAGAGCAGCAAGAATTGTTGGAAAAATTGCATGCGAGT	SLNKEQQELLEKLHASFGYEGEPHKSV
	<u> </u>	ITTGGCTATGAGGGCGAGCGCATAAAAGCGTTTTAGAAACCTGTATTTCTAAAATTAAAGACTGGTTCAAATAAAAG	LETCISKIKDWFK
	OTA STA	GTTGTTGGGATTGTGGATTGCTTTTAGGATGCTTTTAGGACGCTATGATTATAAAAAAAA	
	TAC	TAGECTEGEGEGEGETECATITIETA GEORGE TATA CONTRACTOR AND CONTRACTOR AT TATA CONTRACTOR AND CONTRACTOR AT TATA CONTRACTOR AND CONT	
	<u> </u>	GCTTGCTGGTGAATGCGAGACAGACTTGTTACGCGCTTTCTATGCTAGATTTAAAAACACTAAATGGCGTTTGC	
	CCT	CCTATTTAGCGCACGCGCTCACGGATGAAACCTTTGCTTTATTGAATTTATACGCTCCTAAAGAGGGGGGTTAGTGAAA	
	AAG	AAGACTITATITITAGCATTICCTIACTCAACCACTCTTATTGGATTITTGGCTCGTTGGTGGGGTTCGTTAGTGGGTTC	
	25	<u>GCAITHTCTTTGAC, </u>	
HP0028	1931 CCC	1931 CCGAAATCACTTCTAACACCCGCCACCGCTGCCGCATTTTACCGGTGATTGGAGGGGTTGCGATGGGCATGGGTTA	1932 EITSNTATAAAFLPVIGGVAMGMGYEN
	9 5	GAAAACCA CAGAGCI GACCA CC GAGCCI GAGI GCGACI GCGCG CCGCG GCCCI GCGCG CCC GAGICA CCC	HOSCLLTIPVALSATCAFMLPVVTPPNA
	CTG		STESYELVS IEN
•	AAG	_	
	199		
-	AGT	AGTTAAAGCGAGCTTTAGCCTGTATCTCATTTTAGTGTTGTCATGGGTGGCGGCGTATTTTTAACGGGCGTCCTATAG	
	<u> </u>	ANTIGORATION I AGGGCGTTGGGTTTTTTGGGGTTTATAGGGTTTTTGGTGCAGGGGGGGG	
	<u>L</u>	TITTAGTCGTGGTGCAAGCGATGTGGGGGCGTTTTTGGAGGCAAGCTTTTAGGCAAAACCCCTTTCACGCCC	
	ACT 666	ACTICECCEAATAAAACCTIAGAGGGCGCGTTGATTGGCGTGGTTTTGGCGAGCGTTTTAGGATCGTTTGTGGGCAT GGGGAAATTGAGCGGAGGCTTTTTATGGCGCCTCTTTTTAGTTTTTAATCGCTCTTGTGGCGGTGTTTGGGATTTT	
<u>. </u>	GTA	GTATGAAAGCTATTTGAAAAGAAAGGTCGGTATCAAAGATAGCGGTAAGATTTTACCCGGGCATGGGGGCTTTAG ACCGGTTGGATTCCAT	

•		
c	•	J
Ξ		
r	7	4

02/066501		PC	CT/EP01/15428
1934 PIGALSKALSQLMKGPFYQSFRSKVKKI LSTLPESVNYLASRFEESFKLITPGVFF EELGINYIGPINGHDLSAIIETLKLAKELK EPVLIHAQTLKGKGYKIAE:GRYEKWHG VGPFDLDTGLSKKSKSAII.SPTEAYSNT LLELAKKDEKIVGVTAAMI'SGTGLDKLI DAYPLRFFDVAIAEQHALTSSSAMAKE GFKPFVSIYSTFLQRAYDSIVHDACISS LPIKLAIDRAGIVGEDGETHQGLLDVSY LRSIPNMVIFAPRDNETLKNAVRFANE HDSSPCAFRYPRGSFALKEGVFEPSG FVLGQSELLKKEGEILLIGYGNGVGRA HLVQLALKEKNIECALLDLRFLKPLDPN LSAINAPYQKLYVFSDNYKLGGVASAIL EFLSEQNILKVKSFEIIDEFIMHGNTAL	1936 SKKTQQHSPQDLSNEEATEANHFENL LKESKESSDHHLDNPTETQTNFDGDK SEEITDDSNDQEIIKGSKKKYIIGGIVVA VLIVIILFSRSIFHYFMPLEDKSSRFSKD RNLYVNDEIQIRQEYNRLLKERNEKGN MIDKNLFFNDDPNRTLYNYLNIAEIEDK	1938 VEQVLADLKNFSKEQLAQJAQKNEDF NTGKNSELYQSVKNSVNKTLVGNGLS GIEATALAKNFSDIKKELNEKFKNFNNN NNGLKNSTEPIYAKVNKK+TGQVASPE EPIYTQVAKKVNAKIDRLNJASGLGGV GQAGFPLKRHDKVDDLSKVGLSASP EPIYATIDDLGGPFPLKRHJXVDDLSKV GRSRNQELAQKIDNLNQAVSEAKAGF FGNLEQTIDKLKDSTKKNVMNLYVESA KKVPASLSAKLDNYAINSHTRINSNIQN GANNEKATGMLTQKNPEWLKLVNDKIV AHNVGSVSLSEYDKIGFNÜKNMKDYS DSFKFSTKLNNAVKDIKSGFTHFLANAF	1940 FSGTSOASVFKEDGKEYD WIIRVPDDK KYSVEDIKRLQVRNKYDKLMFLDALVEI TETKSPSSISRYNRGRSVTVLAEPNRN AGVSLGEILTQVSKNTKEWLVEGANYR FTGEADNAKESNGEFLVALATFVLIY MILAALYESILEPFIIMVTMPLSFSGAFF ALGLVHQPLSMFSMIGLILLIGMVGKNA TLLIDVANEERKKGLNIQEAI
1933 GGCCTATTGGAGCCTTATCCAAAGCCCTTAGCCAGCTGATGAAAGGCCCGTTTTACCAGTCTTTCCAGCTCTAAAGTT AAAAAAATCTTAAGCACCTTACCTGAAAGCGGTGAATTACTTAGCGAGTCGTTTTGAAGACTCTTCCAGCTCATCACC CCGGGCGTGTTTTTGAAGAATTAGCAATTACTTAATAGCGCTATTAATTGGAGAACCTTAAAAGGCCAAAAGATTATTGAA ACCTTAAAATTAGCCAAAGAGCTTAAACGGTGCTAATTAGGCCTATTAGGAACCTTAAAAGAT ACCTTAAAATTAGCCAAAGAGCGTTAAACGGTGCTAATTAGGTTTTGGATTTGAAAAAATCCAAAA ACCTTAAAGGGCCTATGAAAAATGGCATGGGGTGCTTTTGATTTGGATTTTGTAAAAAATCCAAAA ACCTTAAAGGGCCTATGAAAAATGGCATATTCTAACACCTTTTGATTTGTGAAAAAATCGTAGGCGTATTTTGAAGAAAATCGTAAAAAATCGCCAAAGGCGTATTTTGAAGAAAATTGATGTGCTTAACCGCTTTTTTGAAGAAAATTGATGTGCTTAACCGCTTTTTTGAAGAAAATTGATGTGCTTATCTAACCTTTTTTGAAGAAAATTGATGTGCTTATCTAGCTTAAAAAAATTGACGCTTTTTTGAAGAAAAATTGATGTGCTTAAAAAAATTGACCTTATCTAGCTTAAAAAAATTGCGCTTATTTTTGAAGAGAGCGCTTTTTTTGCAGAGGCGTTTTTTTGAAGAGCGCTTTTTTTGAAGAGCGCTTTTTTTGAAGAGCGCTTTTTTTT		· · · · · · · · · · · · · · · · · · ·	1939 CTITITICTGGGACTTCTCAAGCGAGCGTGTTCAAAGAAGATGGCAAAGAATACGACATGATCATTAGAGTGCTGAT GACAAGCGCGTTTCTGTAGAAGACATCAAACGCTTGCAAGTGCGTAACAAATACGATAAATTGATGTTTTTTTT
HP0028	HP0028	HP0028	HP0028

1		٠	a
1	Ċ	•	j
,	ė		×

HP0028	1941	1991 TTTAGAGGTGCTTACCCAAGCTAAAAGCATCGCTTTTGATAAAACCGGCACTTTGACTAAAGGGCGTTTTTAAAGTAACGGGCACTTTTAGAGGGCGTTTTTAAAGTAACGGCACTTTAGCGCACTTTAACGCTTTTTGCACTTATCCACGCACG	1942 LEVLTQAKSIAFDKTGTLTKGVFKVTDI VPQNGHSKEEVLHYASCSQLLSTHPIA LSIQKACEEMLKDDKHQHDIKNYEEVS GMGVKAQCHTDLIAGNEKMLDQFHIA HSPSKENGTIVHVAFNQTYVGYIVISDE IKDDAIECLRDLKVQGIENFCILSGDRK SATESIAQTLGCEYHASLLPEEKTSVFK TFKERYKAPAIFVGDGINDAPTLASADV GIGMGKGSELSKQSADIVITNDSLNSLV KVLAIAKKTKSIIWQNILFALGIKAVFIVL GLMGVASLWEAVFGDVGVTLLALANS MRAMRA
HP0028	1943	GCTGTGA AAACCGC TGCGAAA CTTGGTG CTTTTTACG AAAACCCT	1944 SISDLESAVRVNI RNSGAGRVDRDGE TFLVKIQTASLSLEDIGKITVSTNI.GHLH IKDFAKVISQSRTRLGFVTKDGVGETTE GLVLSLKDANTKEIITÜVYÖKLEELKPF LPNGVSINVFYDRSEFTÖKAIATVSKTLI EAVVLIITLFLFLGNLRASVAVGVILPLS
HP0028	1945	1945 ATGGCGCGATGGATGGCGCATCTAAATTCGTCAAAGGCGATGCGATCGCTTCTATCATCATCATCATCATTATCAATATC ATTGGAGGGTTTTTAGTGGCGCGTGTTTCAAAGGGATATGAGCTTTAGCGCTTATCATCTTAACC ATTGGCGATGGGCTTGTGGCGCGTGTTTCAAAGGGATATGATCTTAGCGACCGGTATTTTAGCCACTCGCACCC ATTGGCGATGAAGAAGAGGAGGGATTTGCTTTCCAAACTCATCACACTCACCAATAAAAGCAAAACTTTAGTGATTGTGG GAGCGATTTATTGCTTTTTGCCACTTCCTGGACTCCTTACTTTTTTTT	1946 GAMDGASKFVKGDAIASIIITLINIIGGFL VGVFQRDMSLSFSASTFTILTIGDGLVG QIPALIIATATGIVATRTTQNEEEDFASK LITQLTNKSKTLVIVGAILLLFATIPGLPT FSLAFVGTLFIFIAWLISREGKDGLLTK LENYLSQKFGLDLSEKPHSSKIKPHTPT TRAKTGEELKREEEQAIDEVLKIEFLEL ALGYQLISLADMKQGGDL
HP0028	1947	1947 TGCAAGCCTTGATGAAAAACGCCCCAAAAACCGCCCTTAAAATGCAAAATAACCAACAGATTGAAGTTTTAGTGGGTA GCATTGTGGTGGAGAATCTTAAAAGTCCTCCTGGAAGCGCGATTGCGGTGGATGGTGAAATCATAGAGGCGGA AGGGGAATTAGATGAGAGCATGTTGAAAGGTCCTCCTGGAAGCGGCGTTTATAAAAAAGTCGGCGATAAAGGCTTTTCAG GGACATTCAATAGCGCTCAAAGTTCTAATGAAAGCCGCACGCA	1948 QALMKNAPKTALKMQNNQQIEVLVDSI VVGDILKVLPGSAIAVDGEIIEGEGELD ESMLSGEALPVYKKVGDKVFSGTFNS HTSFLMKATQNNKNSTLSQIIEMIYNAQ SSKAEISRLADKVSSVFVPSVIAISILAF VVWLIIAPKPDFWWNFGIALEVFVSVLV ISCPCALGLATPMSILVANQKASSLGLF FKDAKSLEKARLVNTIVFDKTGTLTNGK PVVKSVHSKIELLELLSLALSIEKSSEHV IAKGIVE

æ	7
•	J
×	ń
•	•

02/066501		PCT/EP01/154
1950 HREVEHLKERVSHGHHIEDDVLLDELL KESEYLAHATCAVCHMCSTLCPLEIDT GKIALNYYQKNPKGEKIASKILNHMQTT TSMARFSLKSARLVQNI.IGSHNLVSLT KGIKKFIKPFPKAFYYMFKNNAYPLENK TLKSEEKVIYFSTCINRSFAPSNKMADK RCIQEVFESLCQKAKVSVMYPNGLNAL CCGKAFINYTDLTKQNNEKNHAIFLQLS DKGKIPIVLDHSACSTHFFKQMKAYKD LKYYDLSVYIEEVLSPKLKFNPINEDIGL YTMCALKLENKEELLFNI.AKKCTLGEIV HKETGCCGFAGNKGFFTPELNESALN GFQAFYQSYDLKRGFSTSTCEIGLSE KTRFSWQHATVVDACTL	LSSURYFTTLETKDP/GFEALIDSEI LSSVDRYFTTLETKDP/GFEALIDSEI SLKAISPMLTDVIEYGLITFFAKGVFVLL DYLYQFVGNWGWAIILLTIVRIILYPLSY KGMVSMQKLKELAPKMKELQEKYKGE PQKLQAHMMQLYKKHGANPLGGCLPL ILQIPVFFAI	1954 DNTPALDNIPKKSCMIVLESAAPLSAFLEKTNARVFARLVLDKEKKVLALAFLEKTEKTNARVPARLVLDKEKKVLALAFLEKTRARVDAFLISTEFLONAFFKMLQHAQIIGHDLKPLI.SFLKAKYQVPLI.SFLKAKYQVPLKELIPHEKIKDFKTI.SFLKAKYQVPLALKELIPHEKIKDFKTI.SFRKGVFENLLSIARELTNALKRULSIARELTDALKRULSIARELTDALKRULSIARELTDALKNULMGMEFQGFKIDAPYFKRLEQEFKNELHVLERGILEGVDFNLNSPKQLSEVLYDKLGLPKNKS.HSTDEKSLLKILDKHPSIALILEYRELNKLFNTYTTPLLRUCKDKNHTFIQTGTATGRESSHSPNLKDNSPKGLIRKGFFASSKEYCLLGNIPVRSPKGLLRKGFFASSKEYCLLGNIPVRSPKGLLRKGFFASSKEYCLLGNIPVRSPKGLLRKGFFASSKEYCLLGNIPVRGFTGANDYVKGNYLREGVFKNN
195		66
1949 CCACAGAGAGGTAGAGCACTTAAAAGGAAAGGGTAAGTCATGGTCATGAGATCAAGTTTTATTAGATGAGCTTTT AAACAGAGGTCGAATATTTTAGCACACTGCGCGGTGTGCCATATGTGTTCCACCCTATGCCTTTAGAAATTG AAACAGAACACCAAGCATTATTCAAAAAAACCCTAAAGGCGAAAAGATCCATTCAAAGATCCTTAATCACA TGCAACCAACCAAGCATGGCTCGTTTTCTTTAAAAAAGCCTTTAGTTCAAAACCTCATAGGCTTCACAACT TGCTACCATCAACCAAAGGGATTAAAAAAATTCATTAAAAAAAGCCTTTTATTACATGCCAAAACCCCAAAAACACG CCTATCCATCAAAAAAAAAA	1951 GCGTGCTTTTAGAAAATAGCGACAAAAAATTGAAAATTGAAGATTTTAGAGACGCTAAAGAAATTGAAGACCTTTTAGAAAAATTGAAGCTTTTGAAGCTTTTGAAGGTTTTGAAGGTTTTGAAGGTTTTGAAGGTTTTGAAGGTTTTGAAGGTTTTGAAGGTTTTGAAGGTTTTGAAGGTTTTTGAAGGTTTTGAAGGTTTTGAAGGTTTTGAAGGTTTTGAAGGTTTTGAAATGAAGCGAATTTGCATTGCATTGCATTGCATTGCATTGCATTTTTTTT	1953 AGACCACCCCCCCCCTAAAAATCATCATCATCATTTGGAAAAGCCCCTTTTGGAGCCTTTTGGAGCCCTTTTGGAGCCCTTTTGGAGCCCTTTTGGAGCCTTTTGGAGCCTTTTGGAGCCTTTTTGGAGTTTTTGGCCCTTTTTGGAGTTTTTGGCCCTTTTTGGAGTTTTTGGCCCTTTTTTGGAGTTTTTAGAGTTTTAGAGTTTTTGGCCCTTTTTTTGGAGTTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTAGAGTTTTTAGAGTTTTTAGAGTTTTTAGAGTTTTTAGAGTTTTTAGAGTTTTTAGAGTTTTTAGAGTTTTTAGAGTTTTTAGAGTTTTTAGAGTTTTTAGAGTTTTTAGAGTTTTTT
HP0028	HP0028	HP0028

02/066501		PCT/EP01
1956 KIALDGVLLNNASVDASLISGEFKPLEL GVNDPILGGYVNVGVPFSYQVSANFQ NSRLSGLLETLKKSFLEKPLIESSANQI ADIFSKAVLFLAFVSFLLWØFGLGGNF EKALMVCISVLVISCPCAFALATPIALVI GVFKNPLIVFKEALFLETLAKVKKIFIDK TGTLTQKEVLLKEKIIYEEFDGRLLKSLL KVREHLAHSAILKSLDGDEVSLEKIEFF AHGLKASYQNETLLVGSLKFLGSMGV DIPMKESANIMVGFAKNETLCALFILEE RLKANAKEVQALQNKGLELEILSGDN ESSVKECAKKLGISNYHAHLTPEDKAÒ TISSYKGVCAMVGDGNNDALALKQAS VSLGFEKSALSKSACDILLLEEDLSLLK KAFDNAQKVYQVLQNIVLSLIYNAILIP VAMLGYINPLIASLSMSASSLLVVLNSL	1958 QQGKEEISVQLPGIKTLEEERRAKDLIS RSAHLQMMAVDEEHNKDAMKMTDLE AQKLGSVLLSDVEMGGKILLKAIPILDG EMLTDAKVYYDQNNQPVVSFTLDAQG AKIFGDFSGARVGKRMAIVLDNKYYSA PVIRERIGGSGQISGNFSVAQASDLAI ALRSGAMSAPIQVLEKRIIGPSLGKDSV KTSIIALVGGFILVMGFMVLYYSMAGVI ACIALVVINLFLIVAVMAIFGATLTLPGM AGIVLTVGIAVDANIIINERIREVLRENEG IAKAIHLGYINASR	1960 EHLDKVIYLDQAPIGKTPRSNPATYTGV MDEIRILFAEQKEAKILGYSASRFSFNV KGGRCEKCQGDGDIKIEMHFLPDVLV QCDSCKGAKYNPQTLEIKVKGKSIADV LNMSVEEAYEFFAKFPKIAVKLKTLMD VGLGYITLGQNATTLSGGEAQRIKLAK ELSKKDTGKTLYILDEPTTGLHFEDVNH LLQVLHSLVALGNSMLVIEHNLDIIKNA DYIIDMGPDGGDKGGKVIASGTPLEVA QNCEKTQSYTGKFLALELK
1955 TAAAATCGCACTAGATGGCGTGCTTTTAAATAATGCGAGCGTGGATGCGTCTTTGATCGTGGGGGAGTTTAAGGCCTTTGGTGGGGGGGG	1957 TCAGCAAGÈTAAAGAAGTTCGGTGCAATTGCCTGGCATTAAGACTTTAGAAGAACGGCGCGCTAAAGACTTAAGACTTTAGAAGAACGGCGCGCTAAAGACTTAAGAACTTAAACATTAAACATTAAACATTAAACATTAAACATTAAACATTAAACATTAAACATTAAACATTAAACATTAAACATTAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAGCAAAAGCAAAAGCAAAACAAAACAAAACAAAACAAAAGCAAAGCAAAAGCAAAGCAAAAGCAAAAGCAAAGCAAAGCAAAGCAAAGCAAAGCAAGCGCATTCAACGCTTCAACGCCTTAAAGAATTTTAAGAATTTTAAGAATTTAAGAATTTTAAGAATTTAAGAAAAAA	1959 GGAGCATTTGGATAAAGTGATTTATTTAGATCAAGCCCCCATAGGCAAAACCCCACGAAGCCACCACGAACCCTGCCACTTACA CGGGAGTGATGGATGAAATCAGGATTTTATTTGCCGAGCAAAAAGAAGCCAAAATTTTAGGCTATAGTGCGAGCGT TTTAGCTTTAATGTTAAAGGGGGGGTGCGAGAAATGCCAAGGCGATGGGGAACTTTAGAAATGCACTTTTT GCCTGATGTGTTTAGTCCAATGCCGTTAGGCTGTAAGGGCGCTAAATACAACCCCCAAACTTTAGAAATCAAGTGAAAG GCAAATCCATTGCCGATGTGTTGAATGCTGTAAGGCGTTATGGAGGCTTATGAATTTTTGCTAAATTGCCTAAAATCGCCG TGAAGTTAAAAATGCGTTATGGATGTGGGCTTAGGCTAAAAAAGAGCCAAAACGCTACGACTTTAAGTGGGGGG GAGGCTCAAAGGATTAGCTAAAATTGAAATTGAGTAAAAAAAA
HP0028	HP0028	HP0821

HD0824	10R1 AT	TTAAAATCCCTAAACAATTAACAAATTAACAAATTAACAAATTAACAAATTAACAAATTAACAAATTAACAAATTAAAA			
1 200	3	GCGCCTTCTAATAACTTGCGTTTTGAAGAAGCCTAATTAACAACAACAACAACAAAAAAAA	1962	1962 LKIAKECLEMIENKDRLIKELE:LKMERLS	(C)
	E	TTICACTTGCATGGGTTTAGGCGAAACTGTATGGATATTTTTATATATA		NNLRFEEALIYRDRIAKIQKIAPFTCMDL	
	<u>6</u>	GTGAAAATGTTCATGCGTGGGGGTAAAATCATTTCTTCAGCGTTTGAAAAAAAA		AKLYDLDIFAFYGASNKAVLVKMFMRG	
•	8	GATGAAGCGATGAAACAAGCATTATCAATCCATCCCATTTTCATTCA		GKIISSAFEKIHSLNGFUTDEAMKQAIIN	=
	<u>အ</u>	TTGCTCTAATGAAAGGCTTAAAAAATTGCAAGAATTAATCTCTCAAAAAAAA		HYGSHLPLMPEQILLNACSNETLKELQ	_
	5	CTAAAAAAGGGGACATAAAAAAAAAAAAAAAAAAAAAAA		EFISHQYSKKIALSIPKKGDKI.ALIEIAM	_
	5	AATGAAGATCTTATTTAGGAAGAAGAAGAACTTAGAAGAAAAACCT		KNAGEIFSGEKTSNEDLILEEARSLFKL	
	N A	ACACAMAGCA CATTATAGCA ACACAMAGA ACACAMAGA I I AAA I AAA I AAA I AAA I AAA I AAAA I AAAA AAAAAA		ECMPYRVEIFDTSHHSSSQCVGGMVV	_
	ΤĀ	TATICE CETACON TO ANOMAL TO THE SECOND TO TH		YENNAFOKNSYRRYHLKGSIJEYTQMS	~
	<u> </u>	CONTRACTOR OF THE CONTRACTOR OF THE CACHE		ELLTRRALDFAKEPPNLWVIDGGRAQ	$\overline{}$
	AA	A A B C C C C C C C C C C C C C C C C C		LNIALEILKSSGSFVEVIAISKEKRDSKA	
	<u> </u>	SCIENTARIO CONTRATO CONTRATO CONTRA C	-	YRSKGGAKDIIHTPSDTFKLL "SDKRLO	~
	8	ANTIFICES.		WVQKLRDESHRYAINFHRSTKLKNMK	_
	<u>{</u>			QIALLKEKGIGEASVKKLLDYI:GSFEAIE	
110000	4000	TANKO GAATATOO GAATAT		KASEQEKNAVLKKRI	
170041	- COS:	1300 1111AG1GGAATTTGTGTGTTCCTTACGCCTAAAAATTAAAAAATTTGAAAAATTTGATGAATTTACCATAAAAATT	1964	LVEYGFRLPSALDNRPLKFDEFIHKNC	
	AT	TOGGCCCTACA CAGGGCCTTTTACA CATTACA CAGGGCA TINGAGCCTTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		OFLFVSATPNKLELELSKKNVAEQIIRP	
	AA.	ANTICARGET CONTROLL IN CONTROLL OF THE CONTROL OF THE CONTROLL OF THE CONTRO	•	TGLLDPKFEVRDSDKQVQDL; -DEIKLV	
	AA	AATTATTATECTE AATTECECE CONTRACTOR OF THE CONTRA		VARGERVLITTLTKKMAEELCKYYAEW	
	<u> </u>	CONTRIBUTE OF THE SAME OF THE	=	GLKARYMHSEIDAIERNHIIRSLRLKEF	
	3 5	THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TO THE TREE TREE TREE TREE TREE TREE TREE		DILIGINLLREGLDLPEVSLVAI WDADKE	
	<u>و د</u>	ACCUSATION AND THE ACCUSATION OF THE ACCUSATION		GFLRSETSLIQTMGRAARNANGKVLLY	
_	2	TACTTACACCULANT SECRET OF THE	_	AKKITQSMQKAFEITSYRRAK QEEFNKI	
	5 5	TACANGA TACANATA TACA	-	HNITPKTVTRALEEELKLRDDEIRIAKAL	
	<u> </u>	MANAGED AND AND AND AND AND AND AND AND AND AN	=	KKDKMPKSEREKIIKELDKKMIRECTKN	
	ξ <u>ξ</u>	CANAGE AND THE CANAGE AND THE CONTROL OF THE CANAGE AND THE CANAGE	_	LDFEEAMRLRDEIAQLRTL	
,	90	OTTIONGAMATINGCILGAATTAAATTAAATTAAATTAAATTAAATTAAATTAAA			
HP0821	1965 AG	1965/AGGGATTAAAAAAGGGTGTTCAAAGACAGGAAAAAAAAAA	7000		
	<u>უ</u>	GCCTATACCGCATTGCTAAAAAAAAAAGACCGATACGTCTATTTATT	0081	1909 GLKAVFKUSKKUACGFIYEISE-FMKAYT	
	TA.	ATTTAACGACTGCCCTTTATGTCAAATACCCTGATTTTGACGCTTTGAAAAAGCTTTTGGTGTCTTATTATTATCCAAA		NAKYBOSOA! WILLAT LFSKTWASIL! IA	
	<u>5</u>	CTTGGATTGCAGGAGGACGATCACGCGCATCAAGCAAACCAGTATCAACATTATCAAAAACGTTAAAAGCAATAAA	<u>-1_F</u>	LIVATEDALANELVOITTU WAGG	
	AGC	AGCGTTGAAACCATCAAAGAGCTTATATTGAATAGCATCGACTCTATAACACCCTTTGATCAATACCTCTATAACTTAT	<u>- 0,</u>	SIDSYNTEDOYI YNI WDSSSVYHSKW	
	<u> </u>	GGGATAGCTCTTCTGTTTATCATAGCAAATGGGTGCGTCCTGTCTTAGCCCTAGCTAATTATTTCATGGCAGATGAAG	ڍِ	VRPVI AI ANYEMADEEKPHEIAMDAET	
	AG	AGAAACCCCATTTTATCGCTATGGATGCCGAAACCCAAGTGGAGCATATTTTGCCACAAACGCCCAAAAAGAGGCCAGT	<u>. </u>	OVEHILPOTPKRGSOWNADFIJKEKRE	
	3 8	CAA! GEAACECEGA! I I GACAAAGAAAAAAAAAAAAAGAAATGGGTAAATAATGGCGAATTTAACCCTTTTAAAGGGT	w	EWVNNIANLTLLKRKKNAHALNGDFDE	
	AA C	AAAAAAAGAACGCGA I GCTTT AAACGGGGGATTTTGA TGAAAAAGAAAAATTTA TGGAGGAAAGAAA	<u>×</u>	KRKIYGGKDTSKVISCYDITKELYSNYR	
	¥ 5	CALINE TETETO A LIBERTAL CACITACA AGASTITET TO THE CONTROL OF THE	<u>×</u>	KWNEKSLOERYKSLYNTITPVLHIE	
	\$	CARALULI GI AI AACACI AI CACGCCI GI I I I ACACAT AGAGG	_		_

HP0389	1967 AATTGTGCT TGGGATCAG	1967/AATTGTGCTTCACGCTTTATAACGCTGTGGGCGATAGCGTGCTGACTTCTACAGGGTATCATTATCCATGTAGGGACTA TGGGGATCAGCTATCAAATACATGGTAGAATAATTGGGAAGAAAAAAAA	1968	1968 LCFTLYNAVGDSVLTSTGIIIHVGTMGS
	ATAACGACT	ATAACGACTGCGCGATTGGGAATGTGCACCCATGCGATATTATGACTCTTGTGCCTATTTTCCACGATGAAAATTGA	•	AINT MYENNWEDNPGINDKDIFT INNDC
	TTGGGTGG	TTGGGTGGGTAGGCGCGTTACGCATGTGATTGATACCGGTTCGGTTACTCCAGGATCGATGAGCACTGGACAGGT	-	VTHVIDTGSVTPGSMSTGQVQRFGDG
	TCAAAGATT			YMITCRKTGANDESFKDWLHESQRSV
	ATGAATCTC	ATGAATCTCAAAGATCGGTTCGCACGCCTAAATATTGGATTCTAGATGAAAGGACTAGGATTGCAGGATGCCATATG		RTPKYWILDERTRIAGCHMIRDLVMEVI
	ATTAGGGAT	ATTAGGGATTTAGTGATGGAGGTCATTAAAGAAGACGGCATTGATTCTTACATGCGATTTATTGATGAGGTGATTGAA		KEDGIDSYMRFIDEVIEEGRRGLISRIKS
1	TGTGCCTTA	GAGGCATATGCGCATAAGGATATTGGCG TGTGCCTTATGCGCATAAGGATATTGGCG	•	MTIPGKYRKVAFVDVPYAHKDIG
HP0389	1969 CTAAAAAT	1969 CTAAAAAATATTTAGAGGCCAGCGCTTATGAGGTCATTTACAACCACCTTTCTTACAACATGAGATTTTAGACAAATA	1970	1970 KKYLEGSAYEVIYNHI SYKHEII DKYLET
	CATAGAGAC	CATAGAGACTAACACGGCTGTTTTGGATCAAAAAGACGATATTTTTCTGTCGCTACGATTTTAAGGCATTTGGG		NTAVEWIKKDDIESVATII RHI GYECI S
	TTATGAGTG	TATGAGTGTTTGAGCGAAATGAGCGCGATAGATTTGTGCGCTAAAAAAGGGCCATTTTGAATTGTTTTATCAGTTCGT		EMSAIDLCAKKGHFELFYOFVGFSDSC
	GGGCTTTAG	GGGCTTTAGCGATAGCTGCAAGAACCGCCGTAGGGTGCGCTGAAGTGCGTTTTGTTGCCTAATGAGAGCGTGGAT		KNRRRVRVKCVLLPNESVDSLSFLYRS
	TCTTTGAGT	ICITIGAGITITITATACCGATCGGCTAATTGGAGCGAAAGGGAAGCGTATGACATGTTTGACAAA		ANWSEREAYÓMLGIVFÓKHPYLKRLIM
	CACCCIAT	CACCCCIATI IGAAACGCCTTATTATGCCGCATGATTGGGCTAGGCCACCCATTATTGCGCTCTTACCCGCTCAAAGG		PHDWVGHPLLRSYPLKGDEFAQWYEV
,	GAGACAGC	GAGACAGCCCAAGAGTGGATGAAAAAGACACTTTCAATTTTTCCAAAATTGGCTTTGAAGAGAGGG		DRIFGKEYKEVVGKEURUSAKVDEKD TENEAKIOVEO
HP0389	1971 GGATGCAAA	GGATGCAAATCCCTGAGAAGGATTTAAGAAAATCAAGCACATGAACAATTGGATGCCTCAAACAAA	1972	1972 MOIDEKOI BKIKHMKNIWMDSTNIIGEID
	тсссетес	TCCCGTGCAAGGCGATCACAATGTGCTTACCTACTTTAACTACCAACGCTCTTTCGTCCCGCCTCAATTAGACGTTT	5	VOGDHINVLTYENYORSEVPPOLDVI S
	TGAGCTATG	TGAGCTATGGAGGAGCGGAGTATTTTACCCAGCACTTTGACACGGTGGAAGCAGGAGCGCGCTACACCTATAAGGA		YGGAEYFTQHFDTVEAGARYTYKDKF
	TAAATTCAG	TAAATTGAGCTTCAATGCGGACTACATCAGGATTTGGGCGCGCGATTTTGCCACCGGGCAGTATTCAGTCTATACAA		SFNADYFRIWARDFATGQYSVYTSGP
	GCGGTCCCA	GCGGTCCCATGAAGGGTAATGTGCGCCCCATTAATGGCTATTCTCAAGGCGTGGAGCTGGAATTGTATTACAGGCC		MKGNVRPINGYSQGVELELYYRPIRGL
	IALIAGAGG	IA I ASAGGET I GCAA I I CCATTI CAACTACATT GACACT GTGTAACCAGCCAT GGCCCTTTAACCGACTT	=-	QFHAAFNYIDTRVTSHGPLTDLNGDVL
	SAACGGGG	SAACSESSA IS ISC AAAASSA ASCA ACCA ACCA IT CCCTTTISTA GCCCTTT CCAATT CATT CTT GACGC		KGTSYNKHFPFVSPFQFILDARYNWRK
	1001 ACAM	I COLITACAMI I GECCO I AAAACCACCACCAI CGG I ATTITATA OT GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		TTIGISSYFYSRAYSGISNSAAGGYYG
		ANTOCON CONTROL OF THE CONTROL OF TH		MOYYSGGNNYESVLNSGYQCEAWCM
·	ATTTGG	ATTTCTGGGAAAACGGGAGACACAACACAACATACAAGGAAGCTTCAAAAAAAA		TOHEGLLPWYWWNIQVSQIFWENGR
	ACAGGGATT	ACAGGG TT GGCTCTACAGGGGTGCAGAGGGTTGCAACCTGCGCGTGGGAAGATCGGGTAACAAGAAAATAATATAAAAGAAAAAAAA		HKV I GSLCIINNIFNIMKYYF I GIGSSPA
	CTAAAGGCT	CTAAAGGCTTTAAAAAGGAGGGGGTTATTGCGCGATGATGAGCCGCTCAAATTAGCCGCTTAGCGATTTTATTGAAA		פרמישופעס או או האווים
	TGATGAAATC	TIGATGAAATCTTCATTTAA	;	
HP0268	1973 ACTTCTTTAA	ACTICTTAAACAAGCTCATTTACACAGGGCAAATCATTCCTGATAGGGGTTCGTGGTTGTATTTTGAATACGATTCTA	1974	1974 TSLNKLIYTGQIIPDRGSWLYFEYDSKD
	AACAAGACA.	AACAAGACATCATCAAAATGTTCTACCCCCTTGTTAAAGTGCCTTATGAAAAAAAA	٠.	VLYARINKRKVPVIILFRAMDYQKQDI
-	ATTAGACGC	ATTAGACGCCAATCAAAGAATGGAATTTGACTTGAAAGATCCTCAAGGCTAATTCTTTTAGCGGTAAAAAAGCT		INMET PLYKYKTENDKYLIPFASLDANG RMEEDI KOPOGKVII JAGKKI TSRKIKE
	CACTTCAAG	CACTTCAAGAAAGATTAAAGAGGTTAAAGAAACCATTTAGAATGGGTGGAATACCCTATGGATATTTTACTCAATCG		LKENHLEWVEYPMOILLNRHLAFPVMV
	CCATTTAGCT	CCATTTAGCTGAGCCTGTTATGGTAGGGAAAGAAGTCTTATTGGACATGCTCACTCA		GKEVLLDMLTQLDKNKLEKIHDLGVQE
	AAAATCCAC	AAAAATCCACGATTTAGGCGTGCAAGAATTTGTGATCATCAACGATCTGGCGTTAGGGCATGACGCTTCCATTATCC		FVIINDLALGHDASIIQSFSADSESLKLL
	AAICIIII I			KOTEKIDDENALAAIRIHKVMKPGDPVT
	CONTINUE	CONTROL OF A CONTR	=-	TEVAKQFVKKLFFDPERYDLTMVGRM
	GATTACATTA	IOTTI GATICCAGARGECTITAACECATGAGGATATTATCACCACGTTAAATACCTCATGAGGATCAAAAAAAA	<u> </u>	KMINHKLGLHVPDYITTLTHEDIITTVKYL MKIKN
HP1236	1975 AGTCGCCAAV GGAATTTGAA	1975/AGTCGCCAAATACAAATATGTAGATGTGTGCCAAATTACTCCTCACAGGGGGAATTACCCCAAAATCAAGATGAAAGCTT	1976	1976 VAKYKYVDVČKLLITGELPKNODESLE
			-	

Г	•
	٩
~	٦

02/066501			PC1/EP0
1978 GKKVKKTYLALAHGLVEKSMKIDKPILT PQNIQKDLHIRSKISPLGKQSITLVEPLS YNPFLDISLLKITPLTGRTHQIRLHLSSV DHRIVGEGLYGVADENVREYLQLKRE NNAPLLMLHAASLEFEFKGAIYKIASPM PERFMPFLKDLSFFY	GOGGIGANA DE LA CONTROL DE LA CONTROL DE LA COGGIGA DE LA CONTROL DEL CONTROL DEL CO	1982 GADEVICUEDILI INSELEMINEAPINE HIGGYLGNAQSLENESI-ENHYLEAPINE ANAVFKSKEINKIPAPLEYSKGNHAKIK QLKLDLSKLRTKFYRLDLFKQHKS	SVHALDVGAMSVFLYAFKTREYGLDL MEDYCGARLTHNAIRIGGVPLDLPPNW LEGLKKFLGEMRECKKLIQGLLDKNRI WRMRLENVGVYTQKMAQSWGMSGIM LRGTGIAYDIRKEEPYELYKELDFDVPV GNYGDSYDRYCLYMLEIDESVRIIEQLI PMYAKTDTPIMAQNPHYISAPKEDIMT QNYALMQHFVLVAQGIMRPPVGEVYAP TESPKGELGFFIHSEGEPYPHRLKIRAP SFYHIGALSDILVGQYLADAVTVIGSTN AVFGEVDR
197	5	96 196	
1977 GCAAAAAAAGTTAAAAAAGATTTAGCACTAGGGCATGGGTTGAAAAAGCATGAAAATTAGACAAACCCAT TCTAACGCCACAAAACATTCAAAAAGATTTTGCATTTGGATCTAAAATTTTTGGCATCAACGCCTT TCTAACGCCACAAAACCATTCAAAAAGATTTTGGATATAAAGCCTTCCTT		1981 TGGTGCTGATGAGGTTTTTTTTTTTTTTTTTTTTTTTTT	1983 CCTTACTCAATTTAGAAATCCCAGGCCGAGGGGGCATGAGCGTTTTTTTT
HP1236	HP1236	HP1236	HP1236

	_	,
1	Ξ	•
Į	C	٦
1	г	•

HP0909	1985 TACCAATTTATCCTAACAAGTGGTGGTTGTCCCGCAAGGTTCGCTCAAAAAGGTTTTTTTAAAAGGCAAG GCGTGGATATTATCCTAACAAGTGGTTGTCTTTTTTACGCCTGATGGGCAAAAAAGGTTATATTGATGGGCG ATGGGGAAAGGGGAATTTTTTTTTT	1986 PIYPNKVVVVPQGSLKKVFFSLKEĞGV DMNALDLLFLRLMGMPKKGYIDMGDG ALRKGDFLVRLIKAKAAQKSATLIPGES RYFFTQILSETYQLETSDLNQAYESIAP RLNGEVIEDGVIWPDTYHLPLGEDAFKI MQTLIGQSMKKHEALSKQWLGYYHKE EWFEKIILASIVQKEAANVEEMPLIASVI FNRLKKGMPLQMDGALNYQEFSHAKV TKERIKTDNTPYNTYKFKGLPKNPVGS VSLEAIRAVIFPKKTDFLYFVKMPDKKH AFSATYKEHLKNINLSNNHF
НРО909	1987 TAGATACTATTCTGAAGTTACTCTTATAGGGGGGGGGGG	1988 DTINLSEVTLIGGGGDSSPFQTFVFSHS QEAVDKSVENLKKFLLESPELKGKVES YHTSTSESQPQLQLKILRQNANKYGVS AQTIGSVVSSAFSGTSQASVFKEDGKE YDMIRVPDDKRVSVEDIRKLQVRNKY DKLMFLDALVEITETKSPSSISRYNRQR SVTVLAEPNRNAGVSLGEILTQVSKNT KEWLVEGANYRFTGEADNAKESNGEF LVALATAFVLYMILAALYESILEPFIIMV TMPLSFSGAFFALGLVHQPLSMFSMIG LILLIGMVGKNATLLIDVANEERKKGLNI QEALLFAGKTRLRPILMTTIAMVCGMLP LALASGDGAAMKSPIGIAMSGGLMISM VLSLLI
5050A	IBBB ICCAAAAGAATI ITAAAAAAGCGATCACCCAACAAATCGCTTATTTTTAAAAGATAAAAGTGCTTTTTATTCTCAATGTTT CAGGCAATGTTTTTTTTTT	1990 ÖKEFKKAITÖÖIAYFLKÜKSAFILNVSG NVFFSFEENPKDLKAIKERLKKTIEPNA DPKAVMRFLNLQASLILECVPQTTCPF DTLLIPTAFSVPVYYANRLGDNPSLFSQ EDKTYHNALIKALNKAYYSLMEGLEKR LNAIKNAEWI.
HP0909	1991 TAAGGTGAAATTGAGTTTTAAAAGCGTGGCTAAAGTGTTGGAAACCATTGATGAAAACAAGTTTAATGAAAATTAAAAAAAA	1992 KVKLŠFKSVAKVLENIDENKFNEIKKNE DEGLRRLEELFLEINQNIKDKISYQMR ETTIKNRKNDAFYDEKGEIREFLDGSL GADKYEIKNSSVREKCLYENFMQVDS EIEKDTIEESNDTKIIVFGKLPR

02/066501		101/2101
1994 AVEHAKKFGISFLSFQETTIAEAMQAM QAQATVLEIDASKKFAKMQETLDFIAER LKNYKKKGVELFHKNNKISGHQAISS DILEKGGIDNFGLKYV, KFGRAGHQAISS VKENPEIIFIWWISPLT "EDVLNNPKFAT IKAIKNKQVYKLPTMD GGPRAPLISLFI	1996 ASHIQGPLLILAGAGSSÄKTKTLTSRLAY LIGVCGVPSENTLTLT-TNKASKEMDE RALKLKNOALIPPLLCTFHRFGLLFLR OHMNILKRACDFSVLDSDEVKTLCKQ LKISNFRASISQIKNGMMDLSMADSEC YKAYELYQNALKKONI.VDFDDLLFLSL KILQDNETIAKETSERYHYIMVDEYQDT NALQLEFLKKLSFTHHNLCVVGDDDQS IYGFRGADISNILNFSKHFKGAKIVKLET NYRSSAEILACANSLISHNQHRHIKTLQ SFKGSHKSVVCKEYLTGKESLDVAY QIKALLKKGENLENIAII.YRLNGLSSIE ESLNALNIPYRLIGALSPYERAEIKDALA FMHLVAKKDDRFFIKRVLNKFPRGLGK ITQEWIFSLLDEGGLNI.EEALKLGAFKD KLNPKNEYALKGFIAM IGRLREAFEISV EEFCSRFLEETNLLKS YEKEDNYEERE GFVKELLTLVKEYFKTNPTHSLLDFLNE SVLDAHNTENAGELOLSYVKERSYF GRKISCSPSVFLEEACILLNODNPPKOD HQKDAPIKYGDLRHKIFGTGRVLGVEK GLSGLCLKINGGGNVYDKISEKFVEKV DNGF	1998 VLNAFI LEDIGELSSWAGDINDLONDL GLFLKKSALDIYDYLLKEGKKDADILRG LERYFYQLFLFFAHIKI TGLMDAKEVLG YAPPKEIAENYAKNALRLKEAGYKRVF EIFRLWHIQSMQGQKIELGFLYLTSIQKII NP
1993 AGCGGTAGAGCATGCGAAAAATTTGGTATATCATTTCTTTC	1999 TGCAGGCACATTCAAGGGCCATTGCTCATTTTAGCGGGAGCGGTAAGACGTTAAGCCTTTAAGCGTTTAAGCGTATAAGCGGTAAAGCGATAAAGCGATAAAGCGATAAAGCGATAAAGCGATTTAAGCGTTTTCACCATTAAGCGATAAAGCGGTTAAAAAGCGGTTTAGCGCTTTTCCACATTAAAGCGATTAAAGCGGTTTAAAAAGCGGTTTTCCATTTCCATTTTCCATTTTCCATTTTCCATTTTCCATTTTCCATTTTTCAAAAAA	1997 GGTTTTAAACGCACCCATCACTTTAGAAGACATTCAAGAATTAAGCTCCAATGCGGGGGGATATGATTAAAAGAAGAGTGCGGGGGGGG
HP0909	HP1478	HP1231

HP0262	1999 TAT	TITAAATTITGAGCCTGAAAGCTCTGTGGCGTTGGCTTTGGCTTTAGGG	2000 LKLOLNDCALNFEPESSVAI GFGFRVG
	ACC		FLGLLHMEVIKERLEREFGLNLIATAPT WYEVHLTDNSIKYYONPSELPPENCIA
	Y E	CCCTGAAAATTGTATCGCTTGCATCAAAGGCCTTTTGTGAGGGCGACGATCATCACGCCGAGTGAATTTTTGGGTA ATTTAATGCAGTTATTGAATAATAAAAGGCATTCAAGAAAAAAAA	CIKEPFVRATITPSEFLGNLMQLLNNK
	ATT.	TTATTCCTTGCCGAGCAATGAAATTGTGATGGATTTTATGACAAACTCAAATCTTGCACTAAAGGGTATGCGAGCTT	MDFYDKLKSCTKGYASFDYEPIENREA
	2	IGA IAI GAGCCIAI AGAGAACAGAGAAGCTAACTTGGTGAAATTAGATGTGAGGGTGGCGGGGGGGTGGGGGTT GAGCTTTCTATCATTATAAATAAAAAAAAAAAAAAAAAA	NLVKLDVRVAGDVVDALSIIIDKNKAYE
	<u> </u>	OCCAAGACAGCTTTTGAAGTCGCTATCCAAGCGAGCGTGGGGAATAAAATCGTCGCCAGAGAACGATCAAATCTG	KGRALVETMKELIPROLFEVAIOASVG
	<u> </u>	TCGGTAAGAACGTAACGGCTAAGTGCTATGGGGGCGATATTACACGAAAAAGAAAACTCTTAGAAAAGCAAAAAGAG	RKLLEKOKEGKKRMKAIGKVELPQEAF
	999	GGGGGTTTAGCTTCTATGGCAAAACTAAAGAACTATGAAATTTTAAAGAAGCGTTTTAGCGATATTAAAGATCGATTA	LAILKID
	ATG	ATGATTITATTAAAGAATTTGGCTTTTCTACTAAAAATGCTTTTTTGAATATTGTCCAAATTGGCCTAGCTGACGG	
НРАЗВЗ	2001 500	TAACCIT AAAAA TGCCTTAAT GTGAT GAT GACCAACTTAAAA CAACATAATAA AAAAAAAAAA	
7070	, –	SCCTIMITION OF STREETS OF STREET STREET STREET STREETS STREET STREETS	Z00Z JELAFSNLKKCLIVDVSELNAYLLAAFSS VVVMEEAAFOHVVODKTFF
	ATC	ATCATGGATATAAAGTCAATTCTTTACACTGAAAAGTCATTAGGATTGCAAGAAAAGGTGTTTTAGTGGTTCAAACG	
	ပ်ပွဲ	GETCAAAATGTAACCAAAAACCAGCTCAAAGAAGTGTTTAAAACTTACTT	
	¥51.0	16AAACAAGAAGG1AAGG1GAAACGC111AGAGGGAAGC1TGGACAAAGAAGAGCTTTAAGAAATTTTATGTGAAA	
	190	OTTOCACACCCAAGCAGACCTTCATGTCGGTGTTTGCACTCTAAAGGATTACCGCAAAAAAGGAAAAAACCAAAAAAAA	
	CTC	CTCACTAAGCTTAAAGCAACAGCAGGGAGAACAATAACGGGCGCATCACCAGCCGCCCACAAAGAGAGAG	
	AAA	<u>AAAAACTCTATCGCATTATTGATTTCAAGCGCAATAAATA</u>	
HP1230	2003 TCT/	A	2004 YDWIKEFVRÖGGEFIAGGSGWLELER
	31 9 0	GCGATCAAGCTATGCCAAACTCATCGCGCAAACCATCTCGCATGTGCTTAATGGCGGATCGCTGTTGGTGAGCGCG	SSYAKLIAQTISHVLNGGSLLVSADSSR
	1 4 C	GATTOTICIAGECACTGGTTTTTATAACTACACTACTACTACTAAACCTAAACCCCAAAGATTTAAAAGAGCGCCCCTTATTGT	HWFLIVYILSNLNPKDLKERPLLSVIDFN
	ATC	ocercentration of the control of the following and the control of	ASSEYPKNDANLSLATIEMTYONPMFW
	<u> </u>	GITTI HATGGTT IT TGAAGAAGGTT AAAAGAATT COTT COTT TAAAAAAAA TAAAAAATT AAAAAAAAAA	TOO I THE SELVICE ON THE SELVICE OF
	ATTC	ATTGCAGCTCTTCAAACTCTTTGAAAACGCGCTTTTTAGCGTGCTATACAATAAGGTTACTCTGTGAAAAACTCCAAC	EDCELEKEMDSELDYKELGEFKEFENAL
	000	CGCCTTATTTATACGGACAATCTTGAAGAGGCCTAGAAGAGACTGCAAGCCTTTTGAACACCACATTAAATTCTAC	
HD1230	SUPPLICATE	AATOOTAAACTTAACTAATACAATAACAAAAAATAAAAAAAA	
007	AAC		ZOUGILALVKONPKVSLIEYENYFSOLKYNPN JASKSDIAFFYAPNÓVI CTTITAKYGALI
	99	\$	KEILSONKVGMHLAHSVDVRIEVAPKIO
	AGC	AGCGCCIAAAATICAAATTAACGCCCA	<u>NA</u>

HP0263	2007 AG	2007/AGCGTGGGCGATCCTTTTGATTTCAAAACAAAATCGGCGCTCTAGCGGAAAAAAAA	
	<u>8</u> :	CATAGATGAATTAAAAAGCTATGAAAATTACGAAATCCCGGTAAGCTTTGTCAATGATAACCCCTATTTGATGACCC	ZUUS SVGDPFDFKNKIGALADKPNEKVIKAID
	A A	AAGCATCAAATACGGCACTAAAAAAGGCGATTTCACGCACCAAACTGAGCTTTTTACGCCCATTTTATCCGTGATGGA	GTKKONETUOTEI FTBII SWITELED
·	35	ACCAMANGE I I AGACGAAGCGATAGAAATAGCCAATTCTACCGGTTACGGGCTGACTAGCGCGTTAGAGTCGTTGG	EALEIANGTONG TOOL OF DEPARTMENT OF DEPARTMEN
<u> </u>	3 5	ACCENTACION OF THE SECOND OF T	FRIEAGNIVINKPTTGANA BOBCON
	- F	THE CHIECECASCCI I I GGGGGGGGTTAAAAATCCGCTGTGGGGGTTTGGGGAAAGTAGGCATTTTCAACTA	KKANANGERINATION CHANGE AND THE SECOND CONTRACTOR OF CONTR
	¥ .	ANY CALGEGRAPH I TELEGRAPH A TELEGRAPH OF THE TOTAL OF TH	DENAL KND SEALENITO CYCYCLERE
	ATC	ATCATTACA A A CATTACA A TECANOLOGICAL CONTROL CONTROL CONTROL CANADA TECANOLOGICAL CONTROL CANADA TECANOLOGICAL CONTROL CANADA TECANOLOGICAL CONTROL CANADA TECANOLOGICAL CONTROL CANADA TECANOLOGICAL CONTROL CANADA TECANOLOGICA CANADA TECANOLOGICAL CANADA TECANOLOGICA CAN	LKRAIFMAKSYAVHYKHEESOTKOVA
	AGT	TARARGEGIGGECTATOCECATORICE AND SOLVE TO THE TOTAL TOT	RGEDNLFSYTKVKSVGYRITEKDTI SO
	Ě	TTCTCAAATCCCTTTAACGCTCAACATAAAAAAAAAAAA	MLGVALACLISQIPLTLSIENERTNKDLT
	AGC	AGCGCTCCAAGCAAGCCCCCCTATTGTTTATGAAAGCTTGCAAAAATTTAGCAAAAATTTAGCAAAAATTTAGCAAAAAATTAAGCAAAAAAAA	FFLECLKALQASAPIVYESLQKFSEKLN
	900	CCGTTATCTCAAAAGCGATTTGGATTTATTGCACGAAAGCGAACCGTTTACCAAAAAAAA	TFNRVRYLKSDLDLLHEQASALGMVLA
	CAT	CATGCCTAAATGGGC	TAKPCLNGREELLYYHLERSVSISYHR
HP0263	2009 TGA	2009 TGATGGCACTAAGTATGATAGGTGGGCGAAGGATTTTACCCCCCCAAGCTATTGGCATAAAACTTCTTGCGCTAATA	YGNLGSRVLRQPTCHK
	ĬĮ.	ATTCTATGAGTCTTTGTATGAATGCCACTAAAATGTGGCCAGCAATCAGGGCCAGGTGGTCATTAACCCTAAGAGGT	ZU10 DG1KYDRWAKDFTPPSYWDKTSCGT
	ALK	ALIGET I GEAT ACAT GGET GAAC GGCT TGTT CCCTAACT ACTAT CCGCT AACT GCT TACT TGCT TG	DOMOCCOMINA I KMWCCSGIPGGVINPR
	<u> </u>	CICAAGGCGCTATCAAGTCTATAAAGCAAATTTGACCTATGATAGCGACAGGGTCCATATGGGGCGTTTTG	GSDBYOLVANI TYPERE IN TABLET
	ACA	ACATIACCGAGCAGGAGCAAATGGATTGGATTTACCAATTGTTCCAAGGGTTTTATGGGACTTTCAAGCTCACTAAAA	GOTT TO TANK! TUSUK!/HMVMGK
00000	ATA	ATATGAAAT	FULL ECECIMOWIYOLFOGFYGTFKLTK
HP0263	71111102	2011 LI I GCAATTAAGGGAAAAGGCAGGATTTAGTTTCTTTAAGGGAGCAGATTTCCGCAATCAGATACCAAAACAAGCAACT	2012 I OI REPODI VSI REDISAIDVONIVOI NI
	ξ <u>Θ</u>	TEGE ATTITUTO CONTROLL OF THE SECOND TO THE	YYPKIDVEDSWI FWIOKPAYATGBEGNI
		CONTROL MANAGEMENT OF THE STATE	FYPGOONTAGYTATI NIEDDIG SI OK
	AAG	44CENCET AND THE SECOND TO THE SECOND TO THE SECOND THE	OSIMLGOLANEKNI AYKKI FIDEKNEDI
		GCCAATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	YRKSLDIARAKIESSKASI DAANI SEANI
	200	CONTROLL STATES AND AND AND AND AND AND AND AND AND AND	KRKYDANI VDETTYI RGI TI'REDAEVA
	ACAC	ACAGEGEGEGTATA ALTA GALCHARATTA CONTRACTOR CONTRACTOR AND ACT ACATTA CAT	YNLALNNYEVOKANYIENSCHKIDDYY
HP0263	2013 ATTC	2013 ATTCH GGGGCT AGGGAATCH A AGGGGATCH A A AGGGGT A AGGGT A AGGT A AGGGT A AGGGT A AGGGT A AGGGT A AGGGT A AGGGT A AGGGT A AGGT A AGGGT A AGGGT A AGGGT A AGGGT A AGGGT A AGGGT A AGGGT A AGGT A AGGT A AGGGT A AGGGT	I
}	200	CCAAAAATTGTAGGGCATGCTTGTGGGGTAAAAAGCAATTAAAAGGCAAGGCAAGGCAAGGCAACATTTAG	2014 FLGLGESEAFKKPSAPKSD/JKGYTLAD
	GTG	GTGGGCAGTCAAGACACCACCACACACACACACACACACA	KIVGHACGVKGILPGTYCEPKVTTVGS
	CITS CITS	CTTTGEGGGGGGTTTTGCCATACCGCCGCTTACCCCAAACCCTAACAAATTTAACAAAAAAAA	ODTTGAMTRDEVKELASLK -DAPFVLQ
	(GGC)	GGCTTTATCACTCAAAGAGGGGGGTGTGGGGTTGCGGGGGGGG	SFCHTAAYPKPSDVSLHATI.PGFITQR
	GAT	GATTGCCTGATACTTTAGGCACAGGGGGGGATAGCCACACCGTTTCCCTTTGGGCATTAGTTTCCCAACAGCAA	GGVALHPGDGVIHTWLNRNGLPDTLG
	991	ICIAGICGCITITIGCAGCGGTTACAGGCACGATGCCCTTGAACATGCCAGAATCTGTGTTGGTGCGTTTTAAAAG	TOTANDI MINDESIA VERMONISIA DELLA PARAN
_	5000	GEGEAPA I GAAT CCI GEGAT CACCTTA A GEGAT TTAGT GAAT GCAAT CCCTTATTAT GCGATTAAAAAA GGGTTACTCA	DI VNAIDYYAIKKEI I TVEKKEKINVEN
	500	OCCUPATION OF THE STANDARD OF	_
	GATG	GATGATTGAATACTTGAAATCCAATATCAACTATAAAAGAAGAAGAAGTGCAGGGGGCTTGCTT	AAACVVRLNKEPMIEYLKSNIKLIDEMIA
_	GAAA	GARAGARACCECCEARATECEA TECTOR A CONTROL LEAF LEAF LEAF LEAF LEATER GENERAL GARACCECT TATGARGATEA GARACTETT	_
	9009	GCCGCTGTCATTGAAATTGATGTGCCAGAAATCACCAATAC	
	TACT	FACTITICA GCGA A GTTT TAGC GGA T	
			_
			TEMECALCMGNCARVKDNAVVFSTS
			III GRIDTKEEVAANI VOEKI EGOVOVAD
			יייייייייייייייייייייייייייייייייייייי

c	4
r	ŋ
c	n

02/066501			PCT/EP01/15428
YMINEN		2016 INTMECATMARGVAEIVAVEATFTRAL PAFVISGLANSSIAEAKORVASALONN DFTFPPLKITINLSPSDLPKSGSHFDLPI ALLIALQKQELAFKEWFAFGELGLDGKI KPNPNIFPMLLDIAIKHPHAKIIAPKANE ELFSLIPNLQCFFVGHFKEALEILGNPE TKADTHTKKLPFKTIELNDKEYYFSDAY ALDFKEVKGAVAKEAALIASAGFHNLI LEGSPGCGKSMINRMRYILPPLSLNEI LEGSPGCGKSMINRMRYILPPLSLNEI LEGSPGCGKSMINRMRYILPPLSLNEI LEGSPGCGKSMINRMRYILPPLSLNEI	2018 YFGEGQICNFDGTTLVQGHRNPWEIVT GEIYPKMADNARLSWGLENNIYNLGHR GYVAKPGGEHDAGLTYIKDLAAGKYKL PWEDHMKIKDGSIYGYPTTGGRFGK
		00 31 A 60 00 00 00 00 00 00 00 00 00 00 00 00	\$\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
		2015 ATTAACACGATGTTTTGCGCCACCATGCAAAGGGGAGTGGCGGAATCGTGGCTGTGGAAGCGACTTTCACAAGGG CTTTGCCGGCGTTTGCATTTCAGGGTTAGCTAATAGCTCTATCCAAGAAGCCAAACAGGGGGTTTGCCTAATCGGCTTTA CAAAATAACGATTTCACTTTCCCGCCTTTAATCGCTTATGCAAAAAGAGGTTGGCTTTTAAAGAGTGGTTTGCCTAAATCGGGAGT CATTTGATTTG	TTGGTGAGGGGCAAÄTCTGTAACTT GGGGAAATCTACCCCAAAATGGCGGGG ATACAAATTGCCTTGGGAGGTACAT TGGGAAATAATCCCTAACCTTGCAT TCAATCAATTTTACGAATAGTTCCAT ATGGCCACAATAGATCATTCCGCT AATGGCCACAAAGATTCCCGCT CAAGATTGACAAAGAATACGGGTGG TTCGTTTGTCAAGGGGGGGGGTTGC AAATATTTTCTATCTCGCTAGGAATAGAAAAT
	 	HP0263	нР0263

~	٦
~	٦
~	1

OSSND OSSND ALLKTF HLREL AYAHG	KSSIAP QYQS VGQG KGKIVK GIDDQ LEAQV 'IALGH QTFAF	VLNAE COKVG AKDV LEIRT LENQI YIMKQ LSPTG KNME VELAK VRNTL
IHPNDDVNMS EITHRLLPSL = EITHRLLPSL = EITHRLLPSL = EITHRLLPSL = EITHRLLPSL = EITHRLLPSL = EITHRLLPSL = EITHRLTSL = EITHRLTSL = EITHRSL = EITHRSL = EITHRSL = EITHRSL = EITHRSL = EITHRSL = EITHRSL = EITHRSL = EITHRR = EITHRLTSL = EITHRR = EITHRR = EITHRR = EITHRR = EITHRR = EITHR	SFGARGSKRO SAVECKKTIKV DKALETCKQOI SAQTCGACQIS ILKDEEIDAIIFE YEKGKRGDI Y DLFIKAPVFFTI	QELVSVYYGM AYDKAHIASVK AYDKAHIASVK SSKDDLVPSEK STLNSYPVLKT STLNSYPVLKT (FLPQVSFFGS) VFVGVAGRMPI LQVSSEQIQAK YLKEYKSLLSS AGLSTNAQVII) KYIVSLANL
2020 EILGGNFREKKLIHPNDDVNWSQSSND TFPTAMHIVSVLEITHRLLPSL ENLLKTF KEKSQOFKEIVKIGRTHLQDATPLTLG QEFSGYASMLEHSKQQILESI.EHLREL AIGGTAVGTGLNAHKELSEKVAEELSQ FSGVKFVSAPNKFHALTSHDANAYAHG AFKALAANLMKIANDIRWLASIPRCGL GELNIPENEPGSSIMPGKVNPTQCEAM TMVAVQVMGNDTAIGIAASQSNFELNV FKPVIIYNFLQSLRLLSDSMESFNIHCA SGIEPNREKIDYYLHHSLMLVTALNPHV GYENAAKIAKNAHKKGISLKESALELKL LSAEDFDKFVVPEK	2022 EDLGSFFEDAFGFGARGSKRJKSSIAP DYLQTLELSFKEAVFGCKKTIKVQYQS VCESCDGTGAKDKALETCKQCNGQG QVFMRQGFMSFAQTCGACQ3KGKIVK TPCQACKGKTYILKDEEIDAIIFEGIDDQ NRMVLKNKGNEYEKGKRGDLYLEAQV KEDEHFKREGCDLFIKAPVFFTTIALGH TIKVPSLKGDELELKIPRNARDKQTFAF RNEGVKHPESS	2024 NEVYRLKKI.STFQELVSVYYGMVLNAE VAETLEEVEKGHYKHFQNALKMQKVG QIARVETLGAQVAYDKAHIASVKAKDV LEVSQLSFNSILSSKDDLVPSEKLEIRT EKNLPDLSFFVSSTLNSYPVLKTLENQI QISKENTKLQIAKFLPQVSFFGSYIMKQ NNSVFEDMIPSWFVGVAGRMPILSPTG RIQKYQASKLAELQVSSEQIQAKKNIME LLVNKTYKETLSYLKEYKSLLSSVELAK ENLKLQEQAFLQGLSTNAQVIIDARNTL SSIVVEQKSVAYKYIVSLANL
2020	2022	2024 1
2019 GAAATTTTAGGGGGTAATTTCAGAGAGAAAACTCATCCACCCTAACGATGACGTGAACATGTCTCAAAGCCTCAAGCTCCAAAGCTCCAAAGCTCCAAAGCTCCAAAGCTCCAAAGAGCTCCAAAGAATTTAAAAGAAATTTAAAAGAAATTTAAAAGAAATTTAAAAGAAATTTAAAAGAAATTTAAAAGAAATTTAAAAGAAATTTAAAAGAAATTTAAAAGAAATTTAAAAGAAATTTAAAAGAAATTTAAAAGAAATTTAAAAGAAATTTAAAAGAAATTTAAAAGAAATTTAAAGAGACTTTTAAAGAGAATTTAAGAGAGCTTAAAGAGACTTTAAAGAGAATTTAAGAGAGCTTAAAGAAATTCGTCTGCGCAATAAAGAATTTAAGAGAATTTAAGAGACGTTAAAAGAAATTGAGAGAATTTAAGAGAATTTAAGAGAATTTAAGAGAATTTAAGAGAATTTAAGAGAATTTAAGAGAATTTAAGAGAATTTAAGAGAAATTTAAGAGAATTTAAGAGAATTTAAGAGAATTTAAGAGAATTTAAGAGAATTTAAGAGAATTTAAGAGAATTTAAGAGAATTTAAGAGAATTTAAGAGAGAATTTAAGAGAATTTAAGAGAATTAAGAGAATTTAAGAGAATTTAAAGAGAATTAATAA	2021 GAAGATTTAGGCTCGTTTTTGAAGACGCCTTTTGGGTTTGGCGCTAGGGGGGGG	2023 AATGAAGTGTATCGTTTGAAAAAGCTTTCCAAGAGCCTTGTGAGCGTGTATTACGGCATGGTGTTAAACGCA 2023 AATGAAGTGTATCGTTTGAAAAGCTTTCCACTTTTCAAGAGCTTTTTTTT
HP0263	HP0263	HP0263

7	7	Г
•	•	٦
r	•	1

02/066501		PCT/EP01/154
2026 ALLQKALKLYALLKPLELNVSIASSFSKI GNLFGRELESFCVKIQPKNTRALNSEK LYLKLFQKGVIARISCEFVCFEVFSLNE KDFEKIALVLEEILNKA	2028 EKQDLSYLFISHDLDVIKAFCDKVLVISE GKVVEMNTIKEVFDNPKHAYTKRLLES RL	2030 FCAIILDLAVGLIKIIY
		2029 ATT-TGCGCTATTATATATATGGACCTAGGGTTAATTAAAATTATTGAGTTGAATTCAAGGAGTAAAACATG GCATTGTATATATTGGAGCGTATGCGGAATTCTTATTGAGAGTTTATTGGGAGTAAAGGAGTAAAAGTTTT GCATTGTAAAACGAGCGAATTCTCGTAATGCGTATGCGAATTCTTTATTGGGAGCTGATTGGGAGCTAGTTATTGGAATTTTC AAGCCGTAGTGCAGTATAAATGGGTGTTTTTTTTTT
HP0263	HP0224	HP0224

2/066501		PC1/EP01/15428
·	2034 QRQAVPLLRSDAPIVGTGIEKIIARDSW GAIKANRAGVVEKIDSKNIYI.GESKEE AYIDAYSLQKNLRTNQNTSFNQVPIVK VGDKVGAGQIIADGPSMDRSELALGK NVRVAFMPWNGYNFEDAIVVSECITKD DIFTSTHIYEKEVDRELKKÜVEFTAD IPDVKTSPKGEIKSTPEERLLTVSAG MILVGKTSPKGEIKSTPEERLLTVSAG MILVGKTSPKGEIKSTPEERLLTVSAG MILVGKTSPKGEIKSTPEERLLTVSAG MILVGKTSPKGEIKSTPEERLLTVSAG MILVGYEKDARVLSAYEEEKAKLDMEHF DRLTMLNREELLRVSSLLSCAILEEPFS HNGKDYKEGDQIPKEEIASII.RFTLASL VKKYSKEVQNHYEITKNNFLEQKKVLG EEHEEKLSILEKDDILPNGVIIKKVKLYIA TKRKLKVGDKMAGRHGNKGIVSNIVPV AD	2036 KKTFFQAPLRFGFIVDFIGYL SLQLGIE MPLVRNVFYTYNNHQERFKPRFNANL SLIVSF
2031 CGTTACAAGTCTTGCAAATCGCTTGCAAAAAGCTTTTCAATAAGAGCATGGGTTTAGAAGAGATAAAAGACGCTTTGCAAG CTTCTATCATCAACAACAGGAATTGCGAGAAATTGTAGAAATTGCCAGTTTTTAGCCTCCCCTTTGTTTG	GCGGTGCCTTATTAAGAA SAGCGATCAAAGCCAATCG AAGAAGCCTATATGATGC CGTTAAAGTGGCGATAA GTTAGGGAAAAATGGCGTT TGCATCATTAACGCTT AAGTCGATATTTACGCCT AAGTCGATATTTAGGG GAAGAGCGCTTTTAAGGG TTTGGAAGAAAAGCCA TATGAAGAAAAAACCA TATGAAGAAAAAAAAAA	2035 CCAAAAAACCITITITCAAGCCCCTTTGCGTTTTGGTTTTATCGTGGATTTTATCGGCTATTTGTTTG
HP0224	HP0224	HP0109

	_
V	
C	'n
•	•

2/066501			PCT/EP01/15428
2038 RYTETRPIAF	2040 GESADEMLETIAHTAPLLPKDKPRYLM GVGTPENILDAISLGVDMFDCVMPTRN ARNATLFTHSGKISIKNAPYKLDNTPIE ENCACYACKRYSKAYLHHLFRAKELTY ARLASLHNLHFYLELVKNARNAILEKRF LSFKKEFLEKYNSRSH	2042 AKEDALKARKKLLNNTHDFLEDLIFRKO KIKELMDHRAKYLSDLENKYKEKEAL EKETRGKILTAKSKAYGDLEQALKONP LYRKLLPNPYAYVLNQETFTKEDRERL SYYYPQVKTSSIFKKTTATTKDKAQALL OMGVFSLDEEGNKKASRLALSYKOAIE EYSNNVSNLLSRKELDNIDYYLQLERN KFDSKAKDIAQKATNTLIFNSERLAFSM AIDKINEKYLRGYEAFSNLLKNVKDDVE LINTLTKNFTNQKLSFAGKQKLCLLVLD SFNFDTQSKKSILKKTNEYNIFVDSDPM MSDKTTMQKEHYKIFNFFKTVVSA	2044 DANHKIISIETNKERYLVILSDKYGLILD KISPKTSKEELIKEAENNIKNSKLGNLYA GKF ZO46 LEYSRĞSVYLQVYQQYYEYFINILARMI ALQKKLEQIKTDIKRVTKLYDKGLTTIDD LQSLKAQGNLSEYDILDMQFALEQINRL TLEYLTNLSVKNLKKTTIDAPNLQLRER QDLVSLREQISARYQNKQLNYYPKIDV FDSWLFWIQKPAYATGREGNYYPGQQ NTAGVTATLNIFDDIGLSLQKQSINLGQ LANEKNLAYKKLEQEKD
2037 CGCTATACAGAAACGCGCCCGGATCGCATTTTAGGAGTGAAGTTACCCAAAGCCTTAAAAGAGCCACGCAGGAGCCAGGAGCCAGGAGCCAGGAGCCAGGAGCCAGGAGCCAGGAGCCATAAAAGAATTAAAAAGAGCCTTGAGAAGCACTCAATAAGCGATTTTAGTAAAAAGCGAGCG	2039 GGGGAAAGCGCTGATGAAATGCTAGAAACCATCGCGCACCCGCCCCTTGCTCCCCAAAGACAAGGCCTCGCTACT TAATGGGCGTAGGCACGCCTGAAAATATCCTAGACGTTTCGGTTTGGATTGCTTTGATTGCGTGATGCCC ACCAGAACGCCAGAAACGCCCATTTCACGCATTCTGCAAAATTCTATCAAAAACGCGCCCTATAAATTGGAT AATACCCCTATTGAAGAAAATTGCGCATGTTATGCTTGCAAACGCTATTTTAAAGACCCATTTAGGG CTAAAGAACTCACTTACGCTGGTTTGGCCAGCTTGCAATTTGCATTTTAGAGCTGGTGAAGAACGCCAGAA ACGCCATTTAGAAAAGCGGTTTTTGAAAAAGAGTTTTTGCAATTTTTGGAGAATACCAGCTCTCATTGAATGAT GGAATGCAAAAAATCTAAAAAGCGGTTTTTACCATCAATAAAAAGGGTTTTTTAAAAAAAA	2041 IGCAAAAGAAGACGCTCTTAAGGCTCGCAAGAAGCTCTTAAACAATACGCCATGATTTCTTAGAAGAAGACTTGATTTTTAG AAAACAAAAAGAAAAAGAAAAAGAAAAACTTAGGACTTAGAAAACAAAAAAAA	2043 GATECGAACCATAAAATTCAATAGAAACCAATAAGGAGCGFTACTTGGTCTTACTAAGCGATAAATACGGCCTG CTITTAGACAAATATATAAGCCCAAAAACATCTAAAGAACTGATTAAAGAAGCTGAAAATATAAAAGAATTCAAAAT TAGGAAATTTATATGCCGGAAAATTCTAAACTACAACTGCTAGGTTGATTATTTGACCCTGTGGATCATTCTA ACAGGAATTTTATTGCCGGAAAATTCTGTCTGTATTGTTACACTGGTTGATTTTAATTTGACCCTGTGGATCATTCTA ACAGGAATTTTTCCTTCTCTTCT
HP0109	HP0261	HP0261	HP0261

70000	2002 SOURCE STREATE A TEXAS CONTINUE OF TRACECT TRACECT TO THE GITATE AND TAKE THE STREAT AND THE STREAT OF TRACECT AND THE STREAT OF THE STRE	2048 PIDESLIKEEVTHSWYQYEDTKEVQLH
HPUZDI	ICCACCCTTATGACGGGCAAACGAACCCGCATTATACCGGTTTAAAAGACGGCGGGGGGGG	PYDGQTNPHYTGLKDGESVGIENKIIPA
	ATCATCCCTGCTAAAGTGCTTGACACTAAAAATAAATAITCTTGGATAAAATGGCCCAGATACGATAGTAAGCCCATG	KVLDTKNKYSWIKSPRYDSKPMEVGPL
	GAAGTAGGTCCTTTAAGTTCCGTAGTGGTTAGCGGCGAAAAACCCTTATGTTACTGAAGTGGCTACGAAGTT	SSV/VGLAAKNPYV/TEVATKFLKDTKL
	TTTAAAAGACACTAAACTGCCTTTAGAGGCGTTGTTTCAACGCTTGGGCGAACAGCTGCAAGGTGTATTGAAGCTA	PLEALFSTLGRTAARCIEAKTIADNGLL
•	AAACGATCGCTGATAATGGCCTTTTGGCGTTTGATGCGTTAGTGGAAAATCTAAAAAGCGATCAAAGCACTTGTGCT	AFDALVENLKSDQSTCAPYHIDKNQEY
	CCTTATCACATTGATAAAAATCAAGAATATAAAGGGCGCTACATTGGTCAAGTGCCAAGGGGCATGCTAAGCCATTG	KGRYIGQVPRGMLSHWVRIKNGVVEN
	GGTGCGTATTAAAAACGGCGTGGTGGAAATTATCAAGCGGTGGTGCCTTCTACTTGGAATGCAGGGCTAGAGT	YQAVVPSTWNAGPRDSQN(2RGAYEM
	TCTCAAAATCAAAACGGGGGTTTATGAAATGAGCTTGATTGGCACTAAAATCGCTGATTTAACCCAGCCTTTAGAAATC	SLIGTKIADLTQPLEIIRTIHSFDPCIACS
	ATTAGEACTATION TO THE TRACE OF THE TRACE OF THE TRACE OF THE TARGET OF THE TRACE OF	VHVMDFKGQSLNEFKVEPN "AKF
	GARTITA A A COLOR DE LA COLOR	
	AAAAAATATTCGGTTTTGGCTTTTTCCATTGGTTTAGGCTTTGAGTTTTTCGCTTTAATCGCTTCA	-
	ACATOCITE TO THE CONTROL OF THE CONT	
	TCATGROTOSTITITITITITITITITITITITITITITITITITI	
100004	2012 TEAAGCT CAAAAA COOCOCAAT COAAT CAAAA GOOTAAA GAAAA TAAAA GOOTAAA GOOTAAAA GOOTAAAA GOOTAAAAAAAAAA	2050 EAQKETPQSNQTPKEMKVK:SISYVGLS
ושבחבו	IT CTT ACATETIC TRACE OF THE TOTAL OF THE TO	YMSDMLANEIVKIRVGDIVDS:KKIDTAV
	CACCECTETT TESCT TO THE TOTAL TO A SECTION TO THE SECURITY TO A SECTION TO THE SE	LALFNQGYFKDVYATFEGGII.EFHFDE
	TCATTTTGATGAAAAAGCCAGGATTGCCGGGGTAGAAATCAAGGGTTATGGGGACTGAAAAGGAAAAAGACGGCTTAA	KARIAGVEIKGYGTEKEKDGI.KSQMGI
	AATCCCAAATGGGGATCAAAAAGGGCGACACTTTGATGAGCAAAAATTAGAGCATGCTAAAAGGGCTTTAAAAACC	KKGDTFDEQKLEHAKTALKTALEGQG
	IGCTTTAGAGGGGGAGGGGTATTATGGGAGCGTGGTGGAGGTGCGCACAGAAAAGGTCAGTGAGGTGCATTATTG	YYGSVVEVRTEKVSEGALLIVFDVNRG
	ATCGTGTTTGATGTGAATAGGGGGGATAGCATTTATATCAACAATCCATTTATGAGGGGAAGCGCGAAATTAAAACGC	DSIYIKQSIYEGSAKLKRRMIE:SLSANK
	ICECATE GA ATT CATTER OF THE CATTER OF THE CATE CONTROL OF THE CATE OF	QRDFMGWMWGLNDGKLRLDQLEYDS
	ACCITTAGATCAACTAGAATACGATTCTATGCGTATCCAAGATGTGTATATGCGTAGGGGTTACTTAGACGCTCATAT	MRIQDVYMRRGYLDAHISSPFLKTDFS
	Tronge CTTTTTGAAAACGGATTTTCTACCCATGACGCTAGGCTTCATTATAAAGTCAAAGGGGTCCAATAC	THDAKLHYKVKEGIQYRISDILIEIDNPV
	AGGATTTCAGACATTTTAATAGAGATTGACAACCCGGTAGTCCCCTTAAAAACCTTAGAAAAAGCGCTTAAAGTGGAAAA	VPLKTLEKALKVKRKDVFNIEHLRADA
	AGGAAAGATGTCTTTAATATTGAGCATTTAAGAGCGGATGCGCAAATTTTAAAAACCGAAATCGCCGATAAGGGTTAT	QILKTEIADKGYAFAVVKPDLDKDEKN
	GCGTTTGCGGTGGTGAGCCAGACTTGGATAAAGATGAAAAAAAA	GLVKVIYRIEVGDMVYINDVIISGNQRT
	GGGCGATATGGTGTAT	SDRIIRRELLIGPKDKYNLTKLRNSENS
		LRRLGFFSKVKIEEKRVNSSI.MDLLVS
		VEEGRIGOLOFGLGYGSYGGLMLNG
		SVSEKNLFGIGUSMSLYANIAIGGGR
		SYPGMPKGAGRMFAGNLSLINPKIFU
		SWYSSTINLYADYRISYUYIQGGGFG
		IVINGERIALGINE I DISELGI INCINO I NELLO
	TAREA TO CONTROL TO A A A SECTION A A A SECTION A A A SECTION A A A A A A A A A A A A A A A A A A A	2052 EAIRSKELOKAEMEROMIALIKKSLEKN
HPUZĐI	2001 CONTROL OCOURT TO CONTROL OCOURT OF THE CONTROL OF THE CONT	RNESLAGEKVLTNYRKSLDF-LQKKRSF
	CATCATATA A CA A A A A A A A A A A A A A	LAKRVFDTLLQDFLFSQALKGQNLASS
	AGCCTCTTCTAATGATGTTGTTTTTGCAAGTGGCGTTTGAAAACTTGCACCAAAGCACTCTGTCTAAAATGTCGCAACT	NDVVLQVAFENLHQSTLSKNISQLSQE
	CANTON	EKELNTQALKVKNSIQKISSIIDEQKTRE
	TIGAGCAAAAAACTCGTGAAGTAACCTTAAAATCCTTGAAAACCGAACAAGATAAGCTCATTTTGAGCATGCAAAAAGA	VTLKSLKTEQDKLILSMQKDYAIYNQRL
	TTATECGATCTACAACCAACGCCTAACCCTTTTAGAAAAAGGCGCCAGAATTTAAAACGCTCTTTTAAAACGCTTGAA	TLLEKERONLNALLKRLNIIKONRENEE
	TATCATCAAACAGAAAACAGAGAAAATGAAGAAAAAGTCAGTTTGAAAAAATCTTCTCAAGGCCTTAGAAGTCAAAGAGT	KVSLKKSSCALEVKCVASSYCNIN IS
	GGCTAGCTCTTATCAAAATATCAACACCACGAGCTATAACGGACCAAAAACGATCGCTCCCTTGAACGATTATGAAGT	YNGPKTIAPLNDYEVVOKFGPYIDPVY
	GGTGCAAAATTTGGCCCCTATATTGACCCGGTTAAAAATTTTAA	וארווו

Ç	2	ς	
¢	٩	r	
(٦	r	

			TO SS SHIP NO AS THE SS OF	•
			SI SNAMII NSRI VNI SRRHTINNIOSEA	
	ATATTGACTCATTCGCCCAACGCTTACAAGCTTTAAAAGACCAAAAATTCGCTTCTTTAGAAAGCGCGGGGGAAGTGT		ORLOALKDOKFASLESAAEVLYOFAPK	
	TGTATCAATTTGCCCCTAAATATGAAAAACCTACCAATGTTTGGGCTAATGGTATTGGGGGGACGAGCTTGAATAATG		YEKPTNWANAIGGTSLNNGGNASLY	
	GCGGCAACGCTTCATTGTATGGCACAAGTGCGGGCGTAGATGCCTACCTTAATGGGGAAGTGGAAGCCATTGTGGG		GTSAGVDAYLNGEVEAIVGGFGSYGY	
	CGG GGAGCCAIGG AIAGCCCITITAATAATCAAGCGAACTCTCTTAACTCTGGAGCCAATAACACTAATTTT	0, 2	SSFNNQANSLNSGANNTNFGVYSRIFA	_
HP0261	2055 AGGGATTTTGGTGTGGGATTTGATCACCGAAGTCAATGGGAAAAAGGTTAAAAACACGAATGAGTTAAGAAATCTAAT	2056	2056 GII VWOI ITEVNGKKVKNTNEI BNI 168	
	CGGCTCCATGCTACCCAATCAAAGAGTAACCTTAAAAGTCATTAGAGACAAAAAAAGAACGCGCTTTCACCCTCACTCT		MLPNORVTLKVIRDKKERAFTLTLAER	
	AGCTGAAAAGGAAAAACCCTAACAAAAAGAAACCATTTCTGCTCAAAACGGCGCGCAAGGCCAATTGAACGGGCTTC		KNPNKKETISAQNGAQGQLNGLQVED	
	PAGE AGARGA I I I AAC I CAAGAAC CAAAA GGTCTATGCGTTTGAGCGATGATGTTCAAGGGTTTTAGTCTCTCAAG		LTQETKRSMRLSDDVQGVLVSQVNEN	
•	ISAN ISANASITICCCCAGCAGAGCAAGCCGGATTTAGAGAAAGGTAAAAGGTAACATTGAAAATTGAAGGTTGAAGTT AAAAGCGTTGCGGATTTTAACCATGCTTTAGAAAAGTATAAAAGGAAAACGAAACGAATTGTAGTTTTAGATTTAAATTGAAGTTAAATT		SPAEQAGFROGNITKIEEVEVKSVADF	
	CAAGGITATAGGATCATTITGGTGAAATGATAGGGGTGGGTCGTTAGTCGCATGTTTTGATTAGAGTGAATGGGGA			
	AGCTTTTAAACTCTCTTTAGAAAGTTTAGAAGAAGACCCTTTTGAAACTAAAGAAACGCTTAGAAACGCTTATCAAACAA GAAACGCTTATCAAACAA ACGAAACTAACAAA ACGAAACTAAAAAAAAAA			
HP0261	2057 GGGGAGCCTTCAGCGTTTGATTTGCAAAGTGGGGCTACCAAAAAAGAACTCAAGCAGTTGCAAATCAATAGTAAGAA	2058	2058 GEPSAEDI OSGATKKEI KOLOINSKNE	
_ _	TITITCTAATATTTTGACCAAATCCATTCGCAAGTAGAGGCTAACACTCAAGCTCAAGAGGGTTTGAGAAGCGTTTA	8	SNILTKIHSQVEANTQAQEGLRSVYEG	
	IGAGGGGCAGGCTAATAAGATTAAAGATCTCAATAACGCTATCCTTTCCCAAGAAGAATCCTTACGAGCCTTAAAAGC	<u>o</u>	CANKIKDLNNAILSCEESLRALKASCEV	
	TICGCAAGAAGIGCAGGCTAACACGCTTAAGCAGCAATCGCAAACTTTAGAGGATTTGAGAGAATGAGATTCACGCTA	<u>o</u>	CANTLKCOSOTLEDLRNEIHANCOAIC	
	ACCAGCAAGTTAAGCCAAGGTTAAAAAAAAAAAAAAAAA	<u>o.</u> :	OLDKONKEMSELLTKLSODLVSQIALIO	
	GELFFORMATA AND CONTRACTOR AND CONTRACTOR AND AND AND AND AND AND AND AND AND AND	Χ.	KALKEQEEKAEKPLKSNAPANKTPSLK	
	TTG>TTGATA&AGGATTGTTTATA	∢ι	AESPKNOEGKTOEKAKIEFDKDLSKOK	
•	CONTROL OF THE PROPERTY OF T	<u>u 2</u>	EIFUEALSFFKNKSYAEAKEKLLWLEA	
	GGCTTATGGGGAAAAGA	<u> </u>	NSTRLTTVRTVLGEVATGER	
HP0261	2059 TAAGGTGGTCCAATCCAACCTGATTATATTTCTACGCATAGCGAATCAGCCTAGACTTGCTCAAGTTATTGAAAAA	2060 K	2060 KVVOSNPDYISTHSESALDILKILKKN	
	AAACCAGATGAATGCAAGCGCGATTGAGATCGCTCACTTGCTCCAATCAAGATGATGTCTGAAAGCTAAAGAGC	0	GMNASAIEIAHLLINGDDDLKAKEGAL	
	AAGCGCCACTITALGALLAGGAGCGTTGTALGCAAGGACTTTAAAAACGCCCACCTTTACAATCTGCAATATT	<u>}-</u>	YDLGALYARIKDFKNAHLYNLQYLQDH	
	ISCAGGAGGAGGAGAAGTIGGAGAAGGGITGIGIGGAGGGGGGGG	<u> </u>	AELDKASVVRARDEKALFSMEGNTÓE	
	AGAATTGAAAGCCCAACTATTGTTTGAAAACAAGCGTTATGCTGAAGGTGTTAAGGCTGTGAAAAAAAA	<u>∠ u</u>	KIARTUKIIQNFPNSNEALKALELKAQLL FENKRYAEVI SMOKNI DKÓSDI IÓKTI	
	TTCCCCTTTGATCCAAAAAGGCTCAATGTCCTTGCTAAAACCCCCATTAGAGAACCATCGTTGTGAAGAAGCCTTAAA	z	NVLAKTPLENHRCEEALKYLSOITTFEF	
	ATATTTATCCCAAATCACAACCTTTGAATTCAGCCCCAAAGAAGAAATCCAAGCCTTTGATTGCTTGTATTTCGCATCG	S	SPKEEIQAFÖCLYFASLKEKAQIIALNAF	
	CTCAAAGAAAAAGCGCAAATCATTGCCCTAAACGCTTTTAAAACGGCTAAAGCCCCTAGCGAGAAATTAATATGGCTTT	¥	KTAKAPSEKLIWLYRLGRNYYRLGDFK	P
	IATICETTI GEGGGGGGATTACTACGGGTTAGGGGATT FTAAAAATTCCACTCTGGCCTCTAAAGACGCTTTAATTCTC	<u>z</u>	NSTLASKĎALILAĞSL	- 1/
HP0261	2061 AAGTTTAAGGAATTTCAAGCCCAAACCGAGGGCGAATTTGGGGGCCTTGGGATCACGGTGGGCATGCGCGATGGC	2062 KI	2062 KFKEFOAOTEGEFGGLGITVGMRDGV	EP
	GTTTTAACCGTTATTGCCCCTTTAGAAGGCACTCCAGCTTACAAGGCTGGGGTTAAGTCAGGCGATAACATTTAAAA	<u> </u>	LTVIAPLEGTPAYKAGVKSGDNILKINN	U1/
	Alichaladocadecacecisasecanis	<u>ŭ ĉ</u>	ESTLSMSIDDAINLMRGKPKTPIQITVV	154
	TGTCTATGTGAAAAGATTAAAGAAACCCCCTTATCTGTATGTGAGAGTGAGT	z a.	KKIVEFKFLVFINIIKUIIKLF3VTVKKIKE I PYLYVRVSGFDKNVTKSVLEGLKANPK	128
	JGG1111AGAAGGC11AAAAGCTAACCCTAAGGCTAAGGGGATCGTGTTGGATTTAAGGG	Ā	(GIVLDLR	

2/066501		PCT/EP01/15428
2064 SFLNAVDGISKTDLSSI NLAEDSAPLNH PNAQKLSLKNAWTRVL.SNHEGLHAQE YAIKRASKMKLAAKLSF.PQIDLSAFYV YLSNPIKMDFASQKQPGVQKATNQIHQ GIQNIQQNIPSQVLTPCIQAGMQGVMQ GIQNIQQNIPSQVLTPCIQAGMQGVMQ GFGALSSTLEAPLLFSKQNVYIGALSIIY PLYMGGARFTMVRIALILMQKDANEVY RLKKLSTFQELVSVYYGMVLNAEVAET LEEVEKGHYKHFQNALKMQKNGALSIIY VETGAQVAYDKAHIASVKAKDVLEVS QLSFNSILSSKDDLVPSSKLEIRTEKNL PDLSFFVSSTLNSYPVLKTLENQIQISK ENTKLQIAKFLQQVSFFGSYIMKQNNS VFEDMIPSWFYGVAGKIMPILSPTGRIQ KYQASKLAELQVSSECIIQAKKNMELLV NKTYKETLSYLKEYKSLLSSVELAKENL KLQEQAFLQGLSTNACIVIDARNTLSSIV VEQKSVAYKYIVSLANI.MALSDHIDLFY EFVY	2066 ALLOKALKLYALLKPLELNVSIASSFSKI GNLFGRELESFCVKIQ¬KNTRALNSEK LYLKLFOKGVIARISCEFVCFEVFSLNE KDFEKIALVLEEILNKA	2068 DEEVMALLIAWNNRIL FLRLLESILISFK HFENPFLTTENFENFNDLNTLFFEVLAK KNSERLPEIK 2070 SLQMDEFLDDLQLSGERINDLEEVVGV NRPEERKEGNFSSRLDVAGITGLQKS FIMRLIPNDYPLESYRIVSAAFNKRIHPI LHVLHNHTGLDLSTAINTPVYASASGV VGLASKGWNGGYGNLIKVFHPFGFKT YYAHLNKIVVKTGEFVKKG
2063 AGCTITITAAATGCTGTTGATGGGATTTCTAAAACCGATCTTTCTTT	2065 CGCATTATTGCAAAAAGCCCTCAAACTCTTTTAAAGCCTTTTAGAATTGAATTGAGGCATAGCCTCTAGCTT TTCTAAAATAGGGAATTTGTTTGGTAGGGAATTAGAATCCTTTTTGCGTGAAAATCCAGCCCAAAAACCCCGTGCTTT TTCTAAAATAGGAACTTTAATTTAA	CGCACCACCCCTA 2067 GATGAAGCCTTTTAACCACCGCATTTTGAAAACTTTTTTAACCGCATTTTAACCCTTTTTTGAAAATCTTTTTTTT
HP0261	HP0261	HP0261

•	_
٠	7
ı	~

.,000301		P(CT/EP01/15428
2072 VWVNNEDRCKGCDICVSVCPAGVLGM GIEKERVLGKVAKVAYPESCIGCVQCE LHCPDFAIYVADRKDFKFAKVSKEADE RSEKVKANKYMLLEETILEGRDK	2074 YKASLTTNAAHLHIGKGGINLSNQASG RTLLVENLTGNITVDGPLRVNNQVGGY ALAGSSANFEFKAGTDTKNGTATFNN DISLGRFVNLKVDAHTANFKGIDTGNG GFNTLDFSGVTGKVNINKLTASTNVAV KNFNINELVYKTNGVSVGEYTHFSEDI GSQSRINTVRLETGTRSIFSGGWFKS GEKLVIDEFYYSPWNYFDARNIKNVET RKFASSTPENPWGTSKLMFNNLTLGO NAVMDYSQFSNLTIQGDFINNQGTINY LVRGGQVATLNVGNAAAMFFSNNVDS ATGFYQPLMKINSAQDLIKNKEHVLLKA KIIGYGNVSLGTNSISNVNLIEQFKERLA LYNNNNRMDICVVRNTDDIRACGTAIG NOSMVNNNPDNYKYLIGKAWKNIGISKT	ANGOSNISY 2076 VFKDSKKDACGFIYEISEFMKAYTALLK KQDRYYYLLRYLPSRYWASILTTALY KYPDFDALKKLLVSYYYQTWIAGGTITR IKOTSINIIKNVKSNKSVETIKELILNSIDS YNTFDQYLYNLWDSSSVYHSKWYRPV LALANYFMADEEKPHFIAMDAETQVEH ILPQTPKRGSQWNADFDKEKREEWVN NIANLTLLKRKKNAHALNGGFDEKRKIY GGKDTSKVISCYDITKELYSNYRKWNE KSL	2078 SVKNLREISVKEKFLWLNAKSYLISVFA PFILLPWIDLLSAFLLYLGFLALFSVLEF FDEDIADIIVAKSKIKTKTKCYRA
202	207	2076	2078
2071 CCGTTTGGGTGAATGAAGGGTGTAAGGGTTGTGATTTTGCGTATCGGTATGCCTGCTGGGGGTTCTTGGCATGCCAAACTTGGGATTGAAAAGGAAAGGGTGTTGGGAAAGGTGGCCAAAGTGCCTACCCAGAGAAGGGTTGCGGTTGCGTTGCGGTTGCGTTGCGGTTGCGTTGCGGTTGCAAAGAATGCGTGCAAAGAATGCGTGCAAAGAATTCGCTAAAGTTTCTAAAGAAAG	2013 GGITATORCATCTITIAGT GGAAATCTAACCGGGAATATCGGCAAGGCGGTATCAATCTGTCCAATCAAGCGCGAATCAAGCGCGAATCAAGCGCGAATCAAGCGCGAATCAAGCGCGAATTTAAGAGCTTTAAGAGCTGAATAATCAAGTTTAAGAGCTGTAAGCGCTTTAAGAGCTGAATATCAAGTTTAAGAGCTGGAATATCAAGTTTAAGAGCTGGTACCGGATACCAAAAAAGCGGCACAGCCACAGCAACTTTAATAAGCGTATTTAATAAGCGATATTTAAGTGGAATTTTAAAAGTTTTAAAGCGTAATTTTAAAAGGTATTTAAAAGGTATTTAAAAGGTATTTAAAAGGTATTTAAAAGGTATTTAAAAGCTTAAAAGCTTAAAAGCTTAAAAAAGCGGAAATTTAAAAAGTTCAATAATAAAAAAGTGGAAATTTAAAAAAAA	2075 AGGIGITICAAAGAGACAGCAAAAAGACGCITIGCGGGITICATCTATGAGATCAGCGAGTTCATGAGAGCCTATACCGCATTACCGCATTACCGCATTACCGCATTACCGCACTTTGCTAAAAAAAA	TITTECECCTITITATCTTECTCCTTEGATTECTTEATECTTATTTEATEGCTGAACGCTAAGGCTATTTGGTTTCGTTTATTTGATTTCGTTATTTTGATTTCGTTATTTGATTTCGTTATTTGATTTCGTTATTTGATTTCGTTGAACGCTTAAGGCGTTTTTAGGCGCTCTTTAGGCGCTCTTTAGGCGCTCTTTAGGCGCTCTTTAGGCGCTTTTAGGCGTTTTTAGGCGTTTTTAGGCGTTTTTAGGCGTTTTTAGGCGTTTTTAGGGGTTTTTAGGGGTTTTTAGGGGTTTTTAGGGGTTTTTAGGGGTTTTTAGGGGTTTTTAGGGGGTTTTAGGGGGTTTTAGGGGGTTTTAGGGGGTTTTAGGGGGTTTTAGGGGGTTAGGTGGCGGGGGGGG
HP0902	70800	HP0902	0

HP0016 207	2079 GCACATTGTTATGAAAACAGGTTAAATCTCGCATGAAAGAAA	2080 AHCYENRLNLA	
208	2081 CTTTAATTITTGATATGCATGCGCCGAATTTGGGGGAGCATTGAGCCAAGGGGTTTCAGGCTTTCATTCA	2082 LIFDMHAPNLGSIEGGVSGFHFIIIPKNI DFKIMIELLPYALSLALVGTIESLLTAKTI DVILKDGVSDKNKETKACIGLGNIISGLI GGMTGCALVGQSIINAKSGAKTRLSTF FAGFSLMVLILVFNEYVVICIPIV	LIFDMHAPNLGSIEGGVŠGFHFIIPKNL DFKIMIELLPYALSLALVGTIESLLTAKTL DVILKDGVSDKNKETKACKGLGNIISGLL GGMTGCALVGQSIINAKSGAKTRLSTF FAGFSLMVLILVFNEYVVKIPIV
200	2083 CGAAGTTTTAGAACAATTTCATGGCGGTTTAAAAAATTTAGAAATTACAAACTAAAAGACGCGTGGGTTTGTGGGGCCGA TCCAAAAGAAGAAGAACAAAGAAAGAAAGAAATTGAAAATTAAAAGCAATTAGAAAACAAAGAAAT TCCAAAAGAAGAACAACAACAACAACAACAATTTGTTTTTTTT	2084 EVLEGFHGGLKNLELQTKRRMGLWGD PKENEEQTLFLEEIENELKQLENKENLK ADNNTEFKEENQDTKEN 2PNDLFSLPL PTQTTINGIKEFVEEPVIETEKKETSQN EPIQEKKERIFKNFFSRIGFDKSIAPTML FEEVRDASVIYHLEKKLGIOYIFYVACFF FGTTALIIIIT	EVLEGFHGGLKNLELQTKRRMGLWGD PKENEEQTLFLEEIENELKQLENKENLK ADNNTEFKEENQDTKENJANDLFSLPL PTQTTINGIKEFVEEPVIETEKKETSQN EPIQEKKERIFKNFFSRIGFDKSIAPTML FEEVRDASVIYHLEKKLGIYIFYVACFF FGTTAI III 17
208		2086 AYMATRTLQNYNERLITLI-VIGFMSCSA RLPIYVLFVGSFFPSSSAG:FVLFCIYILG AVVALVMAKLLKLSVFKGJTESFIMEM PKYRFPSWRMYYFSIYTKSLSYLKKAG TYILVGAILIWFMSQYPKSDAAMKAYK DESI VANKDITI SSF	AYMATRTLQNYNERLITLİYIGFMSCSA RLPIYVLFVGSFFPSSSAG:FVLFCIYILG RVALVMAKLIKLSVFKGJTESFIMEM PKYRFSWRMVYFSIYTKSLSYLKKAG TYILVGAILWFMSQYPKSDAAMKAYK OFSI I VAKDTTI SSF
208	2087 CTGTGATCCATGATTTGAGCCTGATATAGAGGTGTTTATAAAGATTGGCTAGGCATACAGCCCCCAGAAAGACGC TAAGATTGCTCAATCCTTTTTATGAAAGAGGCTTATGCCTCTTGGTGCTAAAAGGTGCC TAAGATTGCTCCAATCCTTATTGAAAGAGGCTTTATGCCTCTTGGTGTTTAATTAA	2088 VIHDFEPDIEVFYKDWLGIQPPERR	COWLGIQPPERR
208	2089 CTAAAGAATTTGCGAGCCTTTTTTCTCAAGATGAAGAAGTCTTGGAAGTGGCGCGATCTTATTTGATCGCTGTGGGC CTCTCAAGCCCCCTAATTGGGTATTTTGTCAAGATGAGTTTTAGAGGGGGCTGGCATTTCTAAAGTCTCAAGTCCACTG CTCTCTCAAGCCCCCTAAGTTTGGGGTATTTTGTGATGGCCATTTTAGAGGGGGCTGGCATTTTAAAGTCTCACTGAAA TATTTTTGTAGTGATCGCATCAGAAACTTTTTTGCGCTCATTCAT	2090 KEFASLFSQDEEVLEVARSYLIAVGLS QAPLIGYFYLDGVFRGAGISKVSLYINT LSLWGLRIMPIYLLIHHFKVEFIFVVIAS ETFLRSFIYYKVFSKGIWKRCGKKA	KEFASLFSQDEEVLEVARSYLIAVGLS QAPLGYFYLDGVFRGAGISKVSLYINT LSLWGLRIMPIYLLLIHHFKVEFIFVVIAS ETFLRSFIYYKVFSKGIWKRCGKKA

ארטטמדו	2004 JTTT.	ACAGG TO TANCOTANA AND CONTROL OF THE CONTROL OF TH	
	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GGATATIGICCGCAAAATGGGCATTCTAAAGAAAACGGCGCACTTGACTAAAGAAGAACAAAAGAAAAAAAA	2092 LEVLTQAKSIAFDKTGTLTKGVFKVTDI
		TATCGCTTTATCCATTCAAAACCAACCAACCAACCAACCA	VPQNGHSKEEVLHYASCSQLLSTHPIA
	S S S S S S S S S S S S S S S S S S S	CGAAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	LSIQKACEEMLKDDKHQHDIKNYEEVS
	ביים האבי	CATCANTIFICATA TO COCCAT CACACACACACACACACACACACACACACACACAC	GMGVKAQCHTDLIIAGNEKMLDQFHIA
		GGCTTATION CONTRACTOR TO CONTRACT OF THE CONTR	HSPSKENGTIVHVAFNQTYVGYIVISDE
	AAA	THE CATE OF THE CASE OF THE CA	IKDDAIECLRDLKVQGIENFCILSGDRK
	(<u>)</u>	COCACCITATION OF A MANAGEMENT OF THE TOTAL O	SATESIAQTLGCEYHASLLPEEKTSVFK
		GGCGATGGCATCATTATTATTATTATTATTATTATTATTATTATTATT	TFKERYKAPAIFVGDGINDAPTLASADV
	A CO	GCAAACCAAAAACCAAAAAAAAAAAAAAAAAAAAAAAA	GIGMGKGSELSKOSADIVITNDSLNSLV
	CTA	CTAAAAAGCATTATTTGGCAAAATATCTTGTTCGCTTTATAAAAAAATATTTTTTTT	KVLAIAKKTKSIIWQNILFALGIKAVFIVL
	TAG	TAGGGAGGTTGTGGGAAGGGGGTGTTTGGGGGATGAGGGGGTTATGGGGGG	GLMGVASLWEAVFGDVGVTLLALANS
	GAG	GAGAGGGGAAAAGCCTIGAACCCTAATAACCAATTAACAAAAAAAAAA	MRAMRA
	AAC	AACTCTAGCGCCTAAGGGGG	
MP0016	2093 TTT	TITAGAAGACATTGGCAAAATCACCGTTTCCACTAATTTAGGGCATTTGCACATTAAGGATTTTGCGAAAGTCATCAG	2094 I FDIGKITVSTNI GHI HIKDEAKAISOEB
	Q S S	CCAGTCTCGCACCCGTTTGGGGGTTTGTTACTAAAGATGGCGTGGGCGAGACCACAGAAGGCTTGGTGGTTTCTTTAA	TRI GEVTKOGVGETTEGI VI SI KOANT
	AAG	<u>AAGACGCTAACACCAAAGAAATCATCACTCAAGTGTATCAAAAACTAGAAGAATTAAAAACCCTTTTTACCGAATGGCG</u>	KEIITOVYOKI FFI KPFI PNGVSINVFY
	191	161CCATTAATGTTTTTTATGATCGCTCAGAATTTACGCAAAAAGCCATTGCCACCGTTTCTAAAACCCTCATTGAAGC	DRSEFTOKAIATVSKTI IEAVVI IIITI FI F
	5	CGITGITITAATCATCATCACGCTCTTTTTATTTTAGGGAATTTGAGGCGAGCGTGGCTGTGGGGGGTGATTTACC	LGNLRASVAVGVII PI SI SVAFIFIKESD
	111	TTANGCTTGTCCGTGGCGTTTATTTTATCAAGTTTAGCGATCTGACTTTAAAATTTGATGAGTTTAGGGGGATTGGTT	LTLNLMSLGGLVIAIGMLIDSAVVVFN
	A C	ATCGCTATAGGCATIGCTCATTGACTCAGCCGTGGTGGTGGTGGAAAACGCTTTTGAAAAATTAAGCGCTAACACTAA	AFEKLSANTKITKI HAIYRSCKFIAVSV
	A C	AACCACTAAACTCCATGCAATCTATCGTTCGTGTAAAGAAATCGCTGTTTCAGTGGTGAGCGGGGTGGTGATCATCA	VSGVVIIIVFFVPILTLOGLEGKMFRPI A
	9	G G	OSIVYALLGTLVLSITIIPVVSSLVLKATP
	ATG	ATGCGCTTTTAGGCACTTTAGTTCTATCATTACAATCATTCCTGTAGTCAGCTCTCTTGTCTTAAAAGCCACGCCCCA	HSETFLT
	AG	I AGCCAAACCI I I I I AACCAAC	
HP0016	2095 CGG	2095 CGGCGATGTTTCTACCGCTAATTCAGGGCTTTATGGAGCGAGC	2096 AMFSTANSGLYGASRMIYGLSKOKMF
	- C	ASSOCIATION CONTINUED CARCAGE CACCACT HAT GCGAT GITTITITICS TITTED TO THE CONTINUED CO	FKVFSQLNRQGTPTYAMFFSLSFSLIG
	TGT	ACCOUNT OF THE PROPERTY OF THE	LLVQIYAKENVVEALINVISFTVIIVWVSV
		CONTRATABAGE CONTRATATION OF A CONTRACT OF A	SVSQYSFRKQYLKAGHSLEDLPYKAPF
	CTAI	CTATGGATAAGGATCAACGCATTGGGATGATTTAA	LPFLQLIGITGCAIGVIGSAMDKDQRIG
HP0016	2097 GGT(GGTGTGGCTCAAAATAGAAATGGTTTTAGGGGCGTTTCTAGCAGGGTTAGTCGTTTCTACTTTTTCCCTCATAAATC	2098 WULKIEMVLGAFLAGLVVSTFFPHKSF
	AGA	AGAATTGATCCACAAGCTCAATGATGTGGGTTTTTGGGTTTTTTGTGCCTTTGTTTTTCATCCATGTAGGCTCTACTTTA	LIHKLNDVGFGFFVPLFFIHVGSTLDLK
	Į te	TO THE PROPERTY OF THE PROPERT	LVFLNPHLILÖGILIVIAMLSLHLITSTLL
		CONTRACTOR CONTRACTOR	WRKYFKEAKHLFSFALGASMPLTFLV
) L	GCT.LIPACITIVITIASIAACCACCACCGCAGCTATTATTAACCAAGCGCAAGCGCAAGCGAAGCGCAAAAAACACACTACGCATTI	TAAVGLKAQAISONTYYALLMAAIFEGV
	TTAA	TARGET TO TARAPTE AND THE CONTROLL OF THE CONT	LFTIAIKILNKKA
	CGAC	C6AGGGTGCAAGTTTTGCATTTCTTTTAAGAAATTTTTGGTGGCTAATCGTGCGATAGGGGGGCTTATCAAGAGGGG	
	CTGT	CTGTTTGGCTGGGCAATTGCAATCAGGGGCGACTGGGATATTTTGAGAAGTGACAAATGAATG	
	GAAC	GAACCTTAATCAAAGGGCGGATCACCAATAAGCCGTTTTCAGCCCTATAAATGGGGGGCATGCTCCTCAAACTCCCG	
	TTAT	TATAAGTGAAATTCATAAAAAGCTCTCTACGGCGTCATCTAAATGGTGCGCGATAGCGACTTTATTATAGCCTTCTT	
	CTAA	CIAAAGCCTTAGAATACAAAGTCCCTCTTCTCAAACGAGAAACAAAACGAAAAAAAA	
	5 L	USTICATORICETORICAGOSATTIGGGTGTAAATGATGTGGTGAATGCCTTGCTGTTGGCACAAATGGCTCAACCAT	-
	5	10.5	

	_
•	7
Ч	۲
~	٦

/066501		PC1/EP01/1542
2100 GLASNNKYSLIGSARATIQLLSFEVVST LTILAPLMVVGSLSLVEINHYQSGGFLD WLVFKQPLAFVLFLIASYAELNRTPFDL LEHEAEIVAGYCTEYSGLKWGMFFLAE YAHLFAFSFVISIVFFGGFNAWGFIPGG IAILIKAGFFVFLSMWVRATYPHVRPDQ LMDMCWKIMLPLALLNIVLTGIIILI	Z102 TQTTPQENLLSTISFEHARIEIDSLGRIK QVYLKDKKYLTPKQKGFLEHVGHLFSS KENAQPPLKELPLLAADKLKFLEVRFL DPTLNNKAFNTPYSASKTTLGPNEQLV LTQDLGTLSIIKTLTFYDDLHYDLKIAFK SPNNLIPSYVITNGYRPVADLJSSYTFSG VLLENSDKKIEKIEDKDAKEIKRFSNTLF LSSVDRYFTTLLFTKDPQGFEALIDSEI GTKNPLGFISLKNEANLHGYIGPKDYR SLKAISPMLTDVIEYGUTFAKGVFVLL DYLYGPVGNWGWAIILTIIVRIILYPLSY KGMVSMQKLKELAPKMKELCIEKYKGE POKLQAHMMQLYKKHGANPLGGCLPL ILQIPVFFAIYRLYNAVELKSSEWILWI HDLSIMDPYFILPLLMGASMYWHQSVT PNTMTDPMQAKIFKLLPLTFIFLITFPA GLVLYWTTNNILSVLQQLIINKVLENKK	2104 LALGWVGEPAIAKLLAALFESINDLREN PIFIHSMSVVIAFLSITFLHVVLGEIVPKS LAIAKSEKATLFAARPLHVFWVVFYPVV RLFDVIAHFFLKKMGINPKEHDGTHSE EELKIIVGESLREGIIDSVEGEIIKNAXDF SDTSAKEIMTPRKDMVCLDEISNSYEEN IDIVLKGHFTRYPYCKGSKDNIIGMVHIR DLLSRSIFTRMHDFNQIVRKMIIVPES ASISQILIKMKKEQIHTALVIDEYGGTAG LLTMEDIIEEIMGEISDEYDLKQEGINKL EEGVFELEGMLDLESVEEALHIEFDKE CEQVTLGG
210	210	210
2099 CCGGGCTTGCCTCTAATAACAAATACTCTTTAATTGGCTCCGCAAGAGGCGACGATCCAACTGCTCAGCTTTGAAGGGGGTGGGT	2101 CCACTCAAACAACCCCCAAGAGATTTGCTAAGCACGATTTCTTTTTGAGCATGCCAGGATTGAAATTTAGCTTTTAGGCAGGATTGAATTTAGGCACCCCAAACAAGGAAAAGGGCTTTTTAGACCATCAAAAGGGCTTTTTAGAGCATGTGGGCCATCAAAAGGGCTTTTTAGACCCATCAAAAGGCCTTTTAGAGCGCTTCAAAAGCCCCTTTTAGAGCGCTTCAAAAACCCCCTTTTAGAGCGCTTCAAAAACCCCCTTTTAGAGCGCTTCAAAAACCCCTTTTAGAGCGCTTCAAAAACCCCTTTTAGAGCGTTCAAAAACCCCTTTTTAGAGCGCTTCAAAAACCCCTTTTTAGAGCGCTTCAAAAACCCCTTTTTAGACCCTTAGATGATTTAAGCGATCATTTAAAAACCCAAATAGAGATTTAGAAAATTCAAAAACCGGAGTTTTAGAAAATTGAAAAATTGAAAAAATTGAAAAAA	2103 ATTAGCTITTAGGCTGGGTGAGCCCGCTATCGCAAAATTGTTAGCCGCGCTGTTTGAGTCTATGGATTTGAGAGAGA
HP0016	HP0016	HP0016

HP1559	2105 GCTCCAAGCATCATAAAGATGGCGTGAGCGTGGCTAAAGAGATTAAATTGAGTTGCCCGGTAGCTAACATGGGCGGCGCGCGC	2106 APSITKDGVSVAKEIELSCPVANMGAQ LVKEVASKTADAAGDGTTTATVLAYSIF KEGLRNITAGANPIEVKRGMDKAEAII NELKKASKKVGGKEETTOVATISANSD HNIGKLIADAMEKVGKDGVITVEEAKGI EDELDVVEGMQFDRGYLSPYFVTNAE KMTAQLDNAYILLTDKKISSMKDILPLLE KTMKEGKPLLIAEDIEGEALTT
HP1559	2107 ACCGCCCAGCTTTTAGAGAAAGAAGGGCGATTTGATAGGGATTTCCGCTTTAGAAGGTGGGTAAGACTTTCGCTGA AACGGACGCTGAAGTGAGCCATTGACTTTTTAGAGTTTTACCCTTACAGGTTAAGGGTGTTGCCAAGAGGAAA ACAAAAAACGCAATTCACCCCTAAAGGCGTGGGGCGTGTTGCCCTATGCCCTTAAGGGTGTTGCCAAGAGGCAAA ACAAAAAACGCAATTCACCCCTAAAGGCGTGGGGCGTGGTCATTGCCCTGTGGGCATTTCTGTA GGCACTATCGCTGCCCCCCTAGCTACGGGCAATCGGGTGATTTACAAGCCCTCAAGTTTGTCTAGCGTAACGGGCT ATAAGCTTTG	2108 TAQLFRERRGDLIGISALEVGKTFAETD AEVSEAIDFLEFYPYSLRVLQEQNTKT QFTPKGVGVVIAPWNFPVGISVGTIAA PLATGNRVIYKPSSLSSVTGYKL
HP1559	2109 AAATCCACCGGTTATGGCGAAGATCTAAAACCCCAAAGGCTTTCAATGACGCACTCATTAAGAGCATGGATATTGAGAGCATGGATATTGAGAGCATGGATATTGAGAGCATGGATATTGAGAGCATTACCCTAGCAACAAACGAGCGTAGCAACAAACGAGAACGTTATTATCTTTCTCAAAAAAGGCTATTGATGGGTTTTGATGGGTTTTTAATCAGCGATTTTAAAAAGGCTTTTAAAAAAGGGTTTTAATCAGCGATTTTAAAAAAGGATTTTAAAAAAGGATTTTAAGCGATGAGGATTAAAAAAGGATTTTAAAGGAGTTTTAAGGGTTTTAAAAAA	2110 KSTGYGEDLKPNAKAFNDALIKSMDIE HYPSVKIRAVVARDSDVRAVPTNKPYY LSQKGYPFDRYQNSLIFQGTPVLITHFN LDKTYAHIGSSFYYGWIKVSDLVYMHD KDIELLTHLKDYVMPIKDKIPLYTDYGD FYTNEVGELFALIPQSQKTPQKPQKK
HP1559	2111 AGCCAAAGTCTATTCCAGCAAGAATAAAAACGCCCAAGAAGCCCATGAAGGGATCAGGCCCACTTCTATTATTTTAG AGCCAAACGCTTTAAAAGACTACCTTAAGCCTGAAGAATTAAGGCTCTATACCTTAATTTACAAACGCTTTTTAGCTTC TCAAATGCAAGACGCTCTTTTGAAAGCCCAAAGCGTGGTTGTGGCTTGCGAAAAAGGCGAGTTTAAAGCGGAGTGGG AGAAAGCTCCTTTTTGATGGCTATTATAAAATTTTAGGCAATGACGATAAGGACAAATTGCTCCCCAATTTGAAAGAAA	2112 AKVYSSKNKNAQEAHEAIRPTSIILEPN ALKDYLKPEELRLYTLIYKRFLASQMQD ALFESQSVVVACEKGEFKASGRKLLFD GYYKILGNDDKDKLLPNLKENDPIKLE
HP1559 HP1559	2113 GAGCAACGCCCATGTTACAGAACCTCCAGCGCTATTCTGAAGCGAGC 2115 AGGCAGGCCCAGCTTACAGAACCTCCAGCGCTTTTACAAAACAGAGCTACATCAAGGTAGAAAAAAGGCAAA 2115 AGGCAGGCCCAGCGCTTTTAGAACATTTTAGAAAACATTTTGAAGAAATTCGTGGATTCCAAATTTTACA TCAGTGCTTTAGAAGAAGAATTGGACAATATCGCTCAAAATAAAGCCGACTACCAGCAAGTCTTAAAGGACTTTTACA GCGCTTCTTTAGGAAGAAGAATTGGACAATATCGCTCAAAATAAGCCGACTACAAAAAACCGGTCAATCAT ACCCCTTTATGGATAAAATTGAACCTGGGAAAAAGAATATCATCTCTCAAAAAGTGCGGAACAATTACCCTAAA GCCCTAAATGCGGTGGGGAATTAGTCAAAAAAAAAA	2114 SNAHVTEPPARYSEAS 2116 GRPSTYAPTISLLÖNRDYIKVEKKÖISA LESAFKVIEILEKHFEENDSKFSASLEE ELDNIAQNIKADYQQVLKDFYYPFMDKI EAGKNIISQKVHEKTGQSCPKCGGEL VKKNSRYGEFIACNNYPKCKYVKQTES ANDEADQELCEKCGGEMVQKFSRNG AFLACNNYPECKNTKSLKNTPNAKE

HP1559	2117	2117 ATTGCGTGCAAGAAAGCGAAAGAATTAGACGATAAAGTCCAAGATAAATCCAAACAAGCTGAAAAAGAAAATCAAATC	2118 JACKKAKELDDKVQDK;3KQAEKENQIN
		AATTGGTGGAAATATTCAGGATTAACAATAGCGGCAAGTTTATTATTAGCCGCTTGTAGCGCTGGTGATACTGATAAA	WWKYSGLTIAASLLLA\CSAGDTDKQI
		CAGATAGAACTAGAACAAGAAAAAAAGGAAGCTGAAAACGCTAGGGATAGAGCGAACAAGAGTGGGATAGAACTAG	ELEGEKKEAENARDRANKSGIELEGER
		AACAAGAAAGACAGAAAACAAAGAAGAGGGATAGAACTCGCTAATAGTCAAATAAAAGGAGAAGAAGAAGAAGAAGAA	QKTNKSGIELANSQIKAEQERQKTEQE
		AAGACAGAACAAGAAAAACAAAAAGCAAATAAGAGTGCGATAGAGTTAGAACAGCAAAAAAAA	KOKANKSAIELEOOKOKTINTORDLIKE
		CAAAGAGATTTGATTAAAGAACAGAAAGATTTCATTAAAGAAACAGAACAAAATTGCCAAGAAAATCATAATCAATTCT	OKDFIKETEONCOENHNOFFIKKLGIK
		ITATTAAAAAATTAGGAATTAAGGGTGGCATTGCTATAGAAGTAGAAGCTGAATGCAAAACCCCTAAACCTGCAAAAA	GGIAIEVEAECKTPKPAKTNQTPIQPKH
		CAATCAAACCCCTATCCAGCCAAAACACCTCCCAAACTCTAAACAACTCTCATTCTCAAAGAGGATCAAAAGCGCAA	LPNSKQPHSQRGSKA()EFIAYLQKELE
		GAGTITATOGCTTATTTGCAAAAAGAGCTAGAATTTCTGCCCTATTCGCAAAAAGCTATCGCTAAACAAGTGAATTTCT	FLPYSQKAIAKQVNFYKPSSIAYLELDP
		ATAAACCAAGTTCTATCGCTTATTTAGAACTAGATCCTAGAGATTTTAAGGTTACAGAAGAATGGCAAAAAGAAAATCT	RDFKVTEEWQKENLKII\SKAQAKMLE
		AAAAATACGCTCTAAAGCTCAAGCTAAAATGCTTGAAATGAGGGATTTAAAACCAGACCCACAAGCCACCACCACCACCACCACCACC	MRDLKPDPQAHLPTSQSLLFVQKIFAD
		CTCTCAAAGCCT1:TTGTTCGTTCAAAAATATTTGCTGATGTTAATAAAGAAATAGAAGCAGTTGCTAATACTGAAAAG	VNKEIEAVANTEKKAEKAGYGYSKRM
		AAAGCAGAAAAAGCGGGTTATGGTTATAGTAAAAGGATGTAGGCATAAGAAAATAAGAACACCATAAAATCGTTTTA	
		GCTTCTAGGA	
HP1559	2119	2119 ATCGCTGAAATCGTGCGTTTGAGAGAAAACGCCCTGAAAAACCACCCTGATGCAACGATGGTTAAAATTTATCATGC	2120 IAEIVRLRENALKNHPD/ATMVKIYHAML
		GATECTTGAGTGTTATGATAATGGGGCTAATTCTAAAGAAAGGTATCTGCCTGGTTCTTTGAAAGTAACACGATTGGC	ECYDNGANSKERYLPGSLKVTRLAPSI
		CCCAAGCATTAAAACGCGCCTAGAAAAACACCCCACAAGCGGGAAAGACCCCTTAGCCTTGATTACATTTCGC	KTRLEKHPTSGKDPLAI.IDYISLYARAIA
		TTTACGCTCGCCCCATTGCTGAAGAAACGCTAGCGGAGGCAAGGTGGTAACCGCCCCCACTAATGGGGCGTGCG	EENASGGKVVTAPTNGACAVVPSVLL
		CGGTGGTGCCAAGCGTGCTTTTATACGCTAAAA	YAK
HP1559	2121	2121 CCAAGAAGGTTGCTATCATTGCCATTCCCAGCTTATTCGCCCTTTCCAAGCTGAGGTGGATCGATATGGCGGGTATA	2122 QEGCYHCHSQLIRPFQAEVDRYGAYS
		GTTTGAGTGGGGAATACGCGTATGACAGGCCATTTTGTGGGGTTCTAAAAGGATTGGCCCTGATTTGCACAGGGTA	LSGEYAYDRPFLWGSKRIGPDLHRVG
		GGGGATTATCGCACAACCGATTGGCATGAAAAGCACATGTTTGATCCTAAAAGCGTTGTGCCGCACAGCATCATGCC	DYRTTDWHEKHMFDPKSVVPHSIMPA
		CGCCTATAAGCATTTATTTACAAAAAAGGGGATTTTGACACCGCTTATGCAGAAGCTTTGACGCAAAAAAGGTTTT	YKHLFTKKSDFDTAYAEALTQKKVFGV
_		TGGCGTGCCTTATGACACAGAAAACGGCGTGAAATTAGGGAGCGTAGAAGAAGGGGAAAAAAGGCTATTTAGAAGAA	PYDTENGVKLGSVEEAKKAYLEEAKKI
		GCTAAAAAAATCACAGCCGATATGAAAGACAAGAGGGTGCTAGAAGCGATTGAGAGGGTGAAGTGTTAGAAATTGT	TADMKDKRVLEAIERGE:VLEIVALIAYL
		GGCTT1GATCGCTTATTTGAATAGCTTGGGTAATTCCAGGATCAACGCCAATCAAAACGCGTAAATAAGGGGTGAATG	NSLGNSRINANGNAK
		ATGGATTTAGAAAGTTTGAGAGGTTTTGCGTATGCGTTTTTTACCATTCTTTTTACGCTCTTTTTGTATGCCTATATTTT	
		TAGCATGTATAGAAAGCAAAAAAAAGGCATTATGGATTATGAGCGATACGGATACTTAGCGTTAAATGATGCTTTAGA	
	.	AGACGAGTTGATTGAACCACGCCATAAAAAGTTCATGATAATGGCATAAAGGAAAGTTGAAATGGATTTTTAAACG	
		ACCATATAAATGTTFTTGGCTTGATTGCAGCGCTTGTGATTTTAGTTTTAACCATCTATGAATCCAGTTCGCTCATTAA	
		AGAAATGCGCGACAGCAAATCTCAAGGTGAGCTTGTAGAAAATGGGCATTTGATTGA	
		AATAATGTGCCAGTAGGCTGGATCGCAAGCTTTATGTGCACGATT	_

GIOCSNTNEVSAKARLGIKUDIEDITI GIOCSNTNEVSAKARLGIKUDIEDITI GIOCSNTNEVSAKARLGIKUDIEKIITTIP APSGDFNAPLKIPTKSLECGEIGIVSLGLK SVTDIANGDTLTDAKNPTSKPIEGFMPA KPFVFAGLYPIETDRFEDLREALLKLGL INDCALNFEPESSVALGFGFRVGFLGLL HMEVIKERLEREFGLNLIATAPTVYYEV HLTDNSIKYVQNPSELPPENCIACIKEP FVRATIITPSEFLGNLMQLLNNKRGIQE KMEYLNQSRVMLTYSLPSNEIVMDFYD KLKSCTKGYASFDYEPIENREANLVKL DVRVAGDVVDALSIIIDKNKAYEKGRAL VETMKELIPRQLFEVAIGAGFLGE KMEYLNQSRVMLTYSLPSNEIVMDFYD KLKSCTKGYASFDYEPIENREANLVKL DVRVAGDVVDALSIIIDKNKAYEKGRAL VETMKELIPRQLFEVAIGAGFLGIL SAEEKIGGONPTSMFDLNKIKYQWADHL VKTMLANTWFAEEVSMNDDKRDYLKL SAEEKIGYDRALAQLIFMDSLQANNLID NINPFITSPEINLCLVRQAYEEALHSHA YAVMVESISANTEEIYDMWRNDMQLK SKNDYIAQVYMELAKNPTEENILKALFA NOILEGIYFYSGFSYF Z128 ĀFIĒSĀSIĒKMĀSKSPPPPLKIĀVÁNNWW GDEEIKFFKKSVLYFILDASSGT NALIKKVENSLISMDMNGRSLEPVFVE KTINTILNLHDKVIGAKDETISAFKNENM FLKDALISMOMNGRSLEPVFVE KTINTILNLHDKVIGAKDETISAFKNENM FLKDALISMOMNGRSLEPVFVE KTINTILNLHDKVIGAKDETISAFKNENM FLKDALISMOEVYEEDKKTIDLLRDELN NKK

				A
HP1559	2131 AGCCCCTAGACAATTCAAGCAAACCCAAACGGGCGCGTATATG GCTTTGGATAACGCCTTAAGAACGCTTTTTATCCATGAATTAGAGC AAAGAGCTTCTCAATGAGCCTGTGGATAAAAAAGAAATTTTGAATT GGGGAATACACCAAACGCCTGAAATTAGTGGAATTCTTATGTTAT GAAAAAGAATTGTTTTAGATGTGGGGGTGTTTTGCAGATAGACA	2131 AGCCCCCTAGACAATTCAAGCAAACCCAAACGGGCGCTATATGCGTCTTTTAAAATTTTTAGACATTCAAAAAAC GCTTTGGATAACGCCTTAAGAACGCTTTTTATCCATGAATTAGAGCGCCTTAAACAGCGAACAATTTAGCC AAAGAGCTTCTCAATGAGCCTGTGGATAAAAAAAGAAATTTTGAATCCCTATGTCAAGAAATCGCCGATCACGCTT GGGGAATACACCAAACGCCTGAAATTAGTGGAATTTTTTTT	2132 SPLDKFKQT LDNALRTLFI LNEPVDKKE KRLKLVEFLI DVGVFLQID	2132 SPLDKFKQTQTGAYMRI.LKFLDIQKNA LDNALRTLFIHELEQPLNSEQQNLAKEL LNEPVDKKENFESLCQE!IADHTHGEYT KRLKLVEFLMLLAYADGILDSKEKELFL DVGVFLQID
НР1559	2133 CGAACGAGAGATTTACGATCTAGACTATGCG CGCAAAAGAGAACGGACATGAACGAAGAGCA GCGGAGGGTTTGAAGATTTACCGATCATTCTA GCTAAACTTCACGCCTAAAAGCCGTTTTTCTTA CGAGTTGTTAGTGAGAGTGCCACAAGGGG GACGCTTCAATAGCGATCACGCTTAAAA AATTAGACGCTGATAGCGTTCATTAAAA ATGTAACCGATAGTAGTATTAGCGTTGCTGATG GCTGGAAAAAGAATTTACCAACGACGCGATG GCTGGAAAAAGAATTTACCAATCGACTTAAAA TTCACAATTTAAGAATTTACCAAAGCACGGGGGGGGGG	CGCAAAGGAGATTTACGATCTAGACTATGCGATCGTCAAAGCATTTAAAAGCATTTAAAAACCAGGCGGGGAACGAAC	2134 EREIYDLD RTDMNEE EDLPIILHE SRESYER KRLNNTEI IAVLSHYE VKKMFVDI VKKMFVDI VKKMFVDI AYLSDIMD SEKFYKTS GAIARFAR ILKDYKIAD ILKDYKIAD ILKDYKIAD ILKDKIAD MQKE	2134 EREIYDLDYAIVKAKDLKPSFTTGGTQK RTDMNEEQIKSIAENFDI?KKIFGSGGF EDLPIILHDGQVIAGNHRIQGMLNFTPK SRFSYERAIKEYYHIDLKPDELLVRVPH KRLNNTEINNLAASSNQGRFNSESDHA IAVLSHYEAKLKELDQKI.DADSIYSLKNI VAKNILNFDKATHPNVTD.SNLALLMFNM PRTKTQGIELLNRWKKEFSNDIKSYEK VKKMFVDNAGSFHNLIHDLNFPKVSLN AYLSDIMDRSFANLKNYJSTSESLKDL SEKFYKTSSLEMFEKSDQSTSDISEILG GAJARFARFDDPSKALFFALRSDNIKKG LKDYKIADVTKDMFNADSKEFKDIDIYD FTHYLLMVNREPNENNFILKRLIEAVKD MQKE
HP1559	2135 CGCTGATGTGATGCGTTCAGGCCCCATCAACO CACCCCATACATGGGGATTTTAAAGCCGTCGC CGCGTTCAATTTGGCTGAAATGCTCATGACTC AGGTGCAAATCCCAGATTTAGAAGAAGTGCAA ACAAGCCTTATGGGGTCGCACAAGACGAGCC GGCTTGCACCATGGGCCTATTGGCTTTCCTAC	CGCTGATGTGATGCGTTCAGGCCCATCAACCGGAATGCCCACTCGTGTGGCTCAAGGCGATGTGAATTTCTTAAGA CACCCCATACATGGGGGATTTTAAAGCCGTCGCGCTCCTGCGAATTTAGAAGAAGCTTACACCGAAACCGTTCG CACCCCATACATTTGGCTGAAATGCTCATGACTCCTGTATTCTTGCTCATGGATGAAACCGTTGGGCATATGTATG	2136 ADVMRSG HPIHGDFK FNLAEMLN QIPDLEEV YGVAQDEI HGPIGFPT	2136 ADVMRSGPSTGMPTRVAQGDVNFLR HPIHGDFKAVALAPANLEEAYTETVRA FNLAEMLMTPVFLLMDETVGHMYGKV QIPDLEEVQKMTINRKEFLGDKKDYKP YGVAQDEPAVLNPFFKGYRYHVSGLH HGPIGFPTEDAKIGGDLIDRLFNKIES
HP1559	2137 GATACGAAAATTTTAATAGGACTTTTTTTGAGGGTGAGAGGGGAAACTCCAAACTCCAAACTCCTTCGTGAAAAGGGCGATGTTTTGTTGCTTTCGTGAAAAGGGCGATGTTTTGTTGCTTTCGCTAAAAAGCAATACCAACGATTCGATACGATTCGATTCTACAGGCGCTTGGAGTAAAAACATTGATGAGGGATTCTAATCAGCAATTGATCAAAAGCATTTTGATGAGGGATTTAAAAAAACAGTAAAAAAAA	2137 GATACGAAAAATITTAATAGGACTTTTTTTGAGCATGGAAGCTGGCGGAAAAGTGTAGCGATTTCAAT GTGAAAGCGACACAAGATTCCAAACTCCAAACTCGCAGGAATTGTGGGATAGCGTTAAGGTTACTGAGGGGGGGG	2138 IRKILIGLFLSFL TQDSKLTLDST DVLLLLYNQDK QYQRYSKIGGA ESDYAYSIAVLN QVGEGVSANN DSKYINAVKVG KITKIYPTVDEN GLFGDGFIQTK	2138 IRKILIGLFLSFLSMEAĞEKVYAIFNVKA TQDSKLTLDSTGIVDSIK/TEGSVVKKG DVLLLYNQDKQAQSDS TEQQLIFAKK QYQRYSKIGGAVDKNTLEGYEFTYRRL ESDYAYSIAVLNKTILRAFFDGVIASKNI QVGEGVSANNTVLLRLV.SHARKLVIEF DSKYINAVKVGDTYTYSIJOGDSNQHEA KITKIYPTVDENTRKVSAFALLSKPMAV GLFGDGFIQTK

MD1550	2139 AAAATTGAACGCCCCAAGGTTTGCCCATCACATCACATC	
3	CTTAATTGCCCGGCAAGGTTGAAAGAAAGCTTCATTCACTTCTAAAAGACCTTTAAAAAAATTAAAAAAAA	Z140/NIERPRVCPICSHELLCEE/FIYCUNLN
	GATAAAGTCATAGAGCAACTTTTGAAGAAAAGCTCATTTTAACGCTCTGGATTTGTATGCTTTAAAATTAGAAGATTT	FOLFERKLIFNALDI YALKI FDI MRI DK
	TAATGCGGCTAGACAAATTAAAAATTAAAAAGCTCAAAATCTATTAGACGCTATTTTAAAAAAGCCAAAAAACCCTCCCT	FKIKKAONLLDAILKSKNPPLWRLINAL
	ATGGCGTTTGATTAACGCTTTAGGGATTGAGCATATTGGTAAGGGAGCGAGTAAAACGCTGGCCAAATACGGCTTAA	GIEHIGKGASKTLAKYGLNVLEKSEAEF
	ATGTGTAGAAAAAAAGCGGAAGCCGAGTTTTTAGAAATGGAAGGCTTTGGGGTGGAAATGGCGCCCTTTAGTCAAT	LEMEGFGVEMARSLVNFYASNOEFIRS
	IIIIAIGCGAGCAAICAAGAAIIIAICCGA	LFELL
HP1559	Z141) I 1941 I GAAAAAAGCGAAAACCTICIA I GGCGAAGATAAAGAAAATIGAATGTTT GAAAATTCCAGCGCGCTA	2142 LIEKAKTFYGEDKEKLNVLIENSSALER
	STATE OF THE STATE	ELKOKNEHLENALKEOEYLKNAWLLE
		MEKOKEIPHNKKLELEKSYQUALNILKS
		EVAUND SUMMERSTANDS CONTROLL OF THE STATE OF
	ACCOMMANACOM	
	TGGGAGTÍTGTTGAAAAAAATCCAAAAA	מייט בייט בייט בייט בייט בייט בייט בייט
HP1559	13	2144 ENLFWGEIDATKRLENVIDLLWDMNIP
	CCIGCITITALITIAGAAAAACATGCCCTTTTGCAAGACATCGCGCGATCTCAAGGGCTGCTTTTGGATAACAAACCT	AFILEKHALLQDIARSQGLLLDNKPCQV
	TGCCAAGTTTTGAATTAGAGGTTTTACGCGCTCTATTAAATAGCCCTATAAAAGGGGGTCTGACTTTTGAATACCGC	FELEVLRALLNSPIKARLTFEYACKHCK
	TGCAAGCATTGCAAACAAATCTTTCCTTTTGAAAGCCATAGGTGTCCTGTGTGTTACCAGTTAGCGTTTATGGATATG	QIFPFESHRCPVCYQLAFMDMVLKISK
	GIGCTTAAAATCTCTAAAGAAAGCTATGGGAGTGGATTGAATGCAAGAAATTGAAATTTTTGCGATGGCTCTTTTT	ESYGSGLNARN
The state of the s		
HP1559	2145 TGAATAGGCAAGGGGGTAGAAAGCTCTTTATTAAAAGGCTCAGAGTATAATGATTTAATGGATCAAAAGGGGTTTTT	2146 EIGKGVESSLLKGSEYNDLMDGKGFLS
	GAGCAAT CETAGCGGAGGGETT TAGGGGGCATGAGCAATGGGGAAGAATCATT GTTAGAGTGCATTTCAAACCC	NRSGGVLGGMSNGEEIIVRVHFKPTPS
	ACGCCAAGCATTTTCCAACCTCAACGAACCATAGACATTAATGGCAATGAGTGCGAATGCTTGTTAAAGGGCAGGCA	[IFQPQRTIDINGNECECLLKGRHDPCIAI]
	TGATCCTTGCGATTAGAGGGAGCGTGGTGTGCGAGAGTTTGTTAGCGTTGGTGTTGGCTGATATGGTATTAC	RGSVVCESLLALVLADMVLLNLTSKIE
1	<u>TCAATTTGACTTCAAAAATAGAGTA</u>	يبيد الم
HP1559		2148 TOAAONRDGSLNNFKNIALTDSLDYLE
	I AGARGAAAACCAA I AAAGGGGG I GCTCCCTTTATATGAGGATTTGAAAAAAAAAAAGGCATCAAAGACAACGAAGGCATCAAAGACAAGGCATCAAAGACAAGGCATCAAAGACAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	EKTNKGVLPLYEDLKENKGIKDTLANQ
	CCACCEAAA I A I A GA I CA I CO COCCO TA I CAGCEGECEAA GA GEATAACAA COAA	NIRVIIGNPPYSAGAKSONDNNONLSH
	AACULI CACACCCAAAGCI I GAAAAA I AGIII A I GAAAAA I ACGGAAAAAA I I CCACA I CI AGAAAG I GI GGGAAAA	PKLEKLVYEKYGKNSTSRSVGKTTRDT
	AUCHCHCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CREADCEBACYAKESWI SAI KII BON
	TATGLE TO ACCUMENT TO A SECRET AND ACCUMENT TO THE SECRET AND ACCUMENTATION TO THE SECRET ACCUMENTATION TO THE SECRET ACCUMENTATION TO THE SECRET ACCUMENTATION TO THE SECRET ACCUMENTATION TO THE SECRET ACCUMENTATION TO THE SECRET ACCUMENTATION TO THE SECRET ACCUMENTATION TO THE SECRET ACCUMENTATION TO THE SECRET ACCUMENTATION TO THE SECRET ACCUMENTATION TO THE SECRET ACCUMENTAT	
	CGGATCGAGGGGGGGGGGTAGCGATTATCTTTTTTGTGAAAGATAAGAGCACTCCTGATAATAAGAGTATTTTTATTATA	FVKDKSTPDNTIFYYEVEDYI KRFAKI
	AGTGGAAGATTACTTGAAAAGAGAAGCCAAACTCAACTGGCTCGCCAATTTTGAAAATTTGGATTTTGTGCTTTTGA	NWLANFENLDFVPFEKITPNDKGDWIN
_		QRNDAFEKLIPLKRDKTLQNDSVFDINS
_	AGACAAAACACTCCAAAACGACAGCGTTTTTGACATCAATTCTCTTGGCGTGGTGAGCGGTCGTGATCCTTGGGTGT	LGVVSGRDPWVYNFSPNILTQSVQKCI
	TCTCCAAACATTTTAACCCAATC	DTYNADLKRFNARFREAFKORAGSVK
	I BUGUGE I I I AUGGAAGU I I UAAAUAUGUGU I CAAAGUG I CAAAGUGGUGAI CI I I AUAAAUAACI TAATGATA IAAGAAATGACCACCGAT	AGDLYKQLNDKEITTOKTKIAWTOGLK

	2149 PACGAACAAGAACCCAATAAAATCGCCTTAGAATTTTATGAAGTTTTGAGCAAGTTTGAGCGCGCGC	2150 NEQEPNKIALEFYEVLSKFEAN/CATPT SYKEMALLSKYGGGIGWDFSLVRSIGS SYNDGHKNASAGTIPFLKIANDVAIAVDOL GTRKGAIAVYLEIWHIDVWAEFILLRKNS GDERRAHDLFPALWVCDLFLKRNS GDERRAHDLFPALWVCDLFLKRNS GDERRAHDLFPALWVCDLFLKRNS GDERRAHDLFPALWVCDLFLKRNLE DAMWTLFDPYECKDLTELYGCDFEKR YLEYEKDPKIIKEYINAKDLWKKILMNYF EAGLPFLAFKDNANRCNPNAHAGIIRS SNLCTEIFQNTAPNHYYMQIEYTDGTIE FFEEKELVTTDSNITKCANKLTSTDILK GKPIYIATKVAKDGQTAVCNLASINLSKI NTEEDIKRVVPIMVRLLDNVIDLNFYPN RKVKATNLQNRAIGLGVMGEAGMLAE
HP1559	2151 ITTACCCACAGACCAGATTTTAAAAAGAGGGGCTAATTTATTCACCAATGCCGAAGGCGATTTCAAAATTTTAAATTCTCAATTCTCAATTCTCAATTCTCAATTCTCAATTTCTCAATTTCTTATTA	HUJAWGS 2152 LPTDTILKRAANLFTNAEAISKLKFSSLS PVRVLYMYNGQLTIENFLPYNLSNVKL SFTDAGGNVIDLGVIETIPKHSK.VLPGE AFDSLKIDPYTLELPKIEATSTSVSDANT QRVFETLNKIKTDLVVNYRNENKFKÖH ENHWEAFTPQTAEEFTNLMLNIMAVLD SQSWGDAILNAPFEFTNKDGGE
HP1559	2153	2154 VALAFLSADSAQANKAIŠNADLIKEIRDL KKIISAQNTEINNLRKVQEVLSGOLGDM RKDILSTRDYCISLRPYIYNWR

066501			PCT/EP01/15428
2164 LDRLCAKALTLLKKQIEPGAKTYLLNNS AGDARALLNLDLSAKIEDPITLKTLQSL RPHSLNDGSYSDDTHYNLTSALIKSLR GSDENASIYYLARLAGGENPEFIARRL VIFASEDIGNANPNALNILAASCLFAVKQ IGYPEARIILSQCVYLACSPKSNTAYRA INQALDCVQKGSLYPIFYHLLPNAKDYL YPHDYNGYVKQDYLEKPLDLVSSQGIG FEKTLLEWLDKIRN	2166 PHSSKIKPHTPTTRAKT GEELKREEEG AIDEVLKIEFLELALGYCILISLADMKOG GDLLERIRGIRKKIASDYGFLMPQIRIRD NLQLPPTHYEIKLKGIVIGEGMVMPDKF LAMNTGFVNKEIEGIPTKEPAFGMDAL WIETKNKEEAIIQGYTIIIDPSTVIATHTSE LVKKYAEDFITKDEVKSLLERLAKDYPT IVEESKKIPTGAIRSVLOALLHEKIPIKD MLTILETITDIAPLVQNDVNILTEQVRAR LSRVITNAF	2168 FAALDKNDPEYPTIQEIKSLIAKPSIDAV LHLHDGGGYYRPVYVDAMLNPKRWG NCFIIDQDEVKGAKFPNILAFANNTIESI NAHLLHPIEEYHLKNTRTAQGDTEMQK ALTFYAINQKKSAFANEASKELPLASRV FYHLQAIEGLLNQLNIPI-KRDF	2170 QLPKSRVRLNEREIYDLDYAIVKAKÖLK PSFTTGGTQKRTDMNEEQIKSIAENFD PKKIFGSGGFEDLPIILHDGQVIAGNHRI QGMLNFTPKSRFSYERAIKEYYHIDLK PDELLVRVPHKRLNNTI∃INNLAASSNQ GRFNSESDHAIAVLSHYEAKLKELDQK LDADSIYSLKNIVAKNLNFDKATHPNVT DSNLALLMFNMPRTKTQGIELLNRWKK EFSNDIKSYEKVKMFVDNGSFHNLI HDLNFFKVSLNAYLSDIMDRSFANLKN YQSTSESLKDLSEKFYYTSSLEMFEKS DQSTSDISEILGGAIARFARFDDPSKAL FEALRSDNIKKGLKDYKIADVTKDMFN ADSKEFKDIDIYDF
2163 ITTAGACAGGCTAAAAGCTTTAACATTGCTCAAAAAACAATTGAGGCGCTAAAAACCTATCTTTTAAA CAACAGCGCTGGCGACGCTAGAGCGTTATTAAACCTTTTAGAGTTTGAGCGCTAAAATGAGAGCCTTAAA CAACAGCGCTGGCGACGCTAGAGCGTTATTAAACCTTTATAGCGATGATACGCATTGATACCTTTACTAGCGC GTTAATCAAATCTTTAAGAGGCGATGAAAACGCTTCCATCTTATTCTGCGCGCCTTGATTGCTGGCGGGGGAAA ACCCGGAATTTATCGCCGAAGGCTGGTGATTTTGCGAGCGCGCTTTTAAGCCCTTAAT TAGCCGCTTCTTGTTTGTTTGTTGGTCAACAGCGTTATAGAGCGCTTTGGATTGCTGATTGCTGAT TAGCCGCTTCTTGTTTGTTTGTCAACAGCGCTTATAGAGCGATCGCTTTGGATTGCTAAT ACTCTACCCTTTTTGTTTGTCTAACAGCGCTAACGCTTAAAGATTTGGAAAAACCCCTTTTAAGCCTTTATGAAAAAGGCTC ACTCTACCCTTTTTTGGAACTCTGCTGCTGCTGCTGCTTTATAAGGCTTTTAAAAAAAA	2165 ACCCCACAGCTCCAAAATCAAACCCCACACCCCAACCAAGGGGTTAAAAAGAGAGAG	2167 TTTGCCGCTTTAGACAAGAATGACCCTGAATACCCCCACTATCCAGGAAATCCAAATCCTTGATTGCAAAACCCGGTATA GACGCTGTCTTGCATTTGCATGATGGCGGTGGGTTTACCGCCCTGTTTATGTTGATGCGATGCTCAATCCTAAGCG GACGCTGTTTATTGCATGATGGCGTGGGTTAAAGGGGCGGAAATTCCCTAATTTGCTTTTGCAAACAACAACAA TACGATTGAGAGTATCAACGCCCATTTATTGCAATTGAAGAGTATCATTTAAAAAACACGCGCACCGCGCAAG GCGATACAGAAATGCAAAAACACCCCATTTATTGCGATCAACAAAAAAAA	2169 CAATTACCCGAAAGCCGAGTGAGGCTAAACGAACGAGATTTACGATCTAGACTATGCGATCGTCAAAGCGAAAGA TTTAAAACCAAGCTTTACCACAGGCGGAGGGGTTTGAAAGGATTTACAAAGCATTGTACAAGAGCATTGCTG AAAATTTTGATCCTAAAAAGATATTTGGTAGCGGAGGGGTTTGAAGAGTTTTTACCGATCATTGTACATGACGGGCAAGTGA TCGCAGGAAACCACAGAATCCAAGGCATGCTAAAGTCTCAAAAAGCCGTTTTTTTT
HP1559	HP1559	HP1559	HP1559

LIDIES	2171 ATTC.	2171 ATT64/C4/CC4C4A444		
} =	GTCC	GTCCAAACAAGTTCAGGAATTGCACCAAAAAGAAGGGGGAATTGAAAGGCTTAAAAAAAA	2172 IEEARKNAFLEQQKGLELLOKELDEKS	ELLOKELDEK
	9006	GCCGATTAAAAGCTGAAAATGAAAAATTGAATGAAAATTGGATTTGGAGAGAAAAAA	KOVOELHOKEAEIERLKRENNEAESRL KAENEKKI NEKI DI EREKIEKAI HEKN	KRENNEAESI Sekiekai Heki
	AS IN IN IN IN IN IN IN IN IN IN IN IN IN	GAAAGGCTGAATTAAGTTGCAAGAAGCAGCAGGAGGCAATTAGAAATGTTAAGAAACGAGTTGAAAAACGCTCAAA	ELKFKOGEEGLEMLRNELKNAGRKAE	NELKNAORKA
	100	TCCCCCTAGATTGCATTGCATTGAAGAAATCAAAAAACCCAAAAA	LSSQQFQGEVQELAIEEFLRQKFPLDCI	EFLROKFPLD
	ATTIC	ATTICAAAATTIGGGGAAAATTTATTATGAGAGAAAATTTATGAGAGAAAACTAAAAAAAA	EEIKKGORGGDCIOVVHTREFONCGKI	'HTREFONCG
ņ	AAGC	AAGCGACATGCGAGATTGGGGCTGATGTGGGGGT	YYESKRTKEFOKAWVEKLKSDMREIG	EKLKSDMREIC
HP1559	2173 ACAA	2173 ACAATAGCGACAAGTTTATTATTATTAGCCGCTTGTAGCACTGGTGATGTTAGTGAACAAATAGAACTAGAACAAGAAAAA	2174 TIATSULI AACSTGDVSEOIEI EOEKOK	FOIFI FOFKOI
	AATAA	CAMMAGAGAGAGAAGTAAGAGAGTAAGAAGTAAGAAGTAGAAGA	TSNIETNNOIKVEGEKOKTSNIETNNOI	KTSNIETNNO
•	S ACA	CHRYLLANDAR AND AND AND AND AND AND AND AND AND AND	KVEGEGOKTEGEROKTEGEROKTEG	TEGEROKTEO
	TCATA	TCATAATCAATTCITTATTGAAAAAGGGAGGAATTAACCCTCCTATATCAAAAAGATATGAAAAATTGAAAAAAAGGAAAAAAAA	EKOKTIKTOKDFIKYVEONCOENHNOF	ONCOENHNO
	TAAAC	TAAACCTGCAAAAACCAATCAAACCCCTATCCACCCCAAAACCCCC	FIEKGGIKAGIGIEVEAECKTPKPAKTN	CKTPKPAKTN
	GATC	GATCAAAAGCGCAAGAGCTTATCGCTTATTTGCAAAAAAAA	QTPIQPKHLPNSKQPRSQRGSKAQEL	SORGSKADEL
	AACA	AACAAGTGGATTTTTATAGACCAAGTTCTATCGCTTATTTAGAACTAGACCCTAGAGATTTAAAAGAAAAAAAA	AYLOKELESLPYSOKAIAKQVDFYRPS	IAKQVDFYRPS
	SCAA	GCAAAAGGAAAATTAAAAATACGCTCTAAAGCTCAAAGCTAAAATGCTTGAAATGAGGAGHTTAAAACCAGACTCACA	SIATLELUPRUPNY JEEWUKENLKIRS KADAKMI EMBSI KODSOAUI STSOSI	WOKENLKIRS
	AGCC	AGCCCACCTTTCAACCTCTCAAAGCCTTTTGTTCGTTCAAAAATATTTGCTGATGTTAATAAAGAAATAAAAGETAAAA		CATE SCAL
	GCTA	GCTAATACTGAAAAGAAAGGAAAAAAGGGGGTTATGGTTATAGTAAAAGGATGTAGGGATAAGAAAAAA	LFV UNIFAD VNKE KVVAN EKKAEKAG	AN EKKAEKAG
3 1 1	ATCG	ATCGITCITAGCITATITATAGTATITTAAAAACTCTATGTTAC	NEW COLOR	
HP1559	2175 TTAAA	ACCCCTATCGCTCAAGAAGAAGTGGATGCATTAGCCCTGGAGTTTGGCACTATTATAGAACAAAAGCTTTTT	2176 KTPIAOFEVDAI AI FEGTIIEOKI ENDE	CTIIEOKI ENDE
-	GATAC	GATAGGGAGCATTTGAATAGCGAAGTGATGGCATTTATTGATAAGCATTATAAAAATCATGTTTTCCATATCGCTTCA	HLNSEVMAFIDKHYKNHVFHIASAAI	AVEHIASAAI H
	1001 1001	SCUSTULI GUALAGUGAATI GCAAGTGTTGTGGGGATTTTTAGGGATCATTAAGTATTTAAGAGCGTTGAAGGGAG	SEI OVI CEEI GIIKVEKSVEGSDDNIKDK	WEGSPONKOK
	3100	CCGCCIAAIAAACCCAAGAICATCGCTAATATCATTCAAAAATACGCCTATAACCCAGGCCGCATGCTAATGATAGG	IIIANIIOKYAVNPGRMI MIGHSVAINVES	
	CGAL	CALAGCETCAATGACAGGGCTCAAGCTAATGAAGGGCGTTTTTGGGTTACAACAGCAGGTTTTGAAAA	ACANEVAFI GYNSKVI KNI VRONICYO	KNI VGONGVO
	WILLY.	ALTIAN GEGEL CAAAACGGCTATCAAGGGAAGTATTTGGAGGCTTTAAGGGGTTTGATTTACAAAACTTTATAAAAG	GKYLESFKGFDLONFIKE	
UDAEEO	AG177	AN AMBUCCARUCTI I AGUCCARON I GI CT I TGTGTT GGCT CATGT CATGACTT CACAGGGTT CAATCGTGC		! ·
800171	1110 1112 1011111		2178 FWEERCNDLSHOILNKILDEDLIMFSVS	LDEDLIMESVS
	GAAG	GAAGTGCATGAAAAAAAAAACAATTACAAAAAAAAAAAA	ENLIRNLIYKSIDTYSKAYESIENEVHEKI	YESIENEVHEK
	CTC	GCTCTATGAAGAAGAATTAAGGCCCCAACTTTTTTTTTT	KHYKRKLPVGSDEYELVFERLYEEELR	FERLYEEELR
	7555	GGGCAAAGTTTTGGGGGTTAGCCGCCAAAGGGGGCTTTTTTGCAA	RKGFL	
	TCATT	TCATTAGCGACCCTAGCTATAAGGGGCAATTTGTGTGTTTTAGCATGCCTCAACAATTGCCATTAGCAATTAGCAATTAGAATTAGAATTAGAATTAGAATTTAGAATTTAGAA		
	AAAGA	AAAGATGATGAATCCTTTTTTCATGCGCAGGGGTTTTAGCGCGCGATTACAACTGAATTTTTTTAAACTGAAGAATTTTTTTT		
	GATT	GATTITAGCTTGAGCGCTTATTGAAAGAGCGTGGCGTTTTAGGGGTTTGTGGCGTTGATACTAGGAGTTTGATAAA		
	ACCTT	<u>ACCTTACGCCATCATGGGTGCTTAATGGTCGCTTCCACGATAGAGCATGACAAAAACAAGCTTGAAG</u>	· .	

~	

2/066501		PC
2180 TKAKNINATILTNITPTLIMDERKSIMQTYD VNHPLECGVCDKSGECELQDMTHLTG VEHQPYAVADDFKALDFWAKALYDPN LCIMCERCYTTCKDNVGENNLKATRAD LHAPDKFKDSMSKDAFSVWSRKQKGII SFVGSVPCYDCGECIAVCPVGALSYKD FAYTANAWELKKIHSTCSHCSAGCLIS YDVRHFDTLGEESKIFRVLNDFYHNPIC GAGRFAFDVSSSPKGSANLKEAQNAL KECEAVRIGGDITNEEAFLIERLRKELD FKIYNQEAYRFQQFLKVLGEIKRPSVEE IKTSHLVVTIGSSIKTEINPLVRYAINNAL KLNKASLIAMHPIKDNALANLCRSSFCI THEVGAEEILGMLLKALNIESAALKSL EDSKQNIVDEAALKALEERKKALEQA EQGCSIGENKAENQEENKTEATTPKEE	2182 VVQSNPDYISTHSESALDLLKLLKKNQ MNASAIEIAHLLINQDCIDLKAKEQALYD LGALYARIKOFKNAHL'YNLQYLQDHAE LDKASVVRARDEKALFSMEGNTQEKIA HYDKIIQNFPNSNEALKALELKAQLLFE NKRYAEVLSMQKNLPKOSPLIQKTLNV LAKTPLENHRCEEALKYLSQITTFEFSP KEEIQAFDCLYFASLKEKAQIIALNAFKT AKAPSEKLI AKAPSEKLI TFPTAMHIVSVLEITHRLLPSLENLLKTF KEKSQQFKEIVKIGRTHILQDATPLTLG QEFSGYASMLEHSKQQILESLEHLRFE	AIGGTAVGTGLNAHKELSEKVAEELSO FSGVKFVSAPNKFHALTSHDAIAYAHG AFKALAANLMKIANDIRWLASGPRCGL GELNIPENEPGSSIMPGKVNPTQCEAM TMVA
72	216	
Z179 CACGAAAACCAACCCCTACATCTCACTAACACCCCAACGCTCATGGATGG	2181 GGTGGTCCAATCCAACCCTGATTATATTTCTACGCATAGCGAATCAGCCCTAGACTTGCTCAAGTTATTGAAAAAAAA	IGGAGCATITAAGAGAATTGGCGGGGGGGCGCGTAGGCACAGGGCTAAACGCTCATAAAGAATTGAGCGA AAAAGTGGCTGAAGAATTGAGCCATTAGCGGCGTGAAATTCGTCTCTGCGCCCAATAAGTTCCATCCA
HP1559	HP1559	

_	٠
٦,	J
u	7
_	-

2/066501			
2186 IKRLSNDRFSQNELNDILMLSLLDGYIO NENKAFSPLLGALEEKFTRLEKLEKER RLLEDKKRFQKDLEERLNFEKMKLERL DLKEDEYERLLEQKKLLSSKEKLNDKIA LALEVLENTHKITHALESVGHSAEFLKS ALLEASALLEKEQAKLEECERLDIEKVL ERLGMLSGIIKDYGSIMHAKERLGHVK NELHNLKEIDSHCETYHKEIERLKTEC! KLCEEISGFRKEYLAGFNALLSAKAKDL LLKSPSLVLEDAPMSEKGAQKLVLNLQ	2188 ISNHEILRPLVEKFDIPYFYAPCDNÖVL HEKEVLEIKNLELKHKVSADLLVLAKY MRILSHDFTKRYENGILNIHHSFLPAFIG ANPYQQAFERGVKVIGATAHFVNESLD AGPIIIQDTLPINHNYSVEKMRLAGKDIE KLVLARALKLVLED	2190 ÉLEILKSYLKIPYTLLETNTLNSKACLKD LSOKISAFFPKLDTONKLLTSLACKIAL ENAITELQNAKNHLETLELFSYHILSAIE NLNLLTRPYETSOMLOSMFSEFCLGK	2192 YNÔFSSĞNĞSĞSKPPCPPYENGENCT AKVPPFTSQDAKNLTNLMLNMMAVFD SKSWEDAVKNAPFGFSDNNLSAPCYS NYSTCVNPYNDGLVDPKLJAKNKGDEY NIENGQTGSVILTPODVIYSYRVTNNLY VNLLPPRGGDLGLGSQYGGPNGPGD DĞTNFĞALGILSPFLDPEILFGKELNKV AIMĞLRDIIHEYGATHNGNMTYQ
			219
TCCAAAACGAAATAGGCGTTTAGCCCCCTTTAGGCGGATATTTTAGTGCTCTCCTTACTGGATGGCTTTAAAAACGAATAGGCGCTTACTGGATGGCTTTAGGCGATTAGAGAAAATAGCCCGATTAGAGAAAATAGCCCGATTAGAGAAAATAGAAAAATAGAAAAAATAGAAAAAATTTAGAAAAAA	2187 ATTICCAACCACGAGATTITACGCCCTTTAGTGGAAAAATTTGACATCCCTTATTTTATGCCCTTGCGACAATCAAG TTTTGCATGAAAAAGAAGTTTTAGAAATCATTAAAAACCTGGAATTAAAGCACAAAGTGAGTG	2189 GGAGCTTGAAATTTTAAAATCTTAAAATCCCTTATACTTTACTAGAGACCAACACCCTAAATTCCAAGGCTTGT TTGAAAGATTTGAGCCAAAAAATCAGCGCCTTTTTCCCCAAACTAGAGACTCAAAACAAGGCTTTACTCGTAGTGCCTAGT TTGAAAAATTGCCCTAGAAAACGCCCATTACTGAAATTGCAAAACGCTAAAAACCATTTAGAAACTTTAGAGCTTTTTT CTTATCACATTTTAAGGGCGATAGAAAACTTGAACTTGCTCACCCGCCCTTATGAAACCAGCAATGCTAGACAGCA TGTTCAGCGATTTTGCTTAGGCAAATGAAACCGCTTAAAAAAACCGTTTTTAGGCCTACTTTAAGA	Z191 ITACAACCAATTITCTAGEGGTAATGGCAGTGGTTCTAAACCCCCATGCCATAGGAAAACCAAGTGCAACTGCAACCAATTITCTAGCGAAGAAAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCAACTGCTTTAAACACTGCAACAACTGCAACTGTTATTCTAAATTGTGGAAGAATAAACGGCCATGTTATTCTAATTGTCAACTGCGTGAAACGGCCCAACAGGAACTGTTATTAACGCCAAGAAGAAATAAAGGAATAACAATAAAAACGGCCAAAACAGGCTCAAGAACAGGCCTCAGAGGAACAGGCCCCAAGAGGGAATTTAAGGCCTAAAAACGGCCAAACAGGCCCCAAGAGGGGGGAATTTAAGGCCTAAAAACGGCCCCAAGAGGGGGAATTTAAGGCCAAGAATAAGGCCCCAAAGGCCCCAATGAAAACAGGCCCCAAGAGGCCCTTAAGGCCATAACAATAAGGCCATAACGCCATAACATAAGGCCATAAGGGAATATTAAGGCCATAACGCCCATAACGCCATAACGCCATAACGCCATAACGCCATAACGCCATAACGCCATAACGCCATAACGCCATAACGCCATAACCCATAACGCCATAACGCCATAACCATGAACAACAACAACAACAACAACAACAACAACAACAACAAC
2	HP1559	HP1559	H 71559
			=

HD1550	2193	ACGGAGTTTTGGCGAAAAGATTGCGAAAAAAAAAAAAAA		
600	<u>.</u>	CGGGGGGTAFCAGCGGATAATTACAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCTTTAAACCCCCC	2194 TEFLAKDCVEKYGILPSQFTDYQGIVG	SIVG
		GGGGGCCTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAA	DSSDNYKGVKGIGSKNAKELLQRLGSL	LGSL
		CACCACACACACACACACACACACACACACACACACAC	EKIYENLDLAKNLLSPKMYRALIHDKAS)KAS
		AGTECCECTTTCCTACCOCCULT AND COCCUTTATION OF THE COCCUTTATION OF TH	AFLSKELATLERGCIKEFDFI.SCAFPSE	FPSE
		GEOTOTICE CONTINUES CONTIN	NPLLKIKDELKEYGFISTLRDLENSPTPL	PTPL
		SCHOOL AND A SCHOOL TO THE SCHOOL I I AND I I I AGACACCCCCCTAIT AGACACCCCCCTTAGACAAC	ILDNAPLLDNTPALDNTPKKSCMIVLES	VLES
		ANCEC A ROCK AND THE ISSUED TO THE STANDARD	AAPLSAFLEKLEKTNARVFARLVLDKE	OKE
		GENTAL STATE OF THE STATE OF TH	KKVLALAFLYEDQGYFLPLEEALFSPFS	SPFS
		ACAGE TO THE CONTROLL TO THE C	LEFLONAFFKMLOHAOIIGHIJLKPLLSF	LLSF
		ANCATT SCRAMMEN AND SECRET FOR THE FORMANCE HELD IN ANAMARIE CONTRACT TO THE SECRET TO THE SECRET TO THE SECRET THE SECRE	LKAKYQVPLENIRIQDTQILAFLKNPEK	PEK
		POWER TO THE STATE OF THE STATE	VGFDEVLKEYLKEELIPHEKIKDFKTKA	₹ ¥
		ASCENSIA AND COUNTRY AND COUNT	EKLELLSVELNALKRLCEYFIFKGGLEE	LEE
		GCCAGAGAAA GCCAGAGAAAA	NLLSLAREIETPFMKVLMGMEFQGFKI	F.K
:	·		DAPYFKRLEGEFKNELHVLERQILELIG	ELIG
HP1559	2195	2195 GGCGAAAGCTGTTGAAGCGTTGTTTAGTGAATTGTGGATAGTTTGGGCATTTATTATAAAATCGGTTTAGCACG	240el CERCI VECERATORI CINARIO ETER	1
		GATTTTACCGGTAAATTGTTCAATGAAATGTATCGCTGGGTTTCACGAAAGACCAATTAAACGATGTGGTGCTC	TOKI ENERAVDIKI CETKOOL KIOKALTO	<u> </u>
		ACACCCCCTTATGTCGCCACGCTTTTAGCTAGACTTTCTAAAGGATAGTTTCGTGTGCGATTTTCCACC		ب کر کا کر کا
		GGAAGCGCTGGGCTATTAGTCGCAAGCATGAATTTGATAGAAGACCCTAAAAAGCCGTATCACTAACACAACACAAAAAAAA		60 A
		ATTAGAGGAAAAAATCGCCCACATTAAAGCCCAAAAAAAA	GLLVADMINLMIEDANKKI I SPEELEUKI	3
		GET GET AND AT CALL AND CONTROL	AHIKAKOLLGIEILSDIHTLAVI.NMILMG	 94
		ACT CONTROL OF THE CONTROL OF THE CAME CAN INTO THE CAME CONTROL OF THE CAME CONTROL O	DGSSQILNQDGLSGFDGKV11NEAFKA	₹ 8
		A STATE OF THE STA	NAFVLNP	
HF1559	7812	Z19/1111GACAAGCCGCTTTTTCGCCAAGGGATTGCGAGCCATAATTTAGGGGTGATTAAGTTTAAGGAAAAGGATTTT	2198 FDKAASFSQGIASHNLGVIKFKEKDFN	N.F.
		AN INSERTIGE I SEATURE I SEATURE I SEATURE I SEATURE SEA SEA SEA SEA SEA SEA SEA SEA SEA SE	GALDLFDSSIASKENASVSAIDALVSAY	SAY
		SACCECTIAL CALL TOCARGA LEGARGA I LIGIAL FALLACTA AAAATTGCGA GA CATTTGTATAAAGACTAT	HLQDEDLYYHYLKIARDTLYKDYKKSF	KSF
		AAAAAA COLITIIA I COLACECTI ACECCICAAA I COLACECE GEGEA GAATITI GAAGCCCTTI CECCCTTA	YSYAYALKSYYAGEYFEALSI-LMHPNS	PNS
		A I SCACCCI AN I CCAACGCC I I I I AAAGCCTAATACGCGCTTAGCGTCTAAATTGTTTTGATGTTTAAAGATGAAA	NAFLKPNTRLASKLFLMFKDETNAYEQ	YEO
		COMPLET I ACCARACION DE LA CARACACION DE LA CONTRO DEL CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DEL CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DEL CONTRO DEL CONTRO DE LA CONTRO DEL CONTRO DE LA CONTRO DEL CONTRO DEL CONTRO DEL CONTRO DE LA CONTRO DEL CON	LOKSANAODELALGLLOARLGHYKOAL	COAL
_		GGCCATTACAAGCAGGCTTTGGAGCATTTGCAGCACTACCCTAAAAGATTTAAACGCTTTGATGGCT	EHLQHYLHNYPKDLNALMALELVSLKK	Ϋ́
		TTSSAATTSSTAATAGCCA AGACACGCTATTAGCCA	GDTLKASEALKLASHTKEDTI.LA	
HP1559	2199	2199/AATGAAGTGTATCGTTTGAAAAAGCTTTCCACTTTTCAAGAGCTTGTGAGCGTGTATTACGGCATGGTGTTAAAACGCA	2200 NEVYDI KVI STEDEI VENAMANANA	
		GAAGTGGCTGAAACTTTAGAAGAGGGGGAAAAAGGCCATTATAAGCATTTCCAAAACGCTTTGAAAATGCAAAAGT	VAFTI FEVERCHYKHEONA! KMOKVO	ب در در
		GGGGCAAATCGCTAGGGTAGAAACCTTAGGCGCTCAAGTGGCTTATGATAAGGCCCATATCGCTAGCGTTAAGGCT	OJARVETI GAOVAYDKAHIASVKAKOV	2 5
		AAAGACGTGTTAGAAGTTTCGCAGCTCTCGTTCAATTCCATTTTATCTAGCAAGGACGATTTAGTGCCTTCAAGCAA	I FVSOI SENSII SEKOI VOSEKI EIDT	<u> </u>
		TTAGAGATCCGCACGGAGAAAAATCTGCCCGATCTGAGCTTTTTTTT	FKNI PDI SEEVSSTI NSYBVI KTI ENDI	
		AAGACTTTAGAAAATCAGATTCAAATCTCTAAAGAAAACGCGAAATTACAGATCGCTAAATTCTTGCCCCAAGTGAGTT	OISKENTKI OIAKEI POVSEERSYIMKO	¥ 5
		TTTTGGCTCTTATATTATGAAGCAAAACAATTCGGTGTTTGAAGACATGATCCCTAGTTGGTTTGTGGGCGTGGCCG	NNSVFEDMIPSWFVGVAGRAMPILSPTG	PTG
		GGCGCATGCCTATTCTTCTCCCACAGGGCGCATTCAAAAATACCAAGGAGCAAATTAGCGGAGTTGCAAGTGAGT	RIQKYQASKLAELQVSSEQICAKKNI	AME.
		AGCGAACAATCCAGGCTAAAAAAAACATGGAATTATTAGTGAATAAGACTTATAAAGAGAGGCTTTCTTATTGAAA	LLVNKTYKETLSYLKEYKSLLSSVELAK	ž
		GAATACAAAAGCITICITICITICITICITICITICITICITICITICIT	ENLKLOE	

v	>
v	1
~	٦

TCTATAAGGGCGGTGTTTAGATGAAAAGTTAAACCGCTTTTAGCGTCAAAGAGTGTCTTGTGTTTTGAGAACGCA TATAGGCTCGTTGTGTCTCAAAAAATGGGCATTTTTCAAAAAAAA

2210 QLPPTHYEIKLKGIVIGEGMVMPDKFLA MNTGFVNKEIEGIPTKEPAFGMDALWI ETKNKEEAIIQGYTIIDPSTVIATHTSELV KKYAEDFITKDEVKSLLERLAKDYPTIV EESKKIPTGAIRSVLQALLHIEKIPIKDML TILETITDIAPLVQNDVNILTEQVRARLS RVITNAFKSEDGRLKFLTFSTDSEQFLL NKLRENGTSKSLLLNVGEL(JKLIEVVSE EAMKVLQKGIAPVILIVEPNLRKALSNQ MEQARIDVIVLSHAELDPNSNFEALGTI HINF	2212 OKEFKKAITQQIAYFLKDKSAFILNVSG NVFFSFEENPKDLKAIKERLIKTIEPNA DPKAVMRFLNLQASLILECVPQTTCPF DTLLIPTAFSVPVYYANRLGINPSLFSQ EDKTYHNALIKALNKAYYSLIMEGLEKR LNAIKNAEWL	2214 SLLEIKKALKKGDQVIAQVSDERFEIAK HHSATHLLQSALREVLGSHVSQAGSLV ESKRLRFDFSHAKALNDEELEKVEDLV NAQIFKHLNSQVEHMPLNQAKDKGAL ALFSEKYAENVRVVSFKEASIELCGGIH VENTGLIGGFRIVKESGVSSGVRRIEAV CGKAFYQLAKEENKELKNAKTLLKNND VIAGINKLKESVKNSQKAPVSIMDLPVE KIHGVNLVVGVVEQGDIKEMIDRLKSK HERLLAMVFKKENERITLACGVKNAPIK ANVWANEVAQIL	2216 IKLFFPPMTSEORKLIAKDAKAMGEKA KVAVRNIRODANNOVKKLEKDKEISED ESKKAQEQIOKITDEAIKKIDESVKNKE DAILKV
2209 TGCAGCTCCCCCCAACGCATTATGAAATCAAACTTAAAGGCATTGTGATTGGTGAGGGCCATGGTGATGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCGCC	2211 CCAAAAGAATTTAAAAAGCGATCACCCAACAATTGCTTATTTTTAAAAGATAAAAGGTGCTTTTATTCTCAATGTTT CAGGCAATGTTTTTTTTTT	2213 ITCACTCCTTGAAATCAAAAAGGGGTAAAAAAGGCGATCAAGTGATGAGCGATGAGCGCTTTGAAGTGAGCGCATGAGCGCTTTGAAGTGAGCGCATGAGCGCTTTGAAGTGAGCGCCTTTAAGAGAGAAGTTTTAGGCTCGCATGTGAGCGCAAGCGGGGGGGG	2215 CGATCAAGCTITITITCCCGCCCATGACAAGTGAGCAAAGAAACTCATCGCAAAAGAGCCCAAAGCGGTGAAAAAAAA
HP0909	HP0909	НР0909	HP0909

GUERTIAMAGCITIAMAGGACCITIANTAMITIAMAGTHGITACAGAAAACAACCAACCATTTTTATATATATATATATAT	HP0909	2217 TA	2217 TAGACTCGCTTTTTACAGAAAACGAACAAGAAAAATCCTAAAAAAACAAGAAAATTCCAATTAATCTTTCAAGCTTA	2218IDSI ETENEDEKII KKOENIDI IEDAXAB	II KKOENIO
ATTITITICOGAMATICACAMOAGOTTITIAACATTATAGAMATICAGGAGCOCCATTITITIAAGA ARCAGOTTITIAGAGCAAAATICTICACAMOAGAGTTITIAACATTATAGAAATICAGGCCCCATTITIAAGA ARCAGOTTITIAGATTATAGATTITIAATITIAATICATATATATATATATATATATATA		<u>₹</u>	CGCCCCTTAATGGCTAAAATCTGCTCGTATCAATCTAAGTTTGTGAGCGCTTTTTATCTTTATACGCAACTCAAAAAAGAGCTTAAAAACCTCAAAAAAAGAGCCTCTATAAAATTGTTAAAAACAAAC	SKOTLYKLHALEKORILELVPNFENNK TKLYLCOFALPYSLTPSPSLLNVFENNK	FVSAFYLYTC EKORILFLVI SLTPSPSLL
ATACCCTACAMACACCTAATITICATIGNATTITICTTIGGATATITIGGATATITIGGATATITICATIGNATITICATION ATACTATITICATION ATACTATITICATION ATACTATITICATION ATACTATICATICATION ATACTATICATICATICATICATICATICATICATICATI		₹ ₹	FELLITIGAMMACATIGGTTTIAGAGCATTTACAAAGCAATTCCCAAAATATGAGCTTTACTCCCATGATAACGGG TTATCTTGCGCGAAAATTCTACCAACAAGCTCGCCCTCATCGCCCACGCTTTCCCCCACGCCCCATTTTTAGAA SAGCTTTTATGGTGCCATAAACATGGGTTTTTAAACATTATAGTCGTTTCTATCAACGCCCCTATTTCAACAAACA	VFLELYKQFPKYELYSHDNGIFILRENS TNKLALIAHAFPTPHFLEKQLLWCHKH	YEL YSHDNGI TPHFLEKOLL
ACCCTAAAAGCGTAGGGTGTTTTTATAGAAGGAAGCAATGAATG		<u> </u>	CCCCTACAAACACCTTAATTTCATTGATTTTCTTTGGATATTCAATCTATTTTGGTAAATAGTTATTATGTATTT ATTTATGTATTTATGTATTTATGTATTTATGTATTTATGTATTTATGTATTAT	GELNIVASINAPISAINIPYKHLNFIDES LDIQSILV	TALL IN LAKE
2219 ITCGGGTAAAGGCGAATTGAGTGAGCAGAGCTTGATTGGTTGG		A T	STAAAAGCGTAGGGTGTTTTTAATGATTTTTTTTTATAGAAAGGAAGCAACATTTTAAAAAATTAAGTTTC SCCTTGTTATCCCTAGGCCTCTTCGCTCAAACAGCGCATGCTAAGCATTTAAAGGGCACGATTGAAAATTACTTCTGA SCTTGAAATCAATTTTTTTGACGAAAAAAACCCGCCCAATCAAT		
TCAGCGCAAGCGGAAGCCTTAAAGGATTCATTAAGCGTTTAAGGATTTTATTAAGCGCTTATGATTTTGATTGA	HP1312	2219 TC	36GTAAAGGCGAATTGAGTATCAATGAGCAGAGCTTGAATCAATGGTTGGGCGGACATGAAGCCATTAAAATGA	2220 PGKGELSINEGSLNÖWLGGHEAIKMK	LNOWLGGHE
CCCACATICTCCAAAGGTATCCTATTTCTTTTTGCTCTTGGGGGGGGG		ST &	SCGCAAGCGGAAGCCTTAAGGCATTGCTAGAGGCTTTGAAGCTTATGATGCTTTTAAGGCCTTAGAGGCCTTATAGGCCTTTAGAGCCTTATAGGCATTTAAGGCTTATAGGCATTTAAGGCATTATAGAGGCATTAGAGGCATTAGAGGCATTAGAGGCATTAGAGGCATTAGAGGCATTAGAGGGAATAGAGGGAATAGAGGAATAGAGGAATAGAAGGAATAGAAGGAATAGAAGGAATAGAAGGAATAGAAGGAATAGAAGGAATAGAAGGAATAGAAGGAATAGAAGGAATAGAAGGAATAGAAGGAATAGAAGA	VMQPLLLTKQEQSVDIKAVVFGGGYSA QAEALRHGISKALNAYDIAFRAILKPKG	SSVDIKAVVFG LNAYDIAFRAI
2221 GAGATGGTGAAAAAGTTTAGAAAATAATGGAAGAAAGTGAAAAGCTTATTTTGGTTTTTGGAATTTGAAGTTTTTTTT		<u>31.</u>	CAATTCTCCAAAAGGTAATCTCTATTTCTTTTTGCCTCTCCTTTGGGGGGGG	LLI RUSKVVERKKYGKRKARRSPQFS KR	KYGKRKARR
PGCCAATAGCCAATATCCTAGCACCACTAGCACCCTAGAGGTTTGGGTAGGCAAGGGCGAGATCA TGGAGATTGATTGCATTTGGGAGTATTTTGCTTACGACACCCTAGAGGGTTTGGGCCAAAAAGAAAAGATTGCTTGGGATTG TGGAGATTATCCGCAAATTTTGATGCTGTTCCCCTAAATCTTTAGTTAG	4P1312	2221 GA	VTGGTGAAAAAACTTTAGAAAATAATGAAGAAAATAAAGATGAAAAGCTTATTTGAATTTGAAGTTTT	2222 DGEKTLENNEENKDEKLILIDEFEVI AN	AKDEKLILIDEFI
TAGGGCTTTATCGCAACGATGTTTGTTGCTCCCACTAATCTTTAGTTGCGGCGGGGGGGG		1 A	.AATAAATTCATTTGGGAGTATTTTGCCTAGCACCCCTAGAGAGTTTGGGTTAGGCAAGGGCGAGATCA (GATTGATGCCTTTTGGGAGTATTTTGCTTACAGACACATTGGCTGACAACAAAAAAAA	KFISRLPNIPSTPREFGLGKGEIMEIDVP	REFGLGKGEIN
CGGGTAATCCGGAAATTTTGAATGCGGTGTATCTTCAAGTCAAAAGCGATGTGGGGCAGTTCCCAGCCCCTTTGGT AGGACATTTATTTATTTATTTATTTATTTATTTATTTATT	-	Ţ	GCTTTATCGCACGATGTTTTGTTGCTCTCCACTAAATCTTTAGTTATCCAGCCGCGAGACATTCTCTTAGTGG	FGSIFAYRHIGSIROKEYRIVGLYRNDV LLLSTKSLVIOPROILLVAGNPEILNAVY	KOKEYRIVGLY
TTGCACAAACATTTAAAGACCTTCACATTCAGGTTTTACCCCACTGCCCGATGTTTTACCATGAATTTT TTGCACAAACATTTAAAGAGCTTCACATTCAGGTTTTACCCCACTAGCCCTAGTTTTACCATGAATTTT TAGCGCTAGAAACATTGAGCTCTACATTTTAGTTTTACCACAAAAGTTTTACCAAAAATTTT TAGCGCTAGAAAAACATTGAGCGAGTTTTAGTTTTTACCAAAAAGTTTTATCCAAAAAGTTTAAAAAACCTTGTATAAAA CAGCCACCCCAGTTTATAAAAACCAACACTTCTGGCTTGTTTTTTTT		90	STATCCGGAAATTITGAATGCGGTGTATCTTCAAGTCAAAGCAATGTGGGGCAGTTCCCAGCCCCTTTGGT	LQVKSNVGQFPAPFGKSIYLYIDMRLQ	APFGKSIYLYIC
TAGGGTAGAAN TOO AND TO	-	₹Ĕ	NOCAL LIAL LA LACATICATA CARGOTT CONTINUE CONTIN	NRKAMMRDVYQALFLHKHLKSYKLYIQ	ALFLHKHLKS
ACCAGAAAAAATGGGCCTAATCGTGGCAGAGAGCTTTTTTTT		TA	GCTAGAAACCGAAAGCATTGAAGTGAATTTTGATTTTTACAGGAAAAACTTTTATCCAAAAAAACTTCCAAAAACTTCAAAAAA	VLHPTSPKFYHKFLALETESIEVNFDFY	FLALETESIEV
CAGCCACACACACACTICTGGCTTGTCTAAAACCTCTCAAAGCGTGGTGGTGTTTGAATGAA	•	S S	GAAAAAATGGGCCTAATCGTGGTAGGCAGAGACTTTTTTATCTAAAAAACACCGAAAGGCCTTGTATAAAA	SKKHRKALYKTATPVYKTNTSGISKTS	TPVYKTNTSG
2223 TTGTGAGATAAACAACCATGACAAACTTAAGCAATACCAAACAGACATGAAGAATTACTAGGGATAGA AATAGATGAAGAGATACTAAAAAAT AATAGATGAAGAGTGCTGGATACTAAACGACTTATCCCAAATTGTATTCTTAAAAAAATACTCTAAAAAAT TTAAAAGATTACAAAGAAACAAAGCGTGGTTAAAGCTTAAACAAAACAAATTAAGGAGGTAATTTTTA CAAAACCCAAAAGAXATTAAACCAAGCCTTTGACAAGTCTAGTCATCAAAAACAGAGATACCATAAAATCACAAG CGAAACTTTCAAAGCAATTGAATTG			UAUCUCASTTTAAAAACCAACACTTGTGGGTTGTCTAAAACCTCTCAAAGCGTGGTGGTATTGAATGAA	QSVVVLNESLDINEDMSSVIFDVSM	VEDMSSVIFDV
	4P1312		GAGATAAACAACCATGACAAACTAAGGGACTTTAAGCAATACCAAAGGGACATGAAAGAGAATTACTAGGGATAGA GATGAAGAGCTGGATACTAAACGACTTATCCCTAATTATTCCAAATTCTAATTAAAAAAAA	2224 CEINNHÜKLTÜFKÖYÖTDMKELLGIËID	COYOTDMKELI
CAAAAUCCAAAAGAXA II AAACCAAGCCITTGACAAGTCTAGTCATCAAAAAGAGAGAGATACCATAAAATCACAAG CGAACTTTCAAAGCAATTTGAATTGATTGAAGATTTGCAAGTAAAAACATGACTAAAGAGCTAAACTCAAA AATGTTAAACAAAAGAGTGGGCTTAATCAATCTATTTAAACGCTTCATTCTA		Ė	AAGATTACAAAGAAAGAAAGCCGTAGGTGTTAAAGTCTAAACAAAACAAAAACAAATTAAGGAGGTAATTTTA	EELU KKLIP YSKLYSLKKYSKKFKRL QRKQSRRC	KLYSLKKYSKR
AATGTTAAACAAAGGCGCTTAATCAATCTATTTAAACGCTTCATTCTA		<u> </u>	AUCCAAAAGAXATTAAAACCAAGGCTTTGACAAGTCTAGTCATCAAAAAACAGACAG		
		\	TTAAACAAAAGAGGGCTTAATCAATCTATTTAAACGCTTCATTCTA		

HP1312		2226 NGVÉIVGLEHLDKVIYI DQAPIGKTPRS NPATYTGVMDEIRILFAEQKEAKILGYS ASRESFNYKGGRCEKCQGDGDIKIEM HFLPDVLVQCDSCKGAKYNPQTLEIKV KGKSIADVLNMSVEEAYEFFAKFPKIAV KLKTLMDVGLGYITLGQNATTLSGGEA QRIKLAKELSKKDTGKTLYILDEPTTGL HFEDVNHLLQVLHSLVALGNSMLVIEH N
HP1312	2227 AGGGGGCGTGATTGAAAGTTTGGGTTATTTGCTTTATGATGTTGGTTTAGAAAATGAAAAGAACAGTTTTAAG GGTGAGCCTTAAAAACCCTAATGGAGCGGTTAGTTTGGACATTTGCCAGCAAGTGAGAAATGAACAGTTTTGAAAACCCTTAT TAGATGTGTGGCGATTTTATTCAAGCCTTATTTTGGAAGTCACTATTGGGGTTAAGAAAGCGTTAAAACAAGCCTTAAAACAAAACCCTTAAAGAAAACGCTTAAAAAAACGCTTAAAAAAACGCTTAAAAAAAA	2228 GGVIESLGYLLYDVSLYKENEGHVLRV SLKNPNGAVSLDICQCVSEIISPLLDVC DFIQDAYILEVSSMGLERTLKTPKHFKL SLGEKVEVKLTNKESFGAVLKDANDLS ADFELEDHAIKSVEYKIJLKKVKTLFEW
HP1312	2229 CATGTCGGTGTTGGACTCTAAAGACATTACCGCAAAAAGCAGTGTCAAAGGCTTACTCACTAAGGCTTAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	2230 MSVLDSKDITAKSSVK3LLTKLKATAG RNNNGRITSRHKERGAKKLYRIIDFKR NKYNIEGKVAAIEYDPYRNARIALVVYP DGDKRYILQPSGLKVGDSVIAAEGGLDI KVGFAMKLKNIPIGTVVHNIEMHPGAG GQLARSAGMSAQIMGIRENKYTIIRMPS SEMRYILSECMASVGVVGNEDFINVSI GKAGRNRHRGIRPQTRGSAMNPVDH PHGGGEGKTGTSGHPVSPWGTPAKG YKTRKKKASDKLIISRKÁH
HP1312	2231 GCAAAAAGACGCTTGCGGGTTCATCATGAGATCAGCGAGTTCATGAAAAACAAAAAAAA	2232 KKDACGFIYEISEFMK-VTALLKKQDRY VYLLRYLPSRYWASILTTALLKKQDRY ALKKLLVSYYQTWIAGGTITRIKQTSIN IIRWKSNKSVETIKELI.INSIDSYNTFDQ YLYNLWDSSSVYHSKIVVRPVLALANY FMADEEKPHFIAMDAETQVEHILPQTP KRGSQWNADFDKEKREEWVNNIANLT LLKRKKNAHALNGDFDEKRKIYGGKDT SKVISCYDITKELYSNYRKWNEKSLQE RYKSLYNTITPVLHIEGQEDDF

	-1000			
HP1312	2233	2233 TGATGAGATGCGAGCCGGAGCGTTTGAGCGCTTCACCAACCGCAAAAAGCGTTTCAGAGAAAACGCGCAAAAAAACCAAAAAAAA	2234	2234 DEMRAGAFERFTNRKKRFRENAOKNA G
	<u>, </u>	OTTTECATGTGAATGAGAGGGGCGTTTAGGCTTTCATAAGAGTTAAAAAAGGGGCGTTGAAGTGAAGCGAATAACAAGATT TTTTGCATGTGAATGAGAGGGGACTTTAGGCTTTCATAAGAGTTAAAAAAGGGCGTTGAAGCGAATAACAAGAT		OKHAKTRNYAQEELDSNKVEGVTEILH 3 VNFBGTI GEHKFI KKGVFANNKIOVEH 1
	<u></u>	CAAGTGGAGCATTTAAACCCGCATTATAAGATGAACTTAAACTCTAAAGCGAGCG		LNPHYKMNLNSKASVKITPLGGLGEIG
	۱ -	C116G61GAGATTGGGGGGAACATGATGGTCATTGAACCCCCAAAAAGCGCGATCGTGATTGAT	<u> </u>	GNMMVIETPKSAIVIDAGMSFPKEGLF
	<u> </u>	GCTGGCATTATCATC		GVDILIPDFSYLHQIKDKIAGIII
HP1312	2235	2235 GCAAGAAACAGATAATTTATTAAAAACATTGAATGTGAAATCGCTTTTAGAAGCCTTGCTTG	2236	2238 QETDNLLKTLNVKSLLEALLVYTPKGYK
	<u>ه ر</u>	OLATARARATITTABANGTITTABANGATITTABANGATITTAGGATATTAGGATATTAGATAGATAGATAGATAG	<u>.</u>	DLNLLERFETGLSGVLEVGILEKRNYAK
	<u>. U</u>	GCGCGTTCCATCACGCCAGTTTAAAACGGGCGAGGAGTTTGTTT	<u>> (</u>	VLKIFAYSKRFYKNLELVFFNYSAFHHS
	4	AAGCTTATATCATTAACACGCCTAAAATCATTACCAAATTTGGTAAAATTTCTTTAATTTTTTAAAAAAGTTAAAAATCATA	<u> </u>	KITKEGKISI IEKIO/KNHKKIOENI OKI I
	<u> </u>	AAAAAATACAAGAAAATTTACAAAAACTCATTTCTTTAGAAAATTTAAAAAAGGAAGG	<u>. 0</u>	SLENLKKEGVKENIAHI I EJEPTPHEV
			×	KDFETNKNFPSQHLNALKYIEMLFYMK
	<u>- </u>	I AAA I GCA I AAAA I ACA I I GAAA I GCOTTTTTA TGAAAAATTTA GAGGGAAAAAA TGCAAAATTGGGGGCTAAAATC	Z	NLERKKLOFGAKIACPNNNERLKAFIAS
	ې د	GCA I GCCCCCAA I AA I AA GGGGCTT GAAAGCGTTT AT GGCTTTTAAACT CACACACAAACC		LPFKLTRDQQNAIKEIQNDLTSSIACKR
	ى رو	SECULI I MANGAZA I CCAAAACGA I CI CACI AGCI CCATAGCGI GCAAGCGI TI GATI ATAGGGGA TGGGGGTGCGG	<u>-i</u>	LIIGDVGCGKTMVILASMVLTYPNKTLL
	<u>) (</u>	CANANCIA I SE ISA I I I AGCGAGGAGGIA I AACTIACCCAAATAAAACCCTTTTAATGGCGCCCACTTCCATTCT	≥.	MAPTSILAKQLYNEALKFLPPYFEVELL
	<u>, c</u>	CSC ANGRATION AND ANGRAGIC HAND AND ANGRAGIC SECOND AND ANGRAGIC SECOND AND ANGRAD AND ANGRAGIC SECOND AND ANGRAGIC SECOND AND ANGRAGIC SECOND AND ANGRAD ANGRAD AND ANGRAD ANGRAD AND ANGRAD AND ANGRAD AND ANGRAD AND ANGRAD AN	크	LGGSYKKRSNHLFETITHVVIGTQALLF
	<u> </u>	CANOMAGGENICAMINETINETINGAAACAATCACECATGEGETTATGEGGAGGGAGGGTTGTTGATAAGC	<u> </u>	DKRDLNEFALVITDEQHRFGTKQRYQL \
	<u>و</u>	פני	ш	EKMASSKGNKPHSLOFSATPIPRTLAL
			<u> </u>	AKSAFVKTTMIREIPYPKEIETLVLHKRD FKIVMEKISEEIAKNHOVIVVYPI VN
HP0954	2237 A	2237 AAAAAGTCGCTCAGGTTTTAGACTATAAGGGCGTGTTTGTGAAAGACTTATCCAAACCAGTGGGCATGCAAAAG	2238IK	2238 KVAGVLDYKGVFVKDI SKPVGMOOKI
	<u> </u>	CTTATGGATATTTCCAAACAAAGGGCTTTAAAATGGGAATTAGAAATCCCTTTAGAGCAGGGCATCAAAGAAGCTTAT	2	MDISKORALKWELEIPLEGGIKEAYEYY
	<u>.</u>	GAGLALIALI GAAGCITI AGAGGTI GAAATAAAATCAAGGCTCTTATGGAGCTATAAAAACGCTCCGCTATTAAG	<u> </u>	LKLLEV
	<u> </u>	CG11AGGCTAGTGGTAGTTGCGATATTGTGATCGTTTTAGCTTCAAACAACTTTGAGCCATTAAAAGGGATTTGGTG TGTGGCTTCGCTCTC		
HP0954	2239 A	2239 AACGCTTTTATCCATGAATTAGAGCAGCCCTTAAACAGCGAAACAGCAAAATTTAGCCAAAGAGCTTCTCAATGAGCC	2240 T	2240 TI FIHEI FOPI NSFOONI AKELI NEPVO
	<u>-</u>	1GTGGATAAAAAGAAAATTTTGAATCCCTATGTCAAGAAATCGCCGATCACACGCATGGGGAATACACCCAAACGCC	<u>×</u>	KKENFESI COEIADHTHGEYTKRI KI V
	<u>- i</u>	TGAAATTAGTGGAATTTCTTATGTTATTAGCCTATGCTGATGGGATTTTGGATAGCAAAGAAAAGAATTGTTTTAGA		EFLMLLAYADGILDSKEKELFLDVGVFL
-		LE LEGEGET I I I LECAGA PACACA CAAGA I I I AACGAGCI I TATGAACT CAATAGA AATT TA GAACT CAATAGA AAT	<u> </u>	OIDNODFNELYDNFERFNAIEIPMSLEE
	₹ (ANTICCCIAIGICI I I AGAAGAAGAGAAAAAGI CI I I I I I I I I I I I I I I I I I	₹.	AKSLFEIQTHTTKQDLEKKALDLSAPYY
	9	GCCTTGGATTTAGCGCTCCCTACTACCATAAAATGAA	Ξ.	

HP0712	2241	2241 GGATTIGCCCTTGCCTTTAGGGGGGCATGGCGATCTATCCCCTTGTATCCCCTTGTAGAGGCGTCAAAAATTTGCTCTTGTGCCTTTAGAGGGGCTCGCTC		LGYQHGFYASLLKTKDCLLTDEYLKYR FS
HP0712	2243	AAGAAACTTAAAACCCCCCITTIAG AAGAAACTTAAAAAAAGTGACCCCCTTTTTTAAGGCCTGATGGCAAGTCTCAAGTGAGGCGTGCT TATGAAAACTTCAAAAAAGGAAAAGGATCGCTTTTTTACCAACATTCCCCAGAAGTTCACAAAAACAT TATGAAAACAACAACAAAAACATCGTTGTCATTTTCCAACACATTTTGCAGAAGTTTTACAAAAAAACAT TAAAAGAAGTTGACGGAAAATTCGTTATCGGTGGCCGAAGGTTTGCGGGCAAAAACAT TACATCCTAACGGAAAATTCGTTATCGGTGGCGCGCAAGGCGGAAAGCCCTAGCGAAAAATCATCGTGGC TACTTATGGGGGGGAGTTGCCCGCTGGCGGGGGGAAAGGCCTTGCGGGAAAAAGCGGCGCGCGC	2244	2244 ALAOKRKDNTLPFLRPDGK SQVSVRY ENNKPVSIDTIVISTOHSPEVSOKHLKE AVIEEIVYKVLSKEYLHDNIK FFVNPTGK FVIGGPQGDAGLTGRKIIVDTYGGSCP HGGAFSGKDPSKVDRSAAYAARYVA KNLVASGVCDKATVQLAYAIGVIEPVSI YVNTHNTSKYSSAELEKCVKSVFKLTP KGIIESLDLLRPIYSLTSAYGHFGRELEE FTWEKTNKAEEIKAFFKR
HP0712	2245	CTITTATGCGATCCACAGAGAGACCCTITTITAAAGATTTAATAGAATTTAGGGGGGTGGGGGGGG	2246	2246 IDGGKEALYGGIACANLLHKNSGITIDIG GGSTECALIEKGKIKDLISLINGTIRIKE MFLDKDLEVKLAKAFIQKEVSKLPFKHK NAFGVGGTIRALSKVLMKRFCYPIDSL HGYEIDAHKNLAFIEKIVMLIKEDQLRL GVNEERLDSIRSGALILSVVLEHLKTSL MITSGVGVREGVFLSDLLR HHYHKFPP NINPSLISLKORFLPHEKHS QKVKKECV
HP0712	2247	GATCGCTITITICCCCCATGAAAAGCCACAGCCAAAAGGTCAAAAAGAATGCGTGAAATTGTTIGAAGCCIIAIUG 2247 CAAAAAACGCGCCCTATAAATTGGATAATACCCCTATTGAAAAATTGCGCATGTTATGCATTGCAATTTGTATTTTAAAAAAAA	2248	2248 KNAPYKLDNTPIEENCACYACKRYSKA YLHHLFRAKELTYARLASLI-INLHFYLEL VKNARNAILEKRFLSFKKEI-LEKYNSRS H

02/066501	<u></u>		PCT/E	P01/1542
2250 GLVIGELLYHKFYQYDEGKLSKLRASIV SAHGFTKLAKAIALODYLRVSSSEEISN GREKPSILSSAFEALMAGVYLEAGLAK VQKIMQNILINRAYKRLDLEHLFMDYKT ALOELTQAGFCVIPTYQLLKEKGPDHH KEFEMALYIQDKMYATAKGKSKKEAEQ QCAYQALQKLKEAK	2252 ISLEENRFKDSGYLKEKLKEAKDLIDAL NLRKATIYKIGLMLLEYQYDFFKGKELR PLKLLDLANEFNHSVSTISRAISNKYLA CERGVFPIKHFFSIALDNSETSNAVIKÖ YLLELIKNEDKKEPLSDAKILELIEEKFH LKMVRRTITKYRQLLNIASSSERKRLYL MRA	2254 YTAPILHTLGLQRYFELVÖNLGGFEALY RETKKAALATQKAVLALGLKIFPKSPSL SMTTIVNEHAKELRNLLKEKYOVÒFAG GOEPYKDALIRINHMGIIPVYKSAYALN ALELALNDLDLREFDGVANATFLKQYY GI	2256 RLHTAFFGINSLLVASLLISGČSI-FKKR NTNAQLIPPSANGLQAPIYPPTNFTPRK SIQPLPSPRLENNDQPVISSNPTNAIPN TPILTPNNVIELNAWAWAWLQNPPFHP LKPWL	2258 LKADNAKÓNRÓSKHKKGAYIMENNYN NNOASLERNELHNTIWKVANELRGSV ÓGWÓFKÓYYLGILFYRYISENMTHYIN KEERKRDPSFDYAKLSDEK
h . m h . (9 h () d				
2249 TGGGTTTGGTGATAGGGGAGTTGCTATACCATAAATTCTACCAATACGATGAGGGAAAACTCTCTAAATTAAGGGCTTCTTCTC CTATTGTGAGCGCCCATGGTTTTACTAAATTAGCGAAAGCGATCGCTTTACAAGGTTTTTTGCGCGTTTCTTCTTCTTCTG AAGAAATTTCTAACGGGAGAAAAAATCATGCAAAATTTACTCAATCGCGCTTTAATGGCTTGGGTTTTTTAGAAAATTTAGAAAATTCAAAGGGGTTTAAAGGGTTTTAGAGCATTTACTCAATTGCGCGCTTTACAAGGGTTTTAGAGCATTTAGAAATTTACTCAATTTTGCGGCTTTAAAAGCGCTTTACAAAAGGGGCCAGTTTACAGGAATTTACCCAATTTTACTCAATTTTACGGACAGTTTACAAAAGGGGCCAGTTACAAAGGGGCCAGTTACAAAGGGGGCGTTTATAAAGGCCGCAATTGCAATTTCAAGCGCTTTATCAAAAGGGGCGCTTATTAAAGGCCGCAATTGCAATGCCATTTTCAAAGCGCTTTTTAAAGGCCCAACGCAATTGGGGAATTTTAAAGGCGCAATTTGAAATGGCGCTTTTTAAAGGGGGGGG	2251 AATCAGTTTGGAAGAAAATCGCTTTAAGGATAGCGGCTATTTAAAAGAAAATTAAAAGGGCTAAAGATTTGATTGA	TACACCGCTCCTATTITACACACTTTAGGGTTGCAACGCTATTTTGAATTGGTGCAAAATTTAGGGGGGCTTTGAAGGG CTCTATAGAGAGACTAAAAAAGCCGCTTTGGCCACTCAAAAAGCCGTTTTAGCTTTAGGTTTAAAAGATTTCCCTAAA AGCCCAAGCTTGAGCATGACAACGATTGTTAATGAGCATGCCAAAGAATTGAGAAACCTTTTAAAAGAAAAAACCGG GTGCAATTTGCGGGCGTCAAGAGCCTTATAAAGATGCGCTCATTCGTATCAACCACATGGGGATCATTCCTGTTTA TAAAAGCGCTTACGCTTTAAAACGCCCTAGAGTTAGCCCTAAACGACTTGGATTTAAAGGGAATTTGATGGCGTGGCGA ACGCAACTTTTTTAAAGCAATATTATGGAATTTAAGGATCACAATGCATTATTCTTATGAAACCTTTTTAAAAGGGGGGCATGAC TTAAGGCCATTTTTTAAAGCAATATTGCGGTGTCCCAGAAGCCCTTGTGTGCGATTGTTATGAAGGCGCCAA TTAAGCCCATTTTTTGAAAGTTGCAAATTTAAGGGAATTAAGGCAATGAAGCCTTGTGTGCGATTTTTTATGACCCCCAA	TGCGTTTGCACACTGCCTTTTTTGGTATTAATTCATTGCTTGTTGCCTCTTTTTGATAAGCGGTTGCAGTCTTTTAAAAAGCGGTTGCAGTCTTTTAAAAAGCGTAACCTAAACGTAACCCCAACCAA	2257 TTTAAAGGCTGACAACGCAAACGGCCAATCAAAACACACAAAAAGGGGGCTTATATCATGGAAAACAGCCAA ACAATAACCAAGCGTCATTAGAACGCAACGAATTGCACAACACCCATTTGGAAAGTGGCTAACGAATTGAGAGGCTCA GTGGATGGCTGGGATTTTAAGCAATACGTTTTAGGCATTCTTTTTACCGCTACATTTCAGAAAACATGACTCATTACA ICAATAAAGAAGAGGCGAAAGCGCGATCCGAGTTTTGATTACGCTAAATTAAGCGATGAAAAG
49 TGGGTTTGGTGATAGGGGAGTTGCTATACCATAANTTCTACCAATACGATGA CTATTGTGAGCGCGCATGGTTTTACTAAATTAGCGAAAGCGATCGCTTTACA AAGAAATTTCTAACGGGAGAAAAAACCCTCTATTTATCAAGCGCTTTTGA AAGAAATTTCTAACGGGAGAAAAAACCCTCTATTTATCAAAGCGCTTTTGC AAGCGGGGTTAAAAGCGGCTTTACAGGAATTTAACCCAAGCGCAATTTTGC AAGAAAAGGGGCCAGACCGTTTACAGGAATTTGAAATGGCTCTATACATTCA GCAAAAGGGCCAGACCGCTTAAAAGAATTGGGGGATTCAAAA TGGGGCGTTTTTAAGGCTCACGACTTTTGGGGGATTCGAAA TAGCGGGATTAAAAATAGACTATGCGCTTTTGGGGGATTGGA TAGCGGGATTAAAAATAGACTATGCGCTATTAGAAATAACAAGCGGGGTTTTTGAAG	51 AATCAGTTTGGAAGAAATCGCTTTAAGGATA TGCGCTAAATTTGAGAAAAGCCACGATTTATA AAGGAATTACGCCCTTTAAAGCCACTATGAGATTT AAGGAATTACGCCCTTTAAAGCCATTAGATTT TCTAATAAATATTTGGCATGCGAAAGGGGGGG ACTTCAAACGCTGTGATTAAAGACTATGTTTT AAGATTTTAGAACTCATTGAAGAAAAATTCCA AACATCGCCTCTTCAAGCGAAAGGGC TTGAGTATCATTTGTCCTTGAAGAAAAGGC TTGAGTATCATTTGTCCTTTAATGTGAGCCTT CGCTATAAAAGATTAGCATTCTGCCCCCCTA	2253 TACACCGCTCCTATTTTACACACTTTAGGGTTGCAACGCTATTTTGAATTGG CTCTATAGAGAGACTAAAAAAGCCGCTTTGGCCACTCAAAAAGCCGTTTTAC CTCTATAGAGAGACTAAAAAGCCGCTTTGGCCACTCAAAAAGCCGTTTTAC AGCCCAAGCTTGAGCATGACAACGATTGTTAAAGATGCCCTCATTCGTATC GTGCAATTTGCGGCGTTAAACGCCCTTATAAAGATGCCCTCAAACGATTGGAATTTGGAATTTAAGGATCAAACGAATGAAATTTAAGGATCACAATGCAATGCAATGAATTTAAGGATCACAATGCAATGCAATTTTAAGGAATTTAAGGCATTTATGCCCTTG TTTAGCGCATTTTTTGAGGAATTTGCGGTGTCCCAGAAGCCCTTG TTTAGCGCATTTTTTGAAAATTGCAAATTTAAGGGAAGTTTATGGCCTTC TTTAGCGCATTTTTTGAAAATTGCAAATTTAAGGAAGTTAAGGCGTCT	SS TGCGTTTGCACACTGCCTTTTTTGGTATTAAT AAAGCGTAACACTAACGCCCAGCTAATCCCCC TCACCCCTAGAAGGCATTCAGCCTCTCCCC CCCACTAACGCTATCCCTAACACCCCCATTCT GCTCCAGAATCCATTTTTACCCTCTCAAGCTAGTTGGGTGGAAAAATGTATGGTTTAAAACGAGAGTCAACGCTCTATTAGAGTGAAGCGTTTAGACGCTCTATTAGAGTTAGAGTTAGACGCTCTATTAGAGTTAGAGTGATTTAGACGCTCTATTAGAGTTAGAGTGAAGCGCTGATTGGTAACAAAATTAGACGCTCTATTAGACTAACAGCGCTGTAAGATTTAGACGCCAGCGATTTTAAAACGAGTGAACGATTTAGACGCCAGCGATTTTAAAACGAGTGAACGATTTAGACGCCAGCGATTTTAAAACGAGCGCAGCGATTTAGACGCCAGCGATTTAGACGCCACGCAACGATTTAGACGCCACGCATTTAGACGCCACGATTTAGACGCCACGATTTACAACGACTTAGACGCCACGATTTACAACGACCATTAGACGCCACGATTTACAACGACTTAGACGCCACGATTTACAACGACTTAGACGCCACAACGATTTACAACGCCACAACGATTTACAACCGCCACAACAACGACTTAAAATTAGACGCCACAACAACGAACAACAACAACAACAACAAAAAA	77 TTTAAAGGCTGACAACGCCAAACGCGCCAATCAAAACACAAAAAAGGGGGGCTTATATGCA ACAATAACCAAGCGTCATTAGAACGCAACGAATTGCACAACACCCATTTGGAAAGTGGCTAAC GTGGATGGCTGGGATTTTAAGCAATACGTTTTAGGCATTCTTTTTACCGCTACATTTCAGAA ITCAATAAAGAAGGGGGAAAGCGCGATCCGAGTTTGGATTACGCTAAATTAAGCGATGAAAAG
				_·
HP0712	HP0712	HP0712	HP0712	HP0712

GCTCTTTTATTCATT 2260 INAPLAQTNALKLGHSLENETALLFIHGV NGAGAGCGAACTCA LHLGYDHEKDKGEORQKESELIKAFN CTAATGCTGACAAAT LPLSLIERTQD AAAAGCGTTTTGA CCAAAGCAGTTTT AAAAGCGTGAGCGAT GTAAAATCCA	TTTGGAAAGCGCCG 2262 APLLDNTPALDNTPKSCMIVLESAAPL GGTGGATAAAGAAA GTTATTTCGCCCTT GATATTAAAACCCTTG ALAFLYEDGGYFLPLEEALISPFSLEFL GANAFKKULKIDKEKKVL ALAFLYEDGGYFLPLEEALISPFSLEFL GANAFKKULGHDLKIPLKSLKAK YQVPLENIRIQDTQILAFLKNPEKVGFD GCATGAAAAAATCA TTTGTGTGAATATTT ARGCGATTTTAATGG KRLEGEFKNELHVLERQILEIGVDFNL NSPKQLSEVLYDKLGLPKNKSHSTDEK SCTAGACAGCGTT NSPKQLSEVLYDKLGLPKNKSHSTDEK SCTAGACAGCCTAAA HENDKHTTFIQTGTATGRISS TTGGCGCTAAA HENDKHTTFIQTGTATGRISS TTGCGCATTCGCCTA KRLEQEFKNELHVLERQILEIGVDFNL NSPKQLSEVLYDKLGLPKNKSHSTDEK SLTATTGCGCCTAAA HENDKHTTFIQTGTATGRISS HENDKHTTFIQTGTATGRISS TTGGCGATTCGCCTAA	2264
2259 GATTAATGCGCCATTAGCTCAAACTAACGCTCTGAAATTAGGACATAGCTTAGAAAATGAGATCGCTCTTTTATTCATT CATGGGGTGTTGCATTTGTTGGGCTATGACCATGAAAAGGACATAGGCTAAAGGAAAAAGAGAACAACAACCCAAAAAAGAGCGTTTAATTGATTG	CGCCCCCTATTAGACAACACGCCCGCCTTAGACAACAACAAAAATCATGGATGATCGTTTTGGAAAGCGCCGCGCCGCCCCGCCCCTATTAGACAACACGCCCCCAAAAACTAAAAAACTAAAAAAGCGCCGTTTGGAGCGCGTTTTGGAGCGCGTTTTGAGAAAACTAAAAAGTTTTTTTT	2263 TAÁCCCCÁTTAAAATGGATTITTGCCAGGCCAAAAACCGGGCGTGCAAAAAGCCACCAACCA
8	8	ž.
HP0712	HP0712	HP0712

363

KGVIARISCEFVCFEVFSLNEKDFEKIAL VLEEILNKA DFKTSSKISEEDLPKIEAKMKEFAKLKL AITKETLTREGALERFKGDELKHAVMS KIGGDAFGVYQQGEFEDLCKGPHLPN TRFLNHFKLTKLGAYLGGDENNEMLI RIYGIAFATKEGLKÓYLFQIEGEKKRÖH RKLGVELGLFSFDDEIGAGLPIW PKC	FSLI FSLI KGD KGD LLGG GAG GAG GAG GAG GAG GAG GAG GAG GA	Z
VLEEILNKA DFKTSŠKISEEDLPK AITKETLTREGALER KIGGDAFGVYQQGE TRFLNHFKI TKLAGA RIYGIAFATKEGLKD	EEDLPKIE EGALERFI YQQGEF YQQGEF TKLAGAY KEGLKDYI KEGLKDYI KAGHKYOY KAGHKYOY KAGHKYOY KAGHKYOY KAGHKKW KAGHKKW KAGHKKW KAGHKKW KAGHKKW KAGHKKW KAGHKKW KAGHKKW KAGHKKW KAGHKKW KAGHKW KAGHKKW KAGHKKW KAGHKKW KAGHKKW KAGHKKW	EEDLPKÍEA EGALERFKC 7YQQGEFEI TKLAGAYL FSFDDEIG ILSOALLR CHSOAN CSFEDIGS CS
2268 DFKTSSKISEEDLPKIEAKMKEFAKLKI. AITKETLTREGALERFKGDELKHAVMS KIGGDAFGVYQGGEFEDLCKGPHLPW TRFLNHFKLTKLAGAYLGGDENNEMLI RIYGIAFATKEGLKOYLFQIEEAKKRDH RKLGVELGLFSFDDEIGAGLPI WIP PKG	68 DFKTSSKISEEDLPKIEAKMKÉFAKLKI AITKETLTREGALERFKGDELKHAVWS KIGGDAFGVYQQGEFEDLCKGPHLPN TRFLNHFKLTKLAGAYLGGDENNEMUL RIYGIAFATKEGLKDYLFQIEEAKKRDH RKLGVELGLFSFDDEIGAGLPLWLPKG ARLRKRIEDLLSQALLLRGYEPVKGPEI LKSDVWKISGHYDNYKENWYFTTIDEQ EYGIKPMNCVGHIKVYQSALHSYRDLP LRFYEYGHIKSGVLHGLLRVÄE FTQDDAHIFGSFEQIQSEVSAILDFTHKI MQAFDFSYEMELSTRPAKSIGDDKVW EKATNALKELKEHRIDYKIDEGGGAF YGPKIDIKITDALKRKWQCGTIQVDMNL PERFKLAFTNEYNHAEQPVMIHRAILG SFERFIALSEHFGGNFFFVAPTQIALI PINEEHHVFALKLKEALKKRDIFVEVLÖ	2268 DFKTSSKISEEDLPKIEAKMKEFAKLKI AITKETLTRECALERFKGDELKHAVMS KIGGDAFGVYQQGEFEDLCKGPHLWI TRFLNHFKLTKLAGAYLGGDENNEMLI RIYGIAFATKEGLKDYLFQIEEAKKRDH RIYGIAFATKEGLKDYLFQIEEAKKRDH RIYGIAFATKEGLKDYLFQIEEAKKRDH RKLGVELGLFSFDDEIGAGLPLWLPKG ARLKRIEDLLSQALLLRGYEPVKGPEI LKSDVWKISGHYDNYKENMYFTTIDEC EYGIKPMNCVGHIKVYQSALHSYRDLP LRFYEYGVYMRHEKSGVLHGLLRYRE FTQDDAHIFCSFEQIQSEVSAILDFTHK MQAFDFSYEMELSTRPAKSIGDDKVW EKATNALKEALKEHRIDYKIDEGGGAF YGPKIDIKITDALKRKWQCGTIQVDMNU PERFKLAFTNEYNHAEQPVMIHRAILG SFERFIALSEHFGGNFFFVAPTQIALI PINEEHHVFALKLKEALKKRDIFVEVLD KNDSLNKKYRLAEK STOOTO EKELDNLSEEDGNESIAYDFSSAKELL ELCÖKHÖKSAEIVRLRENHPDA TMVKIYHAMILECYDNGANSKERYLPG SLKYTRLAPSIKTRLEKHPTSGKOPLAL IDYISLYARAIBEENASGGKVVTAPTNG ACAVAPSVI 1 YAK
GCGGTGATGAGTAGAGTCGCTGCTTTGCCTTTGCCGTGTTTGAGGGGTTTTGAGGGTTTTGAGGTTTTGAGGGGCTGTTTGAGGGGGCTGGGTTTGAGGGGGCTGGGGGGCGGGGGGGG		-0- ⁹ 0-9+4-40
CGCATCTCCCAAACACCGGTTTTTTAAACCATTTTAAGCTCACTAAACTGGGCTGGGGCTTATTTGGGCGGCGATGAA AACAATGAAATGCTCATTAGAATCTATGGAATCGCTTTTGCCACCAAAGGGGTTTAAAAGACTATCTTTTCCAAATAG AAGAGGGGAAAAAACGAGATCACAGAAAGCTAGGCGTGGAGCTAGGGGCTTTTTAGCTTTGATGATGAGATAGGGGC	CGCATCTCCCAAACACCCGTTTTTTAAACCATTTTAAGCTCACTAAACTGGGCGTTTTTTGGGCGGCGATGAA AACAATGAAAAGGATCTAGGAATCTATGGAATCGCTTTTGCCAAAGGGTTTAAAAGACTATCTTTTCCAAATAG AAGAAGGAAAAAACGAGATCACAGAAAGGCTGGGGCTTAGGGGCTTTTTTTT	CGCATCTCCCAAACACCCGTTTTTTAAACCATTTTAAAGCTCACTAAACTGGGGGGCTGAAACAGGCTTGATGCCAATACAAAGACTCCCAAACAGGCGGGGGGGG
) 999	TAAG TATA AAAG TGAA TGAA AATG AAGC	1446 1414 1446 1446 1446 1466 1466 1466

066501			PC1/EPU	
2274 IPCHQRKRVKMGLKRA (THQKAQQIKE) SILLKHYPNQTTELRHKNPYELLVATILS SACTDARVNQITPKLFEKYPSVNDLAL ACTDARVNQITPKLFEKYPSVNDLAL ASLEEVKEIKSVSYFNNKSKHLISMAQ KVVRDFKGVIPSTQKELMSLDGVGQKT ANVVLSVCFDANCIAVDTHYFRATHRL GLSNAKDPIKTEEELSDLFKDNLSKLHH ALILFGRYTCKAKNPLCGACFLKEFCV S	MOLREELPLIEVGOCFROSSNAIFSNTA KDPKNRRIKALNVKGAUALFSRSVLKE LEEFVRGFGAKGLAYLQIKEÐEIKGPLV KFLSEKGLKNILERTDAJVGDIVFFGAG DKKIVLDYMGRIRLKVAETLDLUKGAL NELWYNNFPMFEKTENGYHAAHHPFT MPKNIECEDIEEVEAHAYDVVLNGVEL GGGSIRIHKEEMÖKKVFEKINIHEEEAO KKFGFLLEALKFGAPPHGGFAIGFDRLI MLMTKSHSIRDVIAFPKTOKASCLLTNA PSPINEEQLRELHIRLRIK	2278 LOLDDDNRGFNFHSHTILDMRWDLESE LNAOKVINSYPIVALEKIFRDYGEIKEYK KAHKIAERRAKKPFKNAKDLSEFLSSF SKNKKIHPATLYFOAVKIEVNSELEELK EFLOCARNLKGAILCVISFHSLEDALVK NAFKDYAKNCICDPSSI-KCACSNNHAL GEILTKKPITPSPEEIKNNRRSRSAKMR VFOFKP	NELPYNLSNYLLSTOLOGNIE NFLPYNLSNYKLSFTD, OGNVIDLGVIE TIPKHSKIVLPGEAFDSI. KIDPYTLFLPKI EATSTSVSDANTORVF ETLNKIKTDLVV NYRNENKFKDHENHWEAFTPQTAEEF TNLMLNMIAVLDSOSWG	AYKDNPTCPGSVCYGEKLEAHYGGGK NLSYTGQIGDEIAFDKHHLGLRVWGD VEYAKAQLGQKVGGNTLLSQANYDPN AIKTYDSASNTQGPLVI.QKTPSPQNFL FNNGHFMAFGLNVNVFVNLPIDTLLKL ALKTEKMLFFKIG
2273 AATACCTTGTCAAAGAAGCGTGTGTGAAAATGGGTTTAAAACGCGCGCTAAAAACTCACCAAAAAGCCCAACAAATCAA AGAGCTGCTTTAAAACATTACCCCAACCAACCACGAATTGCGCCATAAAAACCCCTATGAATTATTGGTGGCGAC AGAGTTTAAGCGCTCAATGCACGGACGCTAGAGTGAATTAAACGCCCCAATTGAAAAATACCCGAGCGTGA ACGATTTAGCCCTCGCTTCTTTAGAAGAAGTTAAAGAGATCAATTAAACGCCCCAATTTTAAACAAAAAGCAAGC			2279	2281 TTTTAAAACGAAAAACCACTTTATCTAGGTTTTAGGCTAGGCAAGGAGGCAATGTGAAGGCAATGTGAAGGGGGGGG
HP0100	HP0100	HP0100	HP0100	HP0100

-	
v	2
.7	٠
•	•

2/066501		PCT/I	EP01/15428
2284 GSAAAVAGGLAVAALGSDTGGSIRQP ASYCGCVGLKPTYGRVSRYGLIAYCSS FDQIGPITQNVEDASILFDAISGYDSKD STSANLKPTQTFKNI.NRDKRFKIAVLM DHIKDASNEVQLAYENTLKALKEMGHE IVEKKMLDSHYQISIYYIISMAEASSNLA RFDGVRYGRRAQNIKDLKELYLKSRSE GFGDEVKRRIMLGNFVLSSGYYDAYYL KAQQMRLIIKEQYNKIFEEVDLIFTPVAP KAQQMRLIIKEQYNKIFEEVDLIFTPVAP AHERDLHPFLTYMAINNENLKCYTKTIF HEESSKSIKGMDRWLYPDMVGVRFLH AELSNENLIAFSKKFDTLPIKLVSFELKK EISVHNCRECYFQAISNSSWANEGYLV	GRHIDTHINPQLMDL 2288 VMPRARLDEAYELATIKDSIVLSLGDM MRVPGSYGSLIQAREKGLDARFLYSP MQALEIAKENPTKKVIYIAIGFETTTPMS ASVLWSAKKEKINNLFFHINHILVPPSV SAILKÜPACQINALLAPSHVSVISGAQIY APLVDRFKIPIIVSGFEPVDILESVLMLIK QALNKEAKLEIQYKRAVSFEGNVKAQE LVNACMEVRENFEWRGLGNIKRSALK LKEAFASYDAEEVFKEYLSHKTSKENK ACKCGEILKGIAKPLDCSLFATTCTPQN PIGSCMVSSEGACAAY	2290 IIQRERVDGIIVHFGGQTPLKLAKDLAK MQAPIIGTPFKVIDIAEDREKFSLFLKEL DIKQPKNGMAKSVDEAYSIANVIGFPIIV RPSYVLGGQHIMQILENIEELRHYLESV THALEISPKNPLLIDKFLEKAVELDVDAI CDKKEVYIAGILQHIEEAGIHSGDSACFI PSTLSPEILDEIERVSAKIALHLGVVGLL NIQFAVHQNSLYLIEVNPFLS KALGVPLAKVATRVMVLEDLKEA	2292 KVIŠLKTKIPŠFLKAVMVIPNRAISTKŲS RHLLPKRYSVQESVFNLSHASLMTMAI VQGKWDLLRČCSKORMHQYKRMOTY PVLFAIQKIALENNALMSTLSGSGSSFF NMCYEEDAPKLKQVLSKKFPKFRVAVL OFDNDGVLIEKO
AGCGGGGGGCTATTGCGGGGGGGGGGGTTAGCGGTTTAGGGGGGGG	2287 CGTGATGCCAAGAGCGCCTTGATGAGGTTATGAACTCGCTACTATCAAAGATAGCATTTGATTTTGAGTTTTGGGGGGTTGGATGCGTTTTGAGTTTTGGGGGGTTTGAAGGATAGCATTGAAGGATAGCATTTGATTTGGGGGGTTTGGGGGGTTTTGTATTGGGGGTTTTGAAGGGGGTTTTGTATTGGGGGTTTTGAAGGGGGTTTTGAAGGGGGTTTTGAAGCGGTTTTGAAGCGGTTTTGAAGCGGTTTTGAAGCGGTTTTGAAGCGGTTTTGAAGCGGGTTTTGAAGCGCGTTTTAGCCCTTTAAGCGCGTTTAGCCCTTAACCGCGTTTAGCCCCTAGCCGTTTAGGCGGGTTTTAGGCGGGTTTTAGGCGGGTTTTAGGCGGTTTTAGGCGGTTTTAGGCGGTTTTAGGCGGTTTTAGGCGGTTTTAGGCGGTTTTAGGCGGTTTTAGGCGGTTTTAGGCGGTTTTTAGGCGGTTTTTAGGGGGGTTTTTGAAGGGGGGGTTTTTGAAGGGGGG	CATCATCCAAAGGGAGGGAGTGGATTATCGTGCATTTTGGGGGACAAACCCCTTTAAAACTGGCTAAAGATTTCCAAAAGCTGGCTAAAGATTTCCAAAAAGCTGGCTAAAGATTTCCCAAAAAAAGGGGAAAAATTTTCCCAAAAAAGGGGAAAAATTTTCCCAAAAAAGGGGAAAAATTTTCCCAAAAAAGGGCAAGAGCAAGAGCAAGACAGGGAAAAATTTCCCTATCATTGAGGCCCCAAAAAGGGGCCAACAAGAAATTTAGAAAAACTTGCCTAATTTTGGAAAAGGCCTTATTTGGAAAAGGGGTTATTTGGAAAGCGTTAATTGGAAAGCGTTTAAGAAAAAAAA	TCTTTTTAAAAGCGGTGATGGTGATCCCTAATAGGGCCATTTCCAC TTACAGCGTGCAGGAGGTTTAACCTTTCGCAGGTTTGA SATTTATTGCGTTGTTGCTTTAACCTTTCGCAGGTTTGA SATTTATTGCGTTGTTGCTCTAAAGACAGGATGCAATAAAGCGC SAAAAGATCGCTTTAGAAAATAACGCCCTAATGAGCAGCGCTTTCAGG SAAGAAGACGCCCTAAATAAAGCACGCTTTTGAGCAAGAAATTCCC AATGATGGGGTTCTTATTGAGAAAGACTGAAATTAAAAATTCCC AATGATGGGGTTCTTATTGAGAAAGCTTTGAAA
	HP0100	HP0100	HF0100

/066501		PCT/E
2294 DCMTATGSLSSNASSGISCSATSSTSS TNSFDNSLVATSKVQTINGKEGIGVNS FNLVSQVWSVYNSLKTSEENI QKNANI LCANGTQSGTSSCNSSSGGLSISGNA QLQNILSPTSGTTTNTQAKSNAPKLKA MVVNNNEEEAKTANLAQSSGTTQSP NSTVMGALNTVLQNVSNFQQSIQNAF QNQESNIQAWANAYNTNGSCISGEMT PNNNQDLRIQLRANFYQLINTINQQVPT DMNALINGSQQTQQTSGSASININACA SGMSGSNGNWCYQQWSDSKAYYSG LQSALGYQTQATTQSGSNGGVSTYN VQQTTLTSNGLLNQIITNLKSVNIGSNKT SGNNCYEPNKQQNATTATTDSNLQ KVYNDAQKIANIIASSGNNKGVENGLK QFFEALKNNSSSLSNLCGNGSSGSSG TTCSGWL	2296 EQTNKEYFLKEQLKQIQKELG"DKQRD EDLNQYYQKLESIKPFLKEEAFKEIKKQ IDRLSRTHADSSDSATLQNYIETMLDVP FGQYGKKALDIKHVREQLDKDHYSLKR PKERIVEYFATMQLLEMRRKK FPEKKD KTKGTILCFYGPPGVGKTSLANS	SALEVALUNK KREVKEIIGSEKASA TAN SAIEVSNIKASAMKNETIGSEKASA TAN SAIEVSNIKASAMKNETIGSGULKKVC EKIKSALPFGIISAFKPFKDAFYRDFNH NEGKLLIGAAKSGCIGSSADKI AGLKT RLLYWQDKSVKVDWDKPILIKIJFKGN NYLYRRFCFLLGKHFMDRFLKNNAKAS VKDFMSSKEFVAKYRYTPKGNIFRAK KLQSYLENKRDFIGFVQALNSI.KDNPQ DPFLPNEETSFLVFANEPTIVFNILRDYL LVLAGIFNQQAICYCESKCPIEI.INA
2293 ATGATTGCATGCTGCTGCGGAAGCCTTTCTAGCAATGCTTCTAGCGGGGATTTCATGCTCAGGCCACAAGCTCCACA AGTTCCACAAATAGCTTTGACCTTTTAGTCGCTACCTCCCAAAGGTCCAAACCATCACACGCCAAAAGGTCGGAAAACCAAAAACTTTTAAACCCTTGCAGGGGGTTTATAAAACTTCAAAAACTTCAAAAACTTAAAAACTAAAAACCAAAAATTTTAAGCGCTAATTATGCAAAAATTTTAAGCGCTAATTATTAAGCGCTAATTATGCAAAAACTAAAAGCCCTACTAGTGGAACAACTCAATACTCAAGCCAAAAACGAAAAAAAA	AGAGCAGCTCAAACAAATCCAAAAAGGGCTTGGCACAGACAAACAG AACTAGAAAGCATCAAGCCTTTTTAAAAGAAGAAGCGTTTAAGGAG ACCCATGCGGACAGCTCGGATAGCGCGACTTTACAAAATTATTGA CGGGAAAAAAGCGCTTGACATTAAGCATGTGAGAGAACAACTAGACA AGCGCATTGTAGAATACTTTGCCACCATGCAGCTTTTAGAAATGCGCC CTAAAGGCACGATTTTATGCTTTTATGGGCCTCCTGGCGTGGGTAAA	2297 TGGCTAGGGAAGTGGCTCAAAATAAAACGAAGCGATTCGTTAAGGAGATCATTGGGAGCGAGAAAGCTCTAAAACTAAACTAAACTTAAGGAAACGATTGGGAAAGCCTCTAAAAAACTTAAAAACGGCATTGAAAGCGCTTTAAAAAACGGCGTTTTTAAAAGGGCGCTTTTTAAAAGGGCGCTTTTTAAAGGAATTCAATCATCATCATCATCAATCA
HP0100	HP0100	HP0100

•	2	t	
١	i	Ć	3
•	٠	•	1

KAYTALLK	ILTTALYV IAGGTITR SEULNSIDS SKWVRPV SEULNSIDS SKWVRPV AETGVEH TGVMDEI
2304 VFKDSKKDAČGFIYEISEFMKAYTALLK KQDRYVYLLRYLPSRYWASILTTALYV KYPDFDALKKLLVSYYYQTWIAGGTITR IKQTSINIIKNVKSNKSVETIKELILNSIDS YNTFDQYLYNLWDSSSVYHSKWYRPV LALANYFMADEEKPHFAMDAETQVEH	ILPOTPKRGSQWNADFDKEKREEWVN NIANLTLLKRKKNAHALNGDFDEKRKIY GGKDTSKVISCYDITKELYSNYR 2306 KVIYLDQAPIGKTPRSNPATYTGVMDEI RILFAEGKEAKILGYSASRFSFNVKGG RCEKCOGDGDIKIEMHFLPDVLVQCDS CKGAKYNPQTLEIKVKGKSIADVLVNGS VEEAYEFFAKFPKIAVKLTLMDVGLG YITLGONATILSGGEAGRIKLAKELSKK DTGKTLYILDEPTTGLHFEDVNHLLQVL HSLVAL 2308 TPILTPKINVIELNAWAWAWLQNIPFHP
2304 VFKDSKK KQDRYVY KYPDFDA IKQTSINIII	YNTFDOY LALANYFA ILPOTPKR NIANLTLLI GGKDTSK GGKDTSK RILFAEOK RILFAEOK CKGAKYNI VEEAYEFF YITLGONA DTGKTLYIL HSLVAL 188LVAL
d. (2)	
CATGAAAGCCTA GGCCAGCATTTA TACCAAACTTGG	ATCAAAGAGCTTATATTGAATAGCATCGACTCTTATACACCTTTGATCATATACCTCTATAGAGGGGTTGAAACCTCTTATGGGATAGCTTTATGGATAGCTTATGGGATAGCTCTTTGAAGGGGTTGAAACCTCTTTATGGATAGCTTATGGGATAGCTCTTTTATCATAGGTGAAGGGGTTGGATGCTCTTTATCATAGCTTATGGGATAGCTCTTTTATCATAGCTGAAGAGGGGATAGCTCTTTTATCATAGCTGAAGAGGAAGGA
AGGTGTTCAAAGACAGCAAAAAAGACGCTTGCGGGTTCATCTATGAGATCAGCGAGTTCATGAAAGCCTATACCGCA TTGCTAAAAAAACAAGACCGATACGTCTATTTATGAGGTATCTCCCCTCTAGGTATTGGGCCAGCATTTTAACGACT GCCCTTTATGTCAAATACCCTGATTTTGACGCTTTGAAAAGCTTTTGGTGTCTTATTACCAAACTTGGATTGCAG	A I CAAAGAGCI I ATATT GAATAGCATCGACTCTT ATAACACTTT GATCAATACCTCTATAACTTATGGGATAGCTCTT TATCGCTATGGCAATGGGTGCGTCCTGTCTTAGCCCTAGCTAATTATTCATGGCAGATGAAGAGAACCCCATT TATCGCTATGGAAGAATGGGTGCGTAATTTTTGCCAAAAGGGCAGTCAATGGAACGC GGATTTTGACAAAGAAAGAAGAATGGGTAAATAATTGCCGAAATTTAACCCTTTTAAAGCGTAAAAAGAACGC GCATGCTTAAACGGGGGATTTTGATGAAAAAAAAAA
AGGTGITCAAAGACAGCAAAAAGGACGCITGCGGGITCATCIATGAGATCAGCGAGTTCATGAAAGCCTATACCGCACTTGCTAAAAAAAA	THATCGCTATGGATGCCGAAACCCAAGTGGAGCATATTTTGCCACAAACGCCCCGCAAACGCCCCGCAAACGCCCCCGCAAACGCCCCCGCAAACGCCCCCGCAAACGCAAACGCAAACGCAAACGCCCCGCAAACGCAAACGAAAAAA
GACGCTTGCGG SGTCTATTTATT TTTGACGCTTT SCAAACCAGTAT ATCGACTCTTA	SGTCCTGTCTTA SAAGTGGGGAA WGAATGGGTA WGAATAAGG CCCATAGGCAA GCAAGGGGAT GCCAAGGCGAT GCAAGGCAT AAGAGGCTTAGG AAGAGGACAC AAGAGGAT CTCATTGAATT
ACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	SCAANTGGGTGC ATGCCGAAACCC AGGAATTGAAG AGATTGAAGCCGA TAGATCGAGCCGA TTATTTGCCGAAATTG SCTGTAAGGCCAT AGAATTGAGCTAT AGAATTGAGCTAT AGAATCATCTTTT AGAATCATCTTTTTTTTTT
2303 AGGTGTTCAAAGACAGCAAAAAAGACGCTTGCGG TTGCTAAAAAAACAAGACCGATACGTCTATTTATTC GCCTTTATGTCAAATACCCTGATTTTGACGCTTTC GAGGCACGCGCACAAGCCAGTAT	CTETTTATCATAGEATEGETECATCGACTCGACTCTGTTATCATAGCAATGGGTGCGTCCTGGTATTATCATAGCAAATGGGTGCGTCCTGGGGTTTTTGCAATGGTGCGAATGGTGCGTCCTGGAATGGTGCTGAAATGGAATGTTTTGAAAAAAAA
2303 A	230 230 230 230 230 230 230 230 230 230
HP0105	HP0837 HP0837

2/066501			PCT/EP01/15428
2310 VITNRGGRTCHAAIVAREIGVPAIVGVS GATDSLYTGMEITVSCAEGEEGYVYA GIYEHEIERVELSNMOETÜTKIYINIGNP EKAFGFSQLPNHGVGLAYMEMIILNQI KAHPLALVDLHHKKSVKEKNEIENLMA GYANPKDFYVKKIAEGIGMISAAFYPKP VIVRTSDFKSNEYMRMLGGSSYEPNE ENPMLGYRGASRYYSES YNEAFSWEC EALALVREEMGLTNMKVIAIPFLRTIEE GKKVLEILRKNNLESGKN SLEIYIMCEL PVNVILADDFLSLFDGFSI 3SNDLTQLT LGVDRDSELVSHVFDERNEAMLK	2312 ILADDRATTLEVMAYHMEELELKDEDIA CCLYGASALLQEKHLKNAFETLNKNQN TDYVFTCSPFSASPYRSF SLENGVQM AFKEHSNTRTQDLKTLYHDAGLLYMG KAQAFKEMRPIFSQNSIALELSPLEVQD IAHFRRFRISQAQIQPFEK-XMPVKILCD CFLTSGLGHVRRCEKILSF:IEKLGVEAS LYLHKQNNISAFLEGV.	2314 EQKFTESKSYMEWIKGLYEKSDGPTLK SFDQFWRDGFVEFEIPENARKFVRHA KFRQDPINNKLDTESGKIGIIFSQKCADF KLADFKGHPTWFEPAEWI.GSKMAEIY PFHLISPHPKYRVNSQLDNTWVRNVYK IQGREPVMINELDANKLGIRHGEIVEVF NARGRLLA	2316 RTLELSGYEVMLVRNFTDIDDKIINKAL KENKSIGELSSIYIESYTRULMALNVKK PSLEPKASEYLDAMVGMI=TLLEKNIAY QVSNGDIYLDTSKDKDYGSLSYHNSSI EFGRIGLVQEKRLEQDFV.JWKSYKGD NDVGFDSPLGKGRPGWHIECSSMYFE TLALTNTPYQDIJNAGGADLLFPHHENE ACQTRCAFGVELAKYWM-INGFVNINN EKMSKSLGNSFYKDALKNYDGELRN YLLGVHYRSVLNFNEEDLJVSKKRLDKI YRLKQRVLGTLGGINPNFIKKEILECMQ DDLNVSKALSVLESMLSSTNEKLDQNP KNKALKGEILANLKFIEELL GIGFKDPSA YFQLGVSESSEKQEIENKIEERKRAKER KDFLKADSIREELLKOKIALMDTPQGTI
2309 GGTTATCACTAATCGTGGAGGGCGCATGCCGCTATTGTGGCGAGAGAATTGGCGTGCCAGCTATCGTT GGGGTGAGCGGCGAGGGCGCATTATACCGGCATGGAATCACGGTTTCTTGCGCTGAGGGCCGAAGAGGGC TATGTGTATGCGGGCGATTATGAAAAAATTGAAATTGAAAAAACGGTGGAGGCTTTCTAACCAGGTTTCTAACAGAAAATTTATGCAAAAAAATTGGAAAACCTTTGGAAATTGCAACCAATCAAT	2311 AAATITTAGCGGACGACGACGACTTTAGAGGTGATGGCCTATCACATGGAAGATTAGAATTAAAAGATGAA GATATTGGGTGTTTGTATGGCGCTTCAGGGCTTTTACAGAAAGACTTTAAAAAAAGGCTTTTGAAACTTTAAAAAGGGTATTGCAAATTAAAAACTTTAAAAAACAGGAAAACAAAACGGAAAACAAAACGGAAAAACGGAAAAAA	2313 CGGAGCAGAAATTCACTGAATCTAAGAGTTACATGGAATGGATTAAAGGCCTTTATGAAAAAGGCGATGGCTACT TTGAAATCGTTTGATCAGTTTTGGAGGGATGGTTTTGTGGAGTTTGAAATCCCTGAAAATGCGAGAAAGTTTGTGCGT CATGCGAAATTCAGGCAAGACCCTATTAACAATAAGCTGGATACAGAGAGTGGGAAAATTCAAAATTTTTCTCAAAAA TGCGCGGATTTTAAAACTGGCCGATTTTAAAGGGCATCCTACTTGGTTTGGTTTGAGCCAGCTGAGTGGCTAGGCTCTAAAAT GGCTGAGATTTATCCGTTCCATTTAAACTCCCCCAAAAATACCGTGTCAATAATTCACACTTGGGT TAGGAATGTGTATAAAATTCAAGGCAGAGAGCCTGTAATGATCAATGACCGTATAAAATTAGGCATTAGGCA TGGTGAAATTGTAGAAGTGTTTAACGCTAGGGGAGGGTTGTTAAGGCATTAGGCATTAGGCATTAGGCATTAGGCATTAGGCATTAGGCATTAAGGCATTAAGGCATTAAAATTAGGCATTAGGCATTAGGCAGGGAGGTTGTTAACGGTAGAATTAGGCATTAGGCATTAGGCAATAAAATTAGGCATTAGGCATTAGGCAGGGAGGTTGTTAACAGTTGTAGAAGTGTTTAACGCTAGAGGGGAGGTTGTTAAGGCAGGGAGGTTAGAGAGTGTTTAACGCTAGAGGCAGGGAGGTTAGACAGGAGAGGAGGAGATTAAAATTAGGCATTAAGGCAGAGAGGAGGAGGAGGAGGAGGAGAATTAAAATTAGGCATTAACGCTAGAGAGGCAGAGAGGAGGAGGAGAGGAGAGTATTAAACGCTAAAAATTAGGCATTAAAGGCAGAGAGGAGAGGAGAGAATTAAAATTAAAATTAAGGCATTAAAAATTAACGGTAAGAAATTAAAAATTAAGGCATTAAAGGAGAGGGAGG	2315 GGCGCACGCTTGAATTGAGCGGCTATGAAGTGATGTAAGGAATTTCACAGAATATTGACGATAAGATCAACACACAC
HP1246	HP1246	HP1246	HP1246

<	3
	Ξ,
-	•

	RVEIFFSTDA	TATCGCGCCTAACGACTCCCTAGAGAACAGAATGAAAAACAATCGTGTGGAAATCTTTTTTCAACCGATGCGA
	NOT SESSOCIATION OF THE STANKING TO SESSOCIATION OF THE STANKING TO SESSOCIATION OF THE STANKING TO SESSOCIATION OF THE STANKING THE SESSOCIATION OF THE SESSOCIATION	TAGGGTGAAGTCCTTATACAATACGCGTAAATCCTAATCCAATTGTCTTTTCTTCTTACGGCTCTACCAACCC
28	RIAKIIQKLPKRVHINVRGFTDDTPLVKT	CAATCCAGGGGGGGGGGGGGTGCTTAATTGGAACGGATCGCTAAAAGCATTTAAAAACTCCCTAAAAGGGGTGCATATTAATGT GAGAGGCTTTACGGGATGATACGCCATTAAAAAACCCATTTAAAAAACCAATAAAAAAAA
54	SILKLPSNLLFENATSDAINODMMLYIE	THINGAGCAAATIGATCAAGGCTCTATCTTAAAGCTCCCCTCTAATTTGCTGTTTGAAAAGGCTACTTCAGACGCTAT
/13	PASONTETKATIARKGEGSVLEQIDGG	
01	EAMOPVVVIPPDSGKEEEDMASESSK	TTACGCTCCCAAGCCAGGGCGATGCAGCCGGTTGTAGTGATCCCGCCTGATTCAGGGGAAAGAAGAAGAATG
CP	LYAISAVNKSKVEALKTEFIKIFNYAPKP	I A I CGC I TA I CGC CATTICA GCG G T CAACAA T CCAAAGT G GAAAGC G T TAATAAGATTITAA
1/1	2330 KPTECPAGEKWAVPYADFLSLLLALFIA	2329 CAAACCCACCGAATGCCCCCCCCGCGGTGAAAATGGGGGGTTCCTTATGCGGACTTTTGTCGTTGTTGTTGCTCGCGCTTTT
· C.	INL-KOVQTLVYERNYELGAVFEKNIRFI JDFDSQ:	CCALICACIONE CONTRACA INTERCACIONE CONTRACA
	NA ENLERNE NA EL POLITA DE LA CONTRETA DEL CONTRETA DEL CONTRETA DE LA CONTRETA DEL CONTRETA DEL CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CON	CONTROLL TO A CO
	ISTNAPROESKNIEKREKIECIEKIEGIE	
	KAREALKEVAL COADENIONDO	TGTTATTGAAAATGAAATTCAAAGGGTTTGAAATTCAAAGGGGTTGAAAGTTGAAAGTTAAAAGAATAAAAGAATAAAAGAATAAAAAGAATAAAAAA
		TGATAGAGGGCTTTTTAAAATCATTATGAGCAGTTTGAGGCCTTTTAAAAGAAGGGGGCAAATGCCAGTTTTGTGT
	2328 FTESVI FEMMI FI KAKI I SPINEVSII I IE	2327 GAAACCGAGAGCGTTTTAGAAGAAATGATGCTTTTTTGAAAGCGAAATTATTGAGCCCTGATTTTTATTCTATCCTTT
		JAAGCTTGCGATAGATTTTAAAAGTGGTGTTTTGAGAGAGA
		ATTICITAACCAATCTTAAATACGCCTTACTTTTAACCCATCTCCTTATGGTGCGTAGCGTAAGGATTTTGA
	DTI KKEAI AHEKIAI OEI NOS	ACCCATGCTTTAGAGGACATGCTCAAAAACCCCAGGCTCAAAAAAGAAGAGGGTTAGCACATTTTAAAAATAGCGCTCCA
		GCCCAAACGCCTTTAAACCTTCTAAAGAATCCTTGGGCGCATCGTGTCTTTAAAACAAAC
	DCSILSTLKCDSNSLNLEEEINACLFHL	
		TTAACTGCCCTTAAAAGATTGCAGTATTTAATCCTTCAAATCCAACTGTAAAAAAAA
	KRHONSKPVIGLENPTSKLTFITLTPML	CCCCCATGCTGGATAGCCAATTGAATTTCTTAAAAAATAAAAAAAA
,	2326 TNTNLDKPONKPLNKOVYEGIENCNLC	2325/CACCAATACCAACCTTGATAAGCCCCCAAAATAAGCCCCTTAACAAAGAAGTTTATGAGGGCCATAGAAAATTGCAATCT
		TTCIATGGTTTTTTGAATGGCTTAGGGGCTTATGATTCA
	NLAFNMLGNFAKL	CCGAAAAATTTAGCCTTTAACATGCTGGGGAATTTTGCTAAATTGTGATGTTTCACAAAGCCCTTATTACCTTTATCG
	EDKEAMOIYLMSALNDGYKAVEENRK	CTGTTAGAAGATAAAGAAGCGATGCAAATCTATTTGATGAGCGCTTTGAATGACGGGTATAAAGCCGTAGAAAAA
,	2324 KSGGGMVSVSFNGLGELVDLQIDDSLL	2323 CAAAAGCGGTGGGGAATGGTGAGCGTGAGT1TTAATGGGTTGGGGGAGTTGGTGGATTTGCAAATTGATGACGC
	FCORRECTE	CCTGATATTGATACGGATTTTTGCCAGCGCGTAAGGAAATCATAGAATAC
	DIDPLKYDLLFERFUNPERISMPDIDTD	TTTAAAAATCACGGATATTGACCCTTTGAAATACGATTTGCTCTTTGAAAGGTTTTTAAACCCCGAAAGAATCAGCATG
_	AKEMGIPVGPGRGSAAGSLVAFALKIT	CCGTTATGCTAAGGAAATGGGCATTCCTGTAGGGCCTGGTAGGGGGGGG
-1	2322 ERLEKEIEVITNMKFPGYMLIVWDFIRY	2321 AGAGCGCCTAGAAAAAAAAATTGAAGTCATTACGAACATGAAATTCCCAGGGTATATGCTGATTGTGTGGGGATTTTAT
	KWDSPFKQH	GGACAGGAAAAAAGTCGTGGATAGCCCTTTTAAACAGCACTAAATGTTTGATTAGGGGCTAATAGGGGGCATGCCCTT
_	KKWOERVEVAIKRARHMALIPYIVDRK	ATAGCAAAAAGTGGCAAGAAGGGTGGAAGTAGCGATCAAAAGAGCCCGCCACATGGCTTTAATCCCCTACATTGT
7	2320 DYKDI DMI KHTI SFRYKIMPRRI TGNS	2319 TGACTATAAAGATTTAGACATGCTCAAGCACACGCTATCAGAGGCGCTATAAAATCATGCCAAGGAGATTGACAGGCA
	TGHS	AGCGTTGGAATACTGCGATTTTAATTTTAGTGGATACGACAGGCCATTCGC
_	MSIEAVIDAKDFAKEIEALEYCDFILVDT	ALI LAGCI GGTATGCTAATAAAATGAAAATGAGTGTATAGAAGGGTGATTGACGCTAAGGATTTTGCTAAAGAAATTGA
V	KYKVGIITLDNYRIGALEQLSWYANKMK	CIALICIAGGAIGTIAGCTAAAAATACAAGGTGGGCATTATCACTTTAGACAATTATCGCATTGGGGCTTTGGAGCA
Ÿ	MLVGPTGVGKTTTLAKLAARYSRMLAK	GECCAMANACISCA IC I PATIGETTGTAGGCCCAACAGGCCTGGGGAAAACGACGACTTTAGCTAAATTAGCCGCGCG
	KRYFREVLRKMILCCPEDLNLRÖKRIL	CONTROL STATE CONTROL STATE OF THE CONTROL STATE OF
	KPSHLDEIMQLSLELMPLRMRENSVTI	AAGI GGGA GAAACCCAGCCATTTAGA GAAATCATGCAATTGAGCCTGGAATTGATGATGCCATGCGCAAA
	WDEKNPNSINIPOEFAEIYKLAKOSGM	ACATGTTTGGGATGAGAAAAACCCCAATTCTATTAATATCCCTCAAGAATTTGCAGAAATTTACAAACTGGCCAAACA
	VKQEEEIKDINLQLSKIRDSLKLIQNMF	AAGE AAACAAGAAGAAGAAATTAAAGACATCTGCAATTAAGCAAAATCAGAGACAGCCTGAAACTCATTCAAA
_	2318 EANKODALLOALKDEANHKKEREKRE	ANOTITY CONTRACTOR CON
/([The state of the s	Z31/IAGAGGCTAATAAGCAAAAAAAAAAAAAAAAAAAAAAAAA

066501			
2332 DILSSIFGKGGFSQRFSCNSQGFSGFN 99 FSNFAPENLDITAALNVSVLDTLLGNKK 95 QVSINNETFSLKIPIGVEE:GEKIRVRNK 95 GKTGRTTRGDLLLEIHIEEDEMYRREK DDITQIFDLPLKTALFGGKIEIATWIKTL 1LTIPPNTKAMQKFRIKE KGIKNRKTSH VG	2334 ALAKSAFVKTTMIKEIPYI-KEIE ILVLHK RDFKIVMEKISEEIAKNHJOVIVVYPLVN ESEKIPYLSLSEGASFWUJKRFKKYTT SGODKNKEEVIEFRESGSILLATTLIE VGISLPRLSVMVILAPERLGLATLHQLR GRVSRNGLKGYCFLCTIJGENERLEKF ADELDGFKIAELDLEYRKSGDLLQGGE QSG	2336 KAISQQKIQAKIEELGENYENAIIEGKIV GKNKGGYIVESQGVEYFLSRSHSSLKN DANHIGKRVKACIIRVDKENHSINISRK NROITPFGIFVEAKGIEGI.VHYSEISHK GPVNPEKYYKEGDEVY/KAIAYDAEKR RISLSIKATIEDPWEEIQIKLKPGYAIKV VVSNIEHYGVFVDIGN	OLDKGYYWIETELGWR.KAHGSLLKKI OKPPKNKFKPPKTTIPKIYEASLRLDLR GORSEEALDLLDAFLNDALLGGFEEVLI CHGKGSGILEKF
233	233	233	3
2331 CGATATITTAAGCTCTATTITTGGGAAAGGAGGCTITTCGCAAAGATTTCTCAAAAACTCGCAAAGGCTTTTCTGGCTTTTCTGGCTTTTCTGGCTTTTCTGGCTTTTTT	2333 GCCCTAGGCAAAAGGGGCGTTTGTGAAAACGACCATGATTAGAGAAATCCCTTATCCTAAAGAGATTGAAATCTAGT CTTGCATAAAAGGGGTTTTAAAATAGTGATGGGGAAGAAATCGGGAAGAAATCGCTAAAAACGCTGATGTCGT CTTGCATAAAAGGAGATTTTAAAATAGTGATGGGGAAGAATTTATGGCAAAAACGCT CTATCCGCTGGTGAATGAGGGCGAAAAATCCCGTATTTATGGCGGGGGGGG	2335 AAGGCCATTTCCCAACAAAAGATTCAAGCTAAAATTGAAGAATTAGGCGAAAACTATGAAAACGCCATTATTGAAGGCCAAAGGCCATTATTGAAGGCCAAAACTATTGAAGGCGAAAAGGCGGTTCATTGAAGGCGTTCATTCGTGTGGATAAGGAAAACCATTCTTTTAAAGAATGAAGGCCAAACCATTCGTGTGGATAAGGAAAACCATTCTTTTCTTTAAAGAATGAACCATTCTTTGAAGGAATGTTTGTT	2337 ACAAACCAAGAGATCCCACAAATCATAACGAACTTTCAAGCCAACGAAAAGGGGGGCGCTACAAGAATGAAAGGGGGGTTGGGTTTGAAAGGGGCATGGGAGTTTGAAAAGGGCATGGGAGTTTTAAAAAGGGCATGGGAGTTTTAAAAACGAAGGGGCATTGGAAAACGAACCGAAAACCGAGCGTTTGAAAACAAAACAAAACCGAAAACCGCCTAAAACAAAC
HP1245	HP1245	HP0399	HP0399

066501		PC	T/EP01/15428
2340 SQPKPKKTKEKKKEAPTPIAKKKGGIEI VNTFENQTPPTENTPKVVSHSQIEKAK GKLGEIGKSREALNKLTQSNANNASNA NNAKKEISEVKKOEOEIKRHENIKRRT GFRVIKRNDEVENESENSVTESKKPTQ SAAAIFEDIKKEWQEKDKGEAKKAKKP SKPKATPTAKNNKSHKIDFSDARDFKG NDIYDDETDEILLFDLHEQDNFNKEEEE KEIRQNINDRVRVORKNPWMNESGIK RQSKKRAFRNDNSQKVIQSTTAIPEE VRVYEFAQKANLNLADVIKTLFNLGLM VTKNDFLDKOSIEILAEFHLEISVQNTL EEFEVEEVLEGVKKERPPVVTIMGHVD HGKTSLLDKIRDKRVAHTEAGGITQHIG AYMVEKNDKWVSFIOTPGHEAFSQMR NRGAQVTQIAVINAADDGVKQQTIEA	2342 RAGAFERFTNRKKRFRENAGKNAEYS NHEASSHHKKEHRPNKKPNNHHKQKH AKTRNYAQEELDSNKVEGVTEILHVNE RGTLGFHKELKKGVEANNKIQVEHLNP HYKMNLNSKASVKITPLGGLGEIGGNM MVIETPKSAVIDAGMSFPKEGLFGVDI LIPDFSYLHQIKOKIAGIITHAHEDHIGA TPYLFKELQFPLYGTPLSLGLIGSKFDE HGLKKYRSYFKI	2346 GEMHILMIHILCDCIERHFAHKN 2346 MRHYETMFILKPTLVEEEIKSKIEFYKE VITKHHGVIETSLÖMGMRNLAYEIKKHK RGYYYVAYFKAEPSMIVELERLYRINE DVLRFIVIKYESKKEVEAWHALVÜRAN KKPSHAKEKHEKTEHTHSHHTEEAES VGSHSE	2348 QVIK I ILLELNKMISHIFFISVRALLVGA MSVFLYAFKTREYGLDLMEDYCGARL THNAIRIGGVPLDIPPINVLEGLKKFLG EMRECKKLIQGLLDKNRIWRMRLENV GVYTQKMAQSWGMSGIMLRGTGIAYD IRKEEPYELYKELDFDVPVGNYGDSYD RYCLYMLEIDESVRIIEQLIPMYAKT
	2341 CGAGCCGAGCGTTTGAGCGCTTCACCAACCATGAAGCGTCTCGCACCATAAAACACGAAATTACGCCCAAGAACACGAAATTACGCCCAAGAACACGAAATTACGCCCAAGAACACAGAACTTAGGAACTTCATAAACCCATTAAAGATGAACTTAAACATTAAAACCTTTAAACATTAAAACTTAAAACCTATTAAAACTTAAAAACTAAAAAA	2343 CCAAGAATICCTTTATGATCCACATCTTATGCGATTGCATTGAAGGCATTTCGCTCATAAAAATTAGCCCTAA TTTTGAATTTCTTTAGGGATTTGGTAGTTTTCTATCGTTTGGATGAGTTTTTGCTTGAAGGAATCAATGTTGTTTGGAG TGAGTAGGTATTTCTTGGTAGTTTTCTTACGTTTTGGAAGCTTTTTGGAACCT TGAGTAGGTATTTCTTGCTTATGCTTTTTTTTTT	2347 CÉCAGGGGGGCACGATTITACTAGAGCTTAACCGCATGATCTCACACATCTTTTTATCAGCGTGCATGCTTTAG ATGTGGGGGGCGATGAGGGTGTTTTGTATGCGTTTAAACGAGGGATTAGCATTGGTTGG
HP0399	HP0399	HP1244 HP1244	HP0276

02/066501		PCT/EP01/15428
2350 LOKRGLSLESIKAFKLGLGTNIRIDYGIE NKGLNKDKLIELGVLGKSDNIDOKTYLR FLDRIMFPIYSPSAQVVGFGGRTLKEK AAKYINSPQSKLFDKSSLLYGYHLAKE HIYKORQVVTTEGYLDVILLH(JAGFKNAI ATLGTALTPSHLPLLKKGDPEILLSYDG DKAGRNAAYKASLMLAKEGRRGGVILF ENNLDPADMIANGOIETLKNWLSHPMA FIEFVLRRMADSYLLDDPLEKDKALKE MLGFLKNFSLLLQSEYKPLIATLLQAPL HVLGIRERVSFQPFYPKTEKPNRPQRF AHVSSAPSLEFLEKLVIRYLEDRSLLD LAVGYIHSGVFLHKKQEFDALCGEKLD DPKLVALLLDANIPLKKGGFEKELRLI LRYFERQLKEIPKSSLPFSEKWICLKKA	2352 OKL SLKNAWTRVLSNHEGLHAQEYAIK RASKMKLAAKLSFLPOIDLSA "YVYLSN PKANDFASOKOPGVOKATNOIHOGIQN IQONIPSOVLTPOIOAGMOGY MOGFG ALSSTLEAPLLFSKONVYIGALSIIYPLY MGGARFTMVRIADLMOKDANEVYRLK KLSTFOELVSVYYGMVLNAEVAETLEE VEKGHYKHFONALKMOKVGCIJARVET LGAQVAYDKAHIASVKAKDVLEVSQLS FNSILSSKDDLVPSSKLEIRTEKNLPDL SFFVSSTLNSYPVLKTLENQICIISKENT KLQIAKFLPOVSFFGSYIMKQINNSVFE DMIPSWFVGVAGRAMPILSPTGRIGKYO ASKLAELQVSSEQIOAKKNMELLVNKT YKETLSYLKEYKSLLSSVELAFENKLO GGAFLOGLSTNAQVIDARNTLSSIVVE OKSVAYKYIVSLANLMALSDHIDLFYFF VY	2354 CKCVKEGDVIAFGKYKGAEN DGTEY MVLELEDILGIVGSGSCCHTGINHDHKH AKEHEACCHDHKKH
ATTGATTACG CGATCAGAAA TGGAGGCCG TGCTTATGG TGCTTAAAAA SAGCTTGATG TCGCTAATG TTCCTTGCT ATGGCGGATT TTCCTTGCT SAGAGCGAGT TTCCTTGCT TTCCTTGCT TTCCTTGCT TTCCTTGCT TTCCTTGCT TTCCTTGCT TTCCTTGCT TTCCTTGCT TTCCTTGCT	AATACGCCA TITATGTGTA AGATCCATC CAAGGGGTG SATTGGGGC GCAAAAGA GGTGTTAAA AAATGCAAA TAGCGTTAA GCCTTCAAG CCCTCCAAG TGCCCTCAAG TGCGGT CCCCAAGTG	ACGGCACTG AATCATGAC SGATACAAAA AACGCTGTTA TAAAGATGG AAGTAGCG AAGAAGGTT CATTATTAAT
GTATCAAAGCGTTTAAATTAGGCTTATGCACGAATAGAATTGATTACGAAAAAGCTCATTAGGAAAAAGCCATTAAGGCGTGGCAAGAGGCGATAAGGAATTGAAATTGATTG	AGGGTATTGTCTAACCATGAAGGCTTGCATGCGCAAGAATACGCCA CTAAACTTTCTTTTTGCCTCAAATTGATTGAGCGCATTTTTATGTGTA AGCCAAAAACAACCGGGCGTGCAAAAAGCCACCAACCAAGGGGTG TTCTCAAGTATTAACCCCTCAAATCCAAGCGGGCATGCAAGGGGTG TTAGAAGCCCCCTTATTGTTTTCTAAGCAAAATGTGGTGATTGGGGC SGGGCAAGATTCAAGGCTTGTGAGCGATTTGATGCAAAAAGA TCCACTTTTCAAGAGGTTGTGAGCGTGTATTACGGCATGGTAAA TAGGCGCTCAAGTGGCTTATGATAAGGCCCATATCGCTAGCGTTAA TAGGCGCTCAAGTGGCTTATGATAAGGCCCATATCGCTAGCGTTAA CTCGTTCAATTCCATTTTTGTTAGCAAGGACGATTTGAAATGCCGGT CCAAAGAAACACGAAATTACAGATCGCTAAATTCTTGCCCAAGTG CCAAATTCGGTGTTTTTTTTTT	GCTTTTGGCAAATACAAAGGCGCAGAAATCGTTTTAGACGGCACTG AGGCATTGTGGCTCAGGCTCTTGTTGTTGTACAGGCGCACTG AGGCATTGTGGGCTCAGGCTCTTGTTGTCATACAGGTAACACAC GTCATGATCACAAAAAACCTTAAAAAACATTATTATAAGGATACAAAA GAGAAACCTTTTATTTGAAGGCGTGAGACAACTCCATGACGCTGTTA GTTGATCCAAAAAAGCTATGGCGTTGAGCACTCCATCACAAAAGATGG TGCCCGGTAGCTAACATGGGCGCTCCAACTCGTTAAAAGAAGTAGC ACGACCACAGCGACCGTGCTGTATAGCATTTTTAAAGAAGGTT TTGAAGTGAACGAGGCATGGATAAAGCCGTTATTAAT
GCTTAGCCTAGAGA CTTGAATAAGGACA GGGATCCATCATA GCGGCCAAGTATAT GAACACATCTATAAA WAAACGCCATAGC CTTTTGAGCTATGA GGAGGGGGGT CTTTAGAAAAGA AAGCCCTTAATCGCT ACCCCAAAACGA AAGCCCTTAGTGCAAAAGA	AAAAACGCATGGACT AAATGAAATTAGCGGG AAAATGGATTTTGCC CCAGCAAAATATCCC SCTTTGAGAGGTG CGTTTGAAAAGCTT AACTTTAGAAAGGTT CGAGTTCGCAGGTG CGAGTTCGCAGGTG AACGGGGAAAAATCT AACGGAGAAAAATCT	TTGCAAATGCGTTAAAGAAGGCGATGTGGTTTTGGCAAÁTACAAGGCGCAGAAÁTCGTTTTAGACGGCACTG AATACATGGTGCTAAAAGAACTAGAAGACATTCTAGGCATTGTGGCTCAGGCTCTTGTCATACAGGTAATCATGAC CATAAACATGCTAAAAGAACTAGAAGCATTGTGGCATTGTGGGCTCAAAAAACATTATTATTAATAAGGATACAAAA CATAAAACATGCTAAAGAATTTTCAGATAGCGCGAGAAACCTTTTATTTGAAGGCGTGAGACACTCCATGACGCTGTTA TGGCAAAAGAAATCAAATTTTCAGATAGCGCGAGAAACCTTTTATTTGAAGGCGTGAGACACTCCATGACGCTGTTA AAGTAACCATGGGGCCAAGAGGCAGGAACGTGTTGATCCAAAAAAGCTTGGCGCTCCAAGCATCAAAAGAAGGC CGTGACCATGGCCTGATGAAGAATTGAATT
2349 ATTTGCAAAAAAGGG GCATTGAAAATAAAGG ACCTATTTGCGCTTTT CACCTTAAAAGAAAAA CTATCATTTGGCTAAA CACCAGGCGGTTTT/ AGCCAATCCTAAAGCAAATC TTGCTAAAGAGCAAA CCTATCTTTAGACGA TTTACAAGCGAATAC CTTTTTCAGCCTTTT GTTTGGAATTTTTAGA	2351 TCAAAAACTCCCTTA TTAAGCGAGCGAGTA TCTCTCTAACCCCATT AAGGCATACAAACAT ATGCAAGGTTTGGGC ATGCAAGGTTATTTATC TGCTAATGAAGTGTAT CGCAGAAGTGGCTGA AAGTGGGCCAATTCG GGCTAAAGACGTGTTA CGAATTAGAGAGTCCGC TTTAAAGACTTTAGAA AGTTTTTTGGCTCTTA AGTTTTTTGGCCTTTA	2353 TTGCAAATGCGTTAAAGAAGGCGATGTGATC AATACATGGTGCTAGAACTAGAAGCATCT/ CATAAACATGCTAGAAGCTGGAAGCATTCT/ CATAAACATGCTAAAGAGCCATGAAGCTTGCT/ TGGCAAAGGAAATCAAATTTTCAGATAGCGC AAGTAACCATGGGGCCAAGAGGCAGGAACG CGTGACCTGGCTAAAGAGATTGAATTAAGT AGCAAAACCGCTGATGCTGCCGGCGATGGC/ TGAGGAACATCACGCCTGGCGGCGATGGC/ TGAGGAAAAAAGCCGGCGCTAA
HP0276	HP0276	HP0340 2

•		Г
	٠,	•
	•	١

2/066501		P	CT/EP01/15428
2356 DIKSAKALGIEVKNVSAYSTESVAOHTL ACALSLLGRINDYDRYCKSGEYSOSDL FTHISDIKMGLIKGSQWGVIGLGTIGKR VAKLAQAFGAKVVYYSPKDKKEEYERL SLKDLLATSDIISIHAPLNESTRDLIALKE LQSLKDGAILINVGRGGIVNEKDLAEI 2358 ASVLSALLLVGLGAAPKHSVSANDKRM QDNLVSVIEKQTNKKVRILEIKPLKSSQ DLKMVVIEDPDTKYNIPLVVSKDGNLIIG LSNIFFSNKSDDVQLVAETNQKVQALN ATQONSAKLMAIFNEIPADYAIELPSTN AANKDKILYIVSDPMCPHCQKELTKLR DHLKENTYRMVVVGWLGVNSAKKAAL IQEEMAKARARARGASVEDKISILEKIYS	2360 FFNEYÖLTKNANRKEPERLRSQIISILM KTPKGREILKEYLNEGCILLGE KTPKGREILKEYLNEGCILLGE 2362 LKRIRGÝTERTDVKGQVVIPVRÖEEVK VAVKELLEAGAKAIVICLLÓSHKNAESE	RIVRDIALKEIEKLGKNIPVFASVDYYPQ RKESHRMNTTILEAYAAEPSROTLSKV SNRFKEHGAKFDLRVMATHGGTISWK AKELARTIVSGPIGGVIGSKLLGETLGY DNIACSDIGGTSFDMALIVKSNFNIASD PDMARLVLSLPLVAMDSVGAGAGSFV RIDPHSRSVKLGPDSAGYRVGTCWKD SGLDTVSVTDCHIVLGYLNPDNFLGGLI KLDVDRAKKHIKEQIADPLGISVEDAAA GVIELLDLELKEYLRSNISAKGYSPSDF VCFSYGGAGPVHTYGYTEGLGFKDVV VPAWAAGFSAFGCACADFEYRYDKSV	DIAIPQYSSDKSKIDACKIIQDAWDELTL KVIEEFKINGFSQKDVILRPGYRMQYM GQLNDLEITSPVSKAASVADWEEIVKE YEKTYARVYSESACSPELGFSVTGVIM RGVVATQKPVIPVEKEHGATPPKEAKI GVŘKFYŘHKKWVDADVWQMEKLLPĠ NEVIGPANESDATŤFVIPKGFATRLDK HŘLFHLKEIK
2355 TGGATATAAAAAGCGCGAAAGCTTTAGGCATAGAAGTCAAAAACGTGAGCGCTTATTCTACAGAATCCGTAGCCCAG CACACTTTAGCGTGCCGCATTTGTTGGGGAGCATCATTACGATGATTACGAAAAGCGGGGAATACAG CACACTTTAGCGTGCGCGTTGTCTTTGTTGGGGAGCGTTATTACCAAAAGCGGGGAATACAG TCAAAGCAGCGTTATTACGCAATTACACAGTTTAAAAAGGGAGTCAATGCAAAGGGGGGAATAAAAAGAAGAAGATACAAAAAGAAGAAGTATGAAAAAGAAGCTCGCCAAAGCTTTCGGGGCAAAAGGTATTATCCCCTAAAAAAAA	d (0,0)	CGCTGAAAGCGAGCGGATCGTTAGAGATATAGCGTTAAAAGAATTGAAAAATTGGGTAAAAATTTCCTGTTATTCCTGTTATTCCCTCTATTCCCTCTATTCCCTCTATTCCCTCTATTCCTCTCTGTGCGCTGACCTTCTTTTCTTTTTTTT	
HP0340 HP0340	HP0340 HP0340		

4	٦
r	•
~	٦

2/066501			PCT/EP01/15428
2364 ANMVLDIKNALEGENDPSNKAGKTLDL IVGFKKEYPQDFDELFE:ILKELIQEYEQ NPDEIKQNLKEILK	2366 ENKITKEEYLKIAKECLEMIENKDRLIKE LELKMERLSNNLRFEE	2368 DKEKERAYAFSSFGMPIGSFNISVSHNR GISALIDAVLSALDLNQII EQDLDADILES LETPNNALEEEIJQVGIIGRVNGKSSLL NALTKKERSL VSSVAGITIDPIDETILIG DQKICFVDTAGIRHRGK LGIEKYALER TQKALEKSHIALLVLDVSAPFVELDEKI SSLADKHSLGIILVLNKWDIRYAPYEEIJ ATLKRKFRFLEYAPVITT-SCLKARHIDEI KHKIIEVYECFSKRIPTSLLNSVINQATQ KHPLPSDGGKLVKVYYATQFATKPPQI SLIMINRPKALHFSYKRYLINTLRKEFNF LGTPLILNAKDKKSAQQNI	2370 KNGKI
2363 I GCCAATATGGTTTTGGATATCAAAAACGCTCTTGAGGGCGAAAACGATCCATCAAGCAAG	2365 GCGAGAATAAAATCACCAAAGAAGAATTAAAAAATCGCTAAAGAATGTTTAGAAATGATTGAAAATAAAGACAGGC TCATCAAGGAGCTTGAATTAAAAATGGAGCGCCTTTCTAATAACTTGCGTTTTGAAGAAGC	2367 ACGACAAAGAAAAGGCGAGCTTATGCGTTTTCTTCTTTTGGCGAGGGTTTTAATATTTCCGTTTCCGCACA ATAGAGGCATTAGCAGAACCCTAATTGATGGGGTTTTCTCTTTTTGGATTTAAACCAAATCATAGAGCAAGATTTGGAT ATAGAGGCATTAGCACTTAATTGATGAGGGTTTTGAGAGAGA	2369 AAAAATGGAAAAATTTGATGCGATTGAGTAACGCTGACTTAGAACGATTAAAAAAGCCTGGATGGCGATTGGCTTTTTTTT
H-0340	HP0340	HP0340	HP0340

HP0340	2371	2371 TGATGAGGTGATGCCCAATCCTTACCAACCCAGAAAGGTTTTTAGCGAAGATTCTTTAGAAGATTTAGCGCAATCCAT TAAAGAACATGGTTTGTTGCAACCGGTTTTAGTGGTGAGGAGCGGGGGGTTACCATTTGATCGCCGGTGAAAGGC GCTTAAGAGCGAGCAAATTAGCTAAAATGCCTACGATTAAGGCGATTGTTGTGGATATTGAGCAAGAAAAAATGCGT GAAGTCGCT	2372	2372 DEVMPNPYQPRKVFSEDSLEELAQSIK EHGLLQPVLVVSENGRYHLIAGERRLR ASKLAKMPTIKAIVVDIEQEKMREVA
HP0340	2373	CGTTAAGATGAAAGACTTAGAGCGCGTGTTATTATGAAGCTTATATCGTTAAAGAACCAGGCGGAAGATGGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	2374	2374 VKMKDLERVLYYEAYIVKEPGEAAYDW EGTKLVMKYDILNEEQYGNISRRYEDR EGYAQMGGEAIKDLLEEIDLITILQSLK EEVKDTNSDAKKKKLIKRLKYVESFLNS GNRPEWMMLTVLPVLPPULPLVALD GGKFAVSDVNELYRRVINRNGRLKRL MELGAPEIIVRNEKRMLQEAVDVLFDN GRSTNAVKGANKRPLKSLSEIIKGKOG RFRQNLLGKRVDFSGRSVIVVGPNLK MDECGLPKNMALELFKPHLLSKLEERG YATTLKQAKRMIEQKSNEVW
HP0340	2375	2375 ATTGGGCTGAAGCAGAGATAAACTATCAAAATTTTAATAACGCTAAATACCTCATTGATAAGGTGGTCCAATCCAACC CTGATTATATTTCTACGCATAGCGAATCAGCCCTAGACTTGCTCAAGTTATTGAAAAAAACCAGATGAATGCAAGCG CTGATTGAGATCGCTCACTTGCTCAATCAAGACTTGCTCAAGAGCTAAAGAGCAAGCGCTTTAGGA CGATTGAGATCGCTCACTTGATCAATCAAGATGTTACAAGCTAAAGAGCAAGCGCTTTAGGA GCGTTGTATGCAAGGATCAAGGACTTTAAAAAACGCCTTTACAATCTGCAATATTTGCAGGACCATGCGGAACT GGATAAAGCTTCTGTCGTTAGGGCGC	2376	2376 WAEAEINYQNFNNAKYLIDKVVQSNPD YISTHSESALDLLKLKKNQMNASAIEIA HLLNQDDDLKAKEQALYDLGALYARI KDFKNAHLYNLQYLQDHAELDKASVV RA
НР0340	2377	TGTGAGGATAGAGCAAATCCGCTTGCAACTACGAAAGCTTAAATCCCAACGCAAGGAATTGGGTATCGCTTTTATTGA CTATTTGCAGGCAAATCCGCTTGCAACTACGAAAGCCTTAAATCCCAACGCAAATCGCTGAAATTTCAAGGGGGCTTA AAACTTTGCAGGCTCATGTAAAGCCACTAAAGGGCGCCTGAGCAATTCCAAGGGGGCTTA AAACTTTAGCCAGAGAATTCAAAGACGCGGGGGGGATTGAACAGACGCTGATATTGTTTTTTATATAGA AAACGGCCCATTCTTTCGAATTCAAAGACAGCGGGGGGGATTGAACAGAAAGGTGAAAATTGAAGAGGCGCA AGAGTTGTACTACAAATGAGGCGTACCACAAAATAGACAAAATGACAAAAGCATGAAAAGGTAAAAATGAGGCGCATGAAAAGTTAATGAAGAGGCGCA AGAGTTGTAATCAAAAGTTAATGAAGAAAGGCGTTTAATCGCACCTTTCACGCGCCTATGAAGACATG CCCTAAAAACGCAATTGAAGAAAGGCGTATAATGGATTATGATATGTTAAGTTCACGCGCTATGAAAACTT TCAGGGGGCGTTTCAAAAACTTTAAAGAAAACTTTAAAAACCTTTAATTTTAAGCCTTTTAATTGCCTTTTAATGCCTTTTAATGCCTTTTAATTTTTTTT	2378	2378 VREGIRLGLRKLKSGHKELGIAFIĎYLG LMSGSKATKERHEGIAEISRELKTLARE LEIPIIALVQLNRSLENRDDKRPILSDIKD SGGIEQDADIVLFLYRGYIYQMRAEDN KIDKLKKEGKIEFAGELYLKVNEERRIH KQNGSIEFAEIVAKNRINGATGTVYTRF NAPFTRYEDMPIDSHLEEGGETKVDYD IVTT
HP0950	2379	2379 AGAGACTATTGGCGAGGACATTAGAAGCATTAAAGCATTACAGAAAATGTCCGTGGGTATGGACACCCTAAAG AGTTCTTTTGGACGCAATGATAAAAAAACAGGAAAATGCGATTAAAAGCATGAAGCAGCAAAAATGTGCGGTAAGC AGTTCTTTTTGGACGCAATGATAAAAAACAGGAAAATGCGATTAAAAGCTATAAAGCTATGCGACAAGGCAAAAAGTG GATGACTTCAAACAAGGCAAAGCATTAAACATTAAAAACTATTACCGACAAGGCAAAAAGTG AGTAGGACATTGATTGCTAAAGTGCTTGCTAAGCCATAGACCATAGTTATCCGTCATTTCCCCGACAGAGCAGAGAGAAATGTTTAGCGACACAACTTGGCAACATGACCATAGACTAGACAAAATCAAAAATCAAAAATCATTAAAAATTTTAAGCGACCAAGTTGATTTTGATTAAAAATGTTTTAAGCGACCAAGTGTTTTGATTAGTCATTTGATTTTGATTTGATTTTGATTTGATTTTGATTTGATTTTGATTTGATTTTGATTTTGATTTTGATTTTGATTTTGATTTTGATTTTGATTTTGATTTTGATTTTGATTTTGATTTTGATTTTGATTTTGATTTTGATTTTGATTTTGATTTTTT	2380 380 380 380 580 580 580 580 580 580 580 580 580 5	2380 ETIGEDIRSNIKALQKMSRGYGHPKEFF LDAMIKKGENAIKRIEARKCAVSDDFKQ GMKNINKVINLVKAMRQGKKVSRTLIA KVLANTIDTDAGYCFISPTDLATQLGNI SPRLSKSIVTAIEQAEGVRLNYALIDKIT YNSLHNILSFIFDIDNPLSDQVFERLVIE VPREALKNYKLPQIKNVLTSQIFDGAYH FKS

/066501		PCT/EP01	1/15428	
2382 YMRTDSLNIAKEALEEARNKILKDYGK DYLPPKAKYYSSKNKNAQEAHEARRT SIILEPNALKDYLKPEELRLYTLIYKRFL ASQMQDALFESQSVVYACEKGEFKAS GRKLLFDGYYKILGNDÜKDKLLPNLKE NDPIKLEKLESNAHVTEPPARYSEASLI KVLESLGIGRPSTYAPTISLLQNDÜK VEKKQISALESAFKVIEILEKHFEEIVDS KFSASLEELDNIAQNIKADYQQVLKDF YYPFMDKIEAGKKNISIQKYHEKTGQS CPKCGGELVKKNSRYGEFIACNNYPK CKYVKQTESANDEADCIELCEKCGGEM VQKFSRNGAFLACNNYPECKNTKSLK NTPNAKETIEGVKCPECGGDIALKRSK KGSFYGCNNYPKCNFLSNHKPINKRC EKCHYLMSERIYRKKKAHECIKCKERV	2384 MHFLLHNEGKEUYYEREKWIKEVWUE KYGVFREGKRLEEALKELOELYARSKN ICYKNIKYLHNNPELEDAYRTKKMLKLA LCITGGALLRTESRGAHTRIDYPKRDD EKWLNRTLASWPSAECIDMPTIEYEEL DVMKKMEISPDFRGYGKKGNFIPHPKKE ERDAEILKTILELEKLGKDRIEVQHALM PFELQEKYKARNMRLEDEEVRARGEH LYSFNVHELLDQHINANLKGEHHE	2366 STGVREPDKCTKSFKK;SALMSYDLALG YLVSKNKQYGLKAIEILNAWAKELQSV DTYQSEDNINFYMPYMINMAYWFVKKA FPSPEYEDFIKRMRQY;SQSALNTNHG AWGILFDVSSALALDDNALLHNSANRW QEWVFKAIDENGVIASAITRSDTSDYH GGPTKGIKGIAYTNFAL!ALTISGELLFE NGYDLWGSGAGKRLSVAYNKVATWIL NPETFPYFQPNLIGVHNINAYFIILA	SABB ELGSFIEKKIKAYONYINDLNIGSIDGIIE GHFHLKSGAKIPLNTPIYCPLPSFYYEQ SLFKVSSSVLEPSONKDA	2390 FALKRIKILKAGMLELQIK
				23
2381 CTTACATGAGGACCGATAGCTTGAATATCGCTAAAGAGGCTTTAGAAGAGGGAGG	2383 TATGCATTITITATTGCATAATGAAGGCAAAGAAGATGTGTATGAAATTAGAGAGCGCATGAAAGGAGTCATGGATGA AAAAGTGGGCGTTTTTAGAGAAGGCAAAAGGCTAGAAGAGCCTTAAAGAATTGCAAGAGTTTTTGCACGCTCCA AAAAGTGGGCGTTTTTGCGTGAAAACCAAGAATGCCTGAATTAGAAGAGTTACCGCACCAAAAATGCTCACAAAATGCTCACACAAAATGCTCACAAAATGCTCACACAAAATGCTCACACAAAATGCTCACACAAAATGCCACACAAGAGATTGCACGCTTTAGAGATTGCAAGAATTGCAAGACTTTTAGAGCTTTTAGAGCTTGGCAAAAAGGCTGCACAAAAAGGCTCAAAAAGAATTTGAAAAATGCAAAAATGCAAAAATTTTGAAAAATTTTGAAAAATTTGAAAAAGGCTAGGAAAATGCAAAAAGAAATTTGAAAAAAGAAAAGAAAAGAAAAGAAAAGAAAGAAAAGAAAA	2385 CTTCTACCGGGGTTAGAGAGCCTGATAAATGCACAAAGAGTTTAAAAATCCGCTCTCATGTCCTATGACTTAGCGC TAGGTTATTGGTGAGTAAGAATAAGCAATACGGCTTAAAGGCTATAGAAATTTTAAACGCTTGGGCTTAAGAGGCTTC AAAGCGTGGGATACTTATCAGAGCGAGGATAATATCAATTTTACATGCCTTATTGGTTTGTTGTTGTTGAAAGAGCTTCAAAAGGCTTAATGGTTTGTCAAAAGGCGTTTGTTAAAGAGATAAGAAAAGAGAAAAGAAAAAGAAAAAA	2387/AGAGTTGCAATCTTITATTGAAAAGCGCCTAAAAGCCTATCAAAACTATTAAAGATCTTAACATTGGTAGCATTGACATTGGTAGCATTGACATTGGTAGCATTGACATTGGTAGCATTGACATTGACATTGACATTGACATTGACATTGACATTGACATTGACATTGACATTGACATTGACAGACA	2389 GTTTGCTTTAAAGCGTTTGAAAATCTTAAAAGCTCAAATGTTAGAATTGCAAAAA
HP0950	HP0950	HP0950	HP0950	HP0950

378

2/066501		PC1/EP01/15428
2392 DYDEPLYLISYVAKILGVHPOTLRQYEK EGLIEPSRTDGKMRLYSQRDMDKIKTIL RLTRDMGVNIAGVDIILRLKEKLDELDN LNKELQDALHKHSKNTKTPTKNLNTPT NFYELILFKK	2394 PKPIVIKEDDRPKDFSSFQLTLASPEKI HSWSYGEVKKPETINYRTLKPERDGLF CMKIFGPTKDYECLCGKYKKPRFKDIG TCEKCGVAITHSKVRRFRMGHIELATP VAHIWYNNSLPSRIGTLLGVKMKDLER VLYYEAYIVKEPGEAAYDNEGTKLVMK YDILNECQYQNISRRYEDRGFVAQMG GEAIKDLLEEIDLITLLQSLKEEVKDTNS DAKKKKLIKRLKVVESFLNSGNRPEWM MLTVLPVLPPDLRPLVALDGGKFAVSD VNELYRRVINRNQRLKRLMELGAPEIIV RNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK ANNEKRMLGAVDOLLGK	2396 IISKTDNIEIGDLKLINGGNGEHDONFLV KLIGETANTYLFASEKEKAIKNHÖAKIA RLÜKÜLEELTÖHVOOSNIN DKILENG GLFVSGHDYKYTKDDNPTYVKRMLDN LDSYKYESDDVLDVPYEKLLEISIAIEDT KNPKDYPYINLKELKKLIDSIIDDHGYMA DGFLNEYSNRVSKKGLOILAKLKSMWP SVGKFYFASLKEAIPRHAKEVTDKMISS EEKSIKANQVKLTEAKÖDIDKMEKIIKÜL ESKKNTLSVYLKFGESFTAHYKCÖNLI EVGVKTDKGSWTFNFNR
	2393 ACCTAAACCATTGTCATTAAAGAGGGCCTAAAGACTTTTAGGCTCTTTCCAGCTCAGACGCTAGCCCTGA AAAAATCCATTCTTGGAGATTATGGGGAAGTTAAAAAGGACAGAATTATCGCACCCTAAAAACCTGAACGAGA GGGCTTGTTTTGCATGAAAATTCTTTGGGGAAGTTATGAATGCAATTATCGCACCCTAAAAAGCCTCGCTT CAAAGACATTGGCACATGCGAAAAATGCGGCGTTGGTAATTCCTTGCCGGCAATTCAGGCGTTTTAGGCGTT ATTGAATTGGCCACTTGTGGAAAATGCGGCGTATGTTATTCCTTGCCTTACGCCGTTTTAGGCGTTTAGGCGTT AAGATGAAGGCCTTAGGAGCGCGTGTTGTTATGAATGATGATTCCTTAAAGAACCAGGCGAAGCCGCTTTATGCAA TGAAGGCACTAAGGCGCGTGTTGTTATGAAGGCTTATATGCGTTAAAGAAATTGATTG	ACATAGAAATCCAAGACTTGAAGCTCAATCGTGGCAATTGTGAGCATGATCAAAATT AAACAGCCAATACATACCATGAAAAAAGAAAAAGCGATCAAAAAAGCGATCAAAAATT AAAAAAGCGATTACATACCACCAGCATGTGCAACAATAATCTTGATAAAT TTCCTTAGTTGCCATTATACAAAGCATAATATTGTTAA TTCCTTAGAAAATTTAGAACCTGTGCAACAATAATGTTGTTAA TTAGCTATAAAATTATGAACCTGAGACGTGCCAATATATGTTGTTAA TTAGCTATAAAATTGAATCAGCGTGCTAGAGAGCTATGGGAAAAATTAAT TGGTTATATGGCCGATGCGTACCCTTATATCAACCTTAAAGAGCTATCAAAAAACCCCAAAGAGCTATTTTCGCCTTTTGAAAAAAGGT AAATCCATGTGGCCTAGGGAAATTTTATTTCGCCTTTTGAAAAGGTCAAAACTC TACTGACAAAATGGAAAAATCTATCAAGGCAATCAAGAAAACCTTATCAGTG TTCACAAAATGGAAAAATCTTAGAAAGGTTGGAAAAAA AACAGATAAAAATGGCCAAAATCTCATAGAAGTTGGAAAAAACCTTATAGG AACAGATAAAATCAACAAATCTTTGGAGGCAAAAAACCTTATAGGAACAAAATGGAAAAATCCTTTTGGAGTGCAAAAAACCTTATAGGAGCGTTATAGGAGCGTTATAGGAGCGTTATAGGAGCGTTATAGGAGCGTTATAGGAGCGTTATCAGGACAAAAATCTTTTGGAGTGCAAAAAATCCTTATAGGAGCGTTATAGGAGCGTTATCAGGACAAAAATCCTTTTGGAGTGCAAAAAATCCTTATAGGAGCGTTATAGGAGCGTTATCTTTTGGAGTGCAAAAATGGACACAAAAATCCTTTTTGGAGTGCAAAAAATCCTTATAGGAGCGTTATAGGAGCGTTATAGGAGCGTTATAGGAGCGTTATCTTTTGGAGTGCAAAAATGGACACAAAAATCCTTTTGGAGTGCAAAAATGGACACGAGAAAAATGGACAAAAATCCTTTTGGAGTGCAAAAAATCCTTATAGGAGCAAAAATGGACAAAAATCTTTTGGAGTGCAAAAAATGGACAAAAAATCTTTTTGGAGTGCAAAAATGGACAAAAAATCTTTTTTTT
HP0950	MP0950	HP0950

2/066501		PCT/EP01/15428
2398 SKLDLKDIYAFLKNLDKENFDSRENGR ERIESLLESVNRHKIPLNEGEL DAFDLAI KANSSYYKLSYNLLPLLLSLLSKKTP 2400 EFRSFIDKHYNHSFEPLEVLGYIYALLY SPNYRKRYEDFLKNDYPKILFINNKDL FRALSLGIELIGLHVLNGESLNYSFGK LKDATIGESCYKEEHNPIIKKPSHNEPD QRLYINHSAYFRGVSGEIYDYRIGGYG VLDKYLKSHKNEPCDFDHVTNIIKVIRR TIEIQKTLGFLTSDLPHLKGNDSKALMO EILQNPPPPPPI	2402 LPPKAKVYSSKNKNAGEAHEAIRPTSII LEPNALKDYLKPEELRLYTLIYKRFLASGR QMQDALFESQSVVVACEKGEFKASGR KLLFDGYYKILGNDDKDKLLPNLKEND PIKLEKLESNAHVTEPPARYSEASLIKV LESLGIGRPSTYAPTISLLQNRIYYKVE KKQISALESAFKVIEILEKHFEEIVDSKF SASLEEELDNIAQNKADYQQVI KDFYY PFMDKIEAGKKNIISQKVHEKTISQSCP KCGGELVKKNSRYGEFIACNNYPKCK YVKQTESANDEADQELCEKCGGEMV QKFSRNGAFLACNNYPECKNTKSLKN TPNAKETIEGVKCPECGGDIALKRSKK GSFYGCNNYPKCNFLSNHKPINKRCE KCHYLMASERIYRKKKAHECIKCKERVF LEEDNG	2404 TILRLYKHSLGGESKOFIEDSIYIRYDK EKERLKFLTAQNYNSIFENTVLNHLEFE DNIKKSELNKKFEENTYLRNAY/FKELL NESVENGSISDIDDFVKWFYEHIVLTRII CFEQDSAMQIFQVLNDRGQPL;SPIDILK SSLMQEIKQDSEKRKDFITTWDKLVEA CKSVEGVDIDLEDFFNMYLEYADPSTS KKRADKGLKKVFKDSKKDACGI=YEIS EFMKAYTALLKKQDRYVYLLRYLPSRY WASILTTALYVKYPDFDALKKLLVSYYY QTWIAGGTITRIKQDTSINIIKNVK;SNKSV ETIKELLINSIDSYNTFDQYLYNLWDSS SVYHSKWVRPVLALAN
24 23	240	240
2397 TATCCAAGCTGGATTTGAAAGACATTTATGCGTTTTTAAAAAATTTTAGAAAAATTTTGATTGCAGAGAAATTCAGGAAAATTCAGGAAAATTCAGGAAAATTCAAAGGAATTTTGATTTGCAGGAAAAGGAATTGCAAGGATTGCAAGGATTGCAAGGCTTTTATAGGGATTGCAAGGCTTTTATAGGGATTGCAAGGCTTTTATAGGGATTGAAGCCTTTTATAGGGATTTAAGGGGTTTTAAGGGCTTTTATGTTTTAGGGGTTTTAGGGGTTTTAGGGGTTTTAGGGGTTTTAGGGGTTTTAGGGGTTTTAGGGGTTTTAGGGGTTTTAGGGGTTTTAGGGGTTTTAGGGGTTTTAGGGGTTTTAGGGGTTTTAGGGGTTTTAGGGGTTTTAAAAGAAG	2401 ATTTACCCCCTAAAGCCAAAGTCTATTCCAGCAAGAATAAAAACGCCCAAGAAGAGCCCATGAAGCCCTAATTTACAAACTCTTAATTTACAAACTCTTAATTTACAAACTCTTAATTTACAAACTCTTAATTTACAAACTCTTAATTTACAAACTCTTAATTTACAAACTCTTAATTTACAAACTCTTAATTTACAAACTCTTAATTTACAAACTCTTAATTTACAAAACTCTTAATTTACAAAACTCCCCAAAGCCTTGCTTG	2403 GCACGATITITAAGGCTITATAAACATAGTCTTGGGCAAGAATCTAAAGATTITATTGAAGATAGTATITATGACAGATA CGATAAAGAAAAAGAGCGTCTGAAATTCTTAACCGCTCAAAATTTACAATAGTATTTTTGAAAACACGGTGTTAAACCAT TTGGAGTTTGAAGCGTCTGAAATTCTTAACCGCTCAATAGTATTTTGAAAAACACTTATTTGCGTAACCGTTATT TTGAAGGAGCTATTGAATGGTTGGAAAATGGTTCAATAAGCGATATTGATGATTTTGCAAGTGGTTTTATG AACACATTGTTTTGAACCAGGATCATTTGTTTTGAAAAGCGGATGCAAACCTTTTAGAAGCGTTAAGCCAATGTTTAGAAGCGTTAAGCCCTTAAGCCCTTAAGCCCTTATTTGAAAAAAGAGAGAG
HP1247 HP1247	HP0951	HP0951

	-		
C S S S S S S S S S S S S S S S S S S S	2405	·	2406 SAMKNETIGSGDLKKVCEKIKSALPFGII SAFKPFKDAFYRDFNHNEGKLLIGAAK SGCIGSSADKLAQLKTRLLYWQDKSVK VDWDKPILIKDFFKGNNYLYRRFCFLL GKHFMDRFLKNNAKASVKDFMSSKEF VAKYRYTPKONTERAKKLGSYLENKR DFIGFVOALNSLKDNPGDPFLPNETS FLVFANEPTIVFNLRDYLLVLAGIFNQ AICYCESKCP
HP1489			2408 LYAFESGNEEIKKIASSMLEEKKIKNNO LAFALSLFNGVLEKINEIDALIEPHLKDW DFKRLGSMEKAILRLGAYEIGFTPTÖN PIIINECIELGKLYAEPNTPKFLNAILDSL SKKLTOKPLN
HP1489			2410 IPKÖSVFVÄKEVPPSASVMLKLKFDMK LSPTQILGIKNLIAAAVPKLTIENVKIVNE NGESIGEGDILENSKELALEQLHYKÖN FENILENKIVNILAPIVGGKNKVVARVNA FENSKESTETFDPNNVVRSEGNL EEKKEGASKKQVGGVPGVVSNIGPVQ GLKDNKEPEKYEKSQNTTNYEVGKTIS EIKGEFGTLVRLNAAVVVÖGKYKIALKD GVNTLEYEPLSDESLÖKINALVKÖAIGY NÖNRGDDVAVSNFEFNPMAPVIDNAT LSEKIMHKTQKILGSFTPLIKYILVFIVLFI FYKKVIVPFSERMLEVVPÖEDKEVKSM FEEMDEEEDELINKLGDLRKKVEDÖLG LAASFSEEEVRYEIILEKIRGTLKERPDE
HP1489	2411 ANTGATCGTGGAAAAACAAAAAATTAACACCCCAAACAGAAATCCAAAACATGCAAATCGCGCTCCAAAAAATTAACACAAACACAAAACACAAAAATTAAAAACACAAAAACACAAAAAA		2412 MIVEKOKINTÖTEIÖNMÖJALÖKNNEJIK LKNNÖÖNALLEALKNSFEPSVTIKTÖM EMISÖALGSSSDNAQYIAYNTIGIKAFE ETILKGFETWLKVAMÖKATLIDYNSLTG ÖALFÖSAYAPALSFFSSMGAPFGIIET FTLAPTKOPYLDGLKISACLMEOVIQNY RMIVALIONKI.SDADFÖNIAYLNGINGEI KTLKGSVDLNALIEVAILNAFIN LEKKADLWEEQLKLERETTARNIASSK VIVK

066501				
2414 NGVEIVGLEHLDKVIYLDQAPIGKTPRS NPATYTGVMDEIRILFAEGKEAKILGYS ASRFSFNVKGGRCEKCOGDGDIKIEM HELPDVLVQCDSCKGAKYNPQTLEIKV KGKSIADVLNMSVEEAYEFFAKFPKIAV KLKTLMDVGLGYTLGCNATTLSGGEA QRIKLAKELSKKDTGKTLYILDEPTTGL HFEDVNHLLQVLHSLVALGNSMLVIEH NLDIIKNADYIIDMGPDGGDKGGKVIAS GTPLEVAQNCEKTQSYTGKFLALELK	2416 AGFVKVTILEPMSGESI.DSFTMDLSEL. DIQEKFLKTTHSSHSG:LVSTMVKGTD NSNDAKSALNKIFANINQEIDKKLTQK NLESYQKDAKELKGKRNR	2418 GDGAMAEPLEILFKAAU ILKUAYFEN REVIVMGGASIEKIDSVATISNLSSGIQA SALALALYFKGAKVTLIVSNFPTPLPKEI TSVLVSDTASYENALNISAANNLQKHAL KPLLFNLGAAISDYVPKTISFNYKLKKSEI GETLINIECVONKDILLVSINPNQFYKIGF KAEDNQONAJKNAQNLLKPFKDNGKD CSVVALNLIKDSRPFGSILENELWLFSH HKTQKIPSMNKLEASFKILDFIKDNAL	2420 RLGIQKEIFYISVNEENI:KALLNCYPNA KNIAGFFHLETDYVGLGIDRQMACLAV NNGVVVDAGSATTDLIIKEGKHLGGCIL PGLAQYIHAYKKSAKILEQPFKALDSLE VLPKSTRDAVNYGMVI SVIACIQHLAK NQKIYLCGGDAKYLSAI-LPHSVCKERL VFDGMEIALKKAGILECK	2422 SEQIQAKKNMELLVNK FYKETLSYLKE YKSLLSSVELAKENLKL QEQAFLQGLS TNAQVIDARNTLSSIVVIEQKSVAYKYIV SLANLMALSDHIDLFYEFVY
2413 GAATGGGGTGGAGATTGTAGGGTTGGAGCATTTGGATAAAGTGATTTATTT	2415 AGCCGGGTTTGTCAAGGTTACCATACTAGAGCCTATGAGTGGGGGAATCTTTGGATTCTTTTACGATGGATTTGAGCCGGGCGGG	2417 PAGGCGATGGGGCGATGGCCTTTAGAAATCCTTTTAAAGCGCGCTCAAAGGCGCTCTAAAAGACGCTTTAGTTTTTAAAGCGCTCCTAAAAGACGCTTTTTTTCGAAAGACGCTTTTTCGAAAAGATCTTTTCGAAAGATCTTTTCGAAAGATCTTTTCTTTTCGAAAGATCTTTTCGAAACGTTTCGAAACGTTTTCGAAACGTTTTTTTT	2419 GCGTTTGGGTATTCAAAAGGGAAATTTTTACATTAGCGTGAATGAA	2421 TAGGGAACCAGGCTAAAAAAAACATGGAATTATTAGTGAATAAGACTTATAAAGAGAGACGCTTTCTTATTTGAAA Z421 TAGCGAACAACACTTGCTTTCTAGCGTGGAATTAGCCCAAGGAAAACTTCCAAGAGCGCTTTTTACAAGGC TTAAGCAAAAGCTTGCTTTGATGATGCGAGGAACACGCTTTCTTCTATCGTCGTGGAGCAAAAAGCGTGGCTTA TTAAGCACGAACGCTCAAGTCATTGATGAGGGATTTAAGCGTTAAGGGGA
HP1489	HP1489	HP1489	HP1489	HP1489

c	١
œ	
r	

02/066501	~				1	PCT/EP01/15428
	2424 VEIIRDIADQTNLLALNAAIEAARAGEHG RGFAVVADEVRKLAERTQKSLSEIEANI NILVQSISDTSESIKNQVKEVEEINASIE AI DEVTECNI KI	2426 IGALLVGVGEFYYAIPLSSVLETVRISQ DEIYVGKSVLRLRDEVLSLVRLSDIF KVDAILESNSDVYVVIIGLADGKIGVVD YLIGGEEVVIKSLGYYLKNTRGIAGATV RGDGKITLIVDVGAMMDMAKSIKVNITT L	2428 VFKÖSKKDACGFIYEISEFMKAYTÄLLK KQDRYVYLLRYLPSRYWASILTTALYV KYPDFDALKKLLVSYYYQTWIAGGTITR IKQTSINIIKNVKSNKSVETIKEULNSIDS YNTFDQYLYNLWDSSSVYHSKWVRPV LALANYFMADEEKPHFIAMDAETQVEH ILPQTPKRGSQWNADFDKEKREEWVN NIANLTLLKRKKNAHALNGDF	2430 MRKGHFDGVVQIVLKMFHLVNPTRAY FGKKDAQQLLIIEHLVKDLLLDIEIAPCEI VRDDDNLALSSRNVYLNATQRKQALAI PKALEKIQQAIDKGEKACEKLKKLGLEI	2432 LLKKGRSYGVHLILATQTMRGTDINRSI MAQIANRIALSMDAEDSNSILGDDAAC ELVRPEGIFNNNGGHÖKHHTKMSIPKA PDDFKPFIKKIHRDFNORNLVPVEHKIY NGEKPLEMPNTLKANEMRLHLGKEAD YEQKDLMVGFENSESHLLVVSQDLSA RIALMKLFAÖNFK	2434 KISÍKNÁPYKLDNTPIEENCACYACKRY SKAYLHHLFRAKELTYARLASLHNLHF YLELVKNARNAILEKRFLSFKKEFLEKY NSRSH
	24	247	242	243	243	243
ААААТСАТGTCA	2423 TGTAGAAATCATTAGAGATATTGCTGATCAAACCAATCTTTTAGCCTTAAACGCCGCTATTGAAGCCGCAAGGGCCGCGCGCG	ATTCAAGCTTTACTCGTGGGCGTTCAAGAA AGCCAGGATGAAATTTACACCGTTGATGGC TTCTGATATTTTAAAGTAGATGCTATTTTG AAAATTGGCGTGATCGTGGATTATTTAATCC CTAGAGGCATTGCTGGTGCTACGGTGAGA(TATGGCAAAAAGCATCAAGGTCAATATCAC	2427 AGGTGTTCAAAGACAGCAAAAAAGACGCTTGCGGGTTCATGTGAGGTCGGGGGTTCATGAGAGGCCTATACCGCA TTGCTAAAAAAACAAGACCGATACGTCTATTTGTTGTCCCCTCTAGGTTTTGTTATTACCGCATTTTAACGCT TTGCTAAAAAAACAAGACCGATACGTCTATTTGAAAAAGCTTTTGTTATTACCAAACTTTGCAG GCCCTTTATGTCAAAAAAAAACCGGATTTTGACGCTTTGAAAAACGTTAAAAAACGAATAAGAGCGTTGAAACC GAGGCACGATCACGCGCATCAACCAGTATCAACATTATCAAAAACGTTAAAACTTATGGGATAGCTCTT ATCAAAGAGCTTATATTGAATAGCATCGACTCTTATAACACTTTGATCAATACCTCTATAACTTATGGGAAAAGGCCATT CTGTTTATCATAGCAAATGGGTGCGTCCTGTCTTAGCCCTAGCTAATTATTTCATGGCAGATGAAGAAACGCCATT TTATGGCTATGGATGCGAAACGGAGAAGGGGAATTTTTAAACGCCTTTTAAAGCGTAAAAAGAACGC GGATTTTGACAAAAAAAAAA	2429 CCATGCGTAAAGGGCATTTGATGGGGTTGTTCAGATCGTGTTAAAAATGTTTCATCTTGATTAATCCCACTAGAGCGT ATTTTGGCAAAAAGGACGCCCAACAGCTTTTAATCATTGAGCATTTAGTCAAAGATTTGCTTTTAGACATTGAAATAGC GCCATGCGAGATCGTGCGCGATGACGATAATTTGGCTTTAAGCTCTAGGAATGTTTTGAATGCCACACAAGAA AACAAGCCCTAGCCATTCCAAAAGCTTTAGAAAAATCCAGCAGGCCATAGATAAGGGCGAAAAAGCGTGCGAAAAAA	2431 CCCTACTTAAAAAGGGCCGTAGGGGTGCATTTAATTTTGGCCACTCAAACCATGCGCGGCACTGACATCAATAGTGATAGTGTGCGCGGCGCACTGACATCAATAGTGTGCCACCACCATAGTATTTTGGCTGAAAACACCATAGTATTTTGGCTGAAAACACAATAGTATTTTGGCTGAAAACACACAC	2433 CAAAATTICTATCAAAAACGCGCCTATAAATTGGATAATACCCCTATTGAAGAAATTGCGCATGTTATGCAAA CGCTATTCTAAAGCCTATTGCACCATTATTAGGGCTAAAGAACTCACTTACGCTCGTTTGGCCAGCTTGCACAT CGCTATTCTAAAGCCTATTTGCACCATTTATTAGGGCTAAAGAACTCACTTACGCTCGTTTGGCCCACTTTAAAAAAGAAT TTTGCATTTTTAGACAATACAACTCCCGCTCTCATTGATGGAAAAATACTAAAAAGCGTTTTTTACCATCAATAAA AGTTTCTTAAAAATACAACTCCCGCTCTCATTTTTGATTAAACAAAACCCTATCTTTGATAAAACTCAATAAA AGTTTCTTAAAAATATCGTTTTTAATTTTTGATTAAACAAAACCCTATCTTTGATAAAATTCGGGTGGGT
	HP0391	HP0391	HP1000	НР0031	HP0031	HP0031

WO 02/066501

383

66501				
RKKIASDYGFLMPOIRIRCNLOLPPTHY EIKLKGIVIGEGMVMPDKF:LAMNTGFV NKEIEGIPTKEPAFGMDALWIETKNKEE AIIQGYTI 2438 GGDFNLKDILLNSGARLHLVGNINRAYL	RDYRLALNENSKILFKTHIVPHFKKDTP FKDLQTLAKEHDLIDYYN.GDVDLSNR VALEEILALKPSLLSFSADKFFNSAQAG IIMGQKERVEALKNHPLY?VLRVGKTT TLLFCSLKAWINHQEDITHALNQTKD ALLQKALKLYALLRPLELNSIASSFSKI GNLFGRELESFCVKIOPKNTRALNSEK LYLKLFÖKGVIARISCEFVCFEVFSLNE KDFEKIALVLEEILNKA	2440 HLDLEIDKNAKENIQALLRIPDGAYLSLF TKFDKLNKNEGHRLFLMAPKPFLINTAH FNALSSKYPTLEIVRQTLI.KHLLTNPL FNALSSKYPTLEIVRGTLI.KHLLTNPL	YINYTIGE YINYTIGE YINYTIGE YINYTIGE YINYTIGE YINYTIGE YINYTIGE YINYTIGE YINYTIGE YINYTIGE YINYTIGE YINYTIGE YINYTIGE YINTYTIGE	
2435 ITTAGAACTGGCTTTAGGCTATCAACTCATCAGTCTTGCGGACATGAAACAAGGGGGGGG	2437 TGGGGGGGGATTTTAAACGTTAAAGATATTTAAAAA CTTATTTAAAGACTTTAAAGATTTAAAGATTTAAAAACGAAAATGTCTTTAAAAACCCACAACCCCCATTTAAAAA CTTATTTAAGGGATTACCGCTTGGCTTG	G 2439 CCATTTGGATTTAGAAATTGATAAAAACGCTAAAGAAACATTCAAGCCCTTTTTAAGGCCCGATCAAGGCCTACCTTTC ATACCGCCCATTTTAACGAAATTTGATAAAAACGGCAACACCGCCTTTTTTAAACGCCTCCTAAACCTTTTTAATCA ATACCGCCCATTTTAACGCTTTCTTCAAAATACCCAACCCTTGAAATCGTGCGCCAAACCCTTTTGAACAACCTTTGC ATACCGCCCATTATAAGCCGCAAAAACCATGCTTTTAAAACAAAGATTCCTTTTTTTT	2441 TGGCGTGAAAATCCCGGCTATCAAAGGTATTTGAGGGCCCAATGGGGGCTGATGTGGATTACAGGCGTTGATG 2441 TGGCGTGAAAATCCCGGCTATCAAAGGTTTTAAAGCTCTTTTTAAGGGCTTATAAAGAGGCTTTTTAACTTTTTTTT	GGCTATACTOCATEGGGATTGCAGGAAGATTTGCACGCAAAGCTCACATCAAGCGATCAAGGAGCGATCAAG Z443 CAATGTACGGGGATTGCAAGGAAGATTTACAAGAGCGTTAAGACCATTAGGGGCTTTAGGGGCTTTTGT CGCTATAAATTTAAAAAAGTGGTTTTACAAGAGGCTAGAGCGTTAAGGCGAATTAGGGGCTTTAGGGGCTTTTGT CGCTTACTTCAGGGCGCGAATTAGACGATGAAAATGCGAATTAGCTAAATTAAGGGCATCAACAGA CTGGTTACTTCAGGGCGCGAATTAGACGCTGCGGGCGCGGGATTTGGAGAATTTTTAAGAGATTTTAAGAGAATTGCGGGC AGAATTGGGCTTAACCACAATTTAGGGCGGGCGGGATTTCTTCCCTAAGATTTTTTTT
	,,		-	
HP0031	HP0031	HP0031	HP0705	HP0705

2/066501				PC1/.	EP01/154
2446 GFDYQIIACKDFKESELAKEVISYFKPN TKAILFPEFRAKKNDDLRSFFEEFLQLL GGLREFYQALENKOETIIIAPISALLHPL PKKELLESFKITLLEKYNLKDLKDKCKFY YGYEILDLVEVEGEASFRGDIVDIYAPN SKAYRLSFFDTECESIKEFDPITQMSLK EDLLEIEIPPTLFSLDESSYKDLKTKVEQ SPLNSFSKDLTSFGLWFLGEKAQDLLI VYKSIISPRALEEIQELASLNELDCERFK FLKVLENAQGYEDLEIHAHALEGFIALH SNHKITLLAPNKTILDNAI	2448 VYPYDIARHRAAWVRDKAKALEFPLKL LVEEIK	2450 YCIIFAHDLKQIQANYDLSKLKELLNNH FKQRLAFRCNGENLSAIKKDLPLLTNEL NALFVELSKDSHTEFRPFSL	2452 DKVLKGEKAFLITYEDKFFPSTKEELSM ILSSLFQWKEAWARGDFERYMRFYNP NFTRYDGMKFNAFKEYKKRVFAKNEK KNIAFSSINVIPYPNSQNKRLFYVVFDQ DYKAYQHNKLSYSSNSQKELYIEIENN QVSIIMEK	2454 CFLCDAKLERSVALAQGFILAHPSCLK AKSLNLEKIQAFFRTQSTIDLETEEVEE LWRTLNLGF	2456 LALKGERRLSGKSALDKRAYGPGÖHG ORRAKTSDYGLQLKEKOKAKMMYGIS EKOFRSIFVEANRLD
2445 GGCTTTGATTACCAAATACTCGCTTGTAAGGATTTTAAAGAATCCGAGCTCGCTAAGGAGTCGTAAGGAGTCTTAAGGCTATTTTAAGCTCAAAAAAAA	2447 GCGTCTATCCTTATGATATTGCCAGGCATAGGGCGGCATGGGTTAGGGAAAGCCAAAGCGTTAGAATTCCCTTTA AAATTATTGGTAGAAGAGATAAAATAATGGCTAAATTCAATCAA	2449 AGTATTGCATCATCTTTGCGCACGACCTCAAACAGATTCAAGCTAATTACGATCTTAGCAAGTTAAAAGAATTGTTAAAA CAACCACTTCAAACAACGCCTGGCCTTTAGGTGTAATGGTGAGCACTTTAGGCGCTATCAAAAAAGGATTTACCTCTATT AACAAACGAACTCAACGCGCTATTTGTAGAGCTTTCTAAAGGACTACTGAATTCAGACTTTCAGGCTTATAGGG TCAAAAAAAGGGGGGAGTAAAAAGGACTATAATCTTTTTTGAAGTGCTTTCAAAACCTTTTGCGTGGTGGTTT GCGTAACCAAGCGAGCGATTTTTTTTTT	2451 ATGACAAAGTGTTAAAAGGCGAAAAAGCGTTCCTCATCACCTATGAAGACAAGTTTTTCCCAAGGCCCAAAGAATTTTT TGAGCATGATTTTAAGCTCCCTTTTTCAATGGAAAGGAGCCTGGGCTAGGGGCGATTTTGAACGCTACATGCGTTTTT ATAACCCCAATTTCACTCGCTATGACGGCATGAAATTTAACGCTTTTAAAGAGTATAAAAAAAGGGTGTTTGCAAAAA ACGAAAAAAAAGAGTTTTTCCTCTATCAATGTGATCCCTTACCCCAACTCTCAGAACAACGCTTGTTTATGT GGTGTTTGACCAAGATTATAAAGCCTACCAGCATAACAAGCTCTCTTATAGCTCCAAATTCTCAAAAAGAACTGTATAAAGAACAAGCTTATATAAAGAAAAAAAA	2453 CTTĞTTİTİTATĞCGATGCAAATTAGAGCGTTCTĞTCĞÇİTİTAGCĞCAAĞĞĞTTTATTCTAĞCGCACCCCTCTTĞTT GAAAACTGTTĞT TGAAAAGCGTAAAATTTAĞAAAAAAAAAAAAA GAAAAGAATTTAĞAAAAAAAAAA	2455 ITTTAGCCTTAAAAGGTGAAAGGCGATTGAGCGGGAAGAGCGCGCTAGATAAAAGGGCTTATGGGCCAGGCCAGCAT GGGCAAAGACGCGCTAAGACTTCTGATTACGGGTTGCAATTGAAAGAAA
HP0705	HP0032	HP0274	HP0274	HP0274	HP0274

4	3
œ	э
~	٦

AWGÁTGÁGTTT GIGGTAGAAAAGTGGTGCATGAG AWGÁTGÁGTT TO GIGGTAGAAAAGTGGTGCG TIGTCAAACCTGATTTT TAGAAAAGTGGTGCG TIGTCAAACCTGATTTT TAGAAAAGTTT TAGAAAGCGAATTT TAGAGCATTT TAGAAAGCGAATTT TAGAGCAATTT TAGAGCAAACGAAACG	CT/E	KEEGKKKSYAILAEATARFAGNYAAEN		STATGCCATTTTAGCGGAAGCGACAGCCCGTTTTGCGGGTAATTATG
			1000	2467 ATTAAAAGCATGATTTTAGAGCAATTAGAAGAATTAGAAGGAGCCCAAAAAAAA
		ISRIQNLSQEDPFNTYDPFSW;JIFKEK TLSLKDEGAFNAMLKSLYYEKS;APELT YLLSQRNK		CCTTTTCGTGGCAATTTTAAGGAAAAACCTTGAGTTTGAAGAT CTGTATTATGAAAAAAGGCGCTCCTGAATTGACCTATCTTTTAAGCCAA
		AVVDDDFSKDRAIFWQYLVSKKKTL ERLSQSPALNLYSLYASRKLKTTPSYRI		AAGAAAAAACTTTAGAACGCCTTTCACAAAGCCCAGCTTTAA
		NAOTFILGINEILRKKPSKALKYFERSE		CAGCAACGCGAAACCTTTTTTATTCTAGGGATTAATGAAATCT TGAACGATCAGAAGCGGTTGTCAAAAGAGAATAATGAAAA
		SYEKKLOJFEKHIPIKELNRLLDENYPAF INRLIYQVILDPKLDHFKDAJ TKSNATHS		CCGCTTGATCTATCAGGTTATTTTAGATCCTAAATTGGATCAT
		LEILQSKHVSASLFKANAQVFSALFNHL		AAAAGCTCCAAATTTTTGAAAACCATTTAAAACATTAAAACAATTAAAACAAAC
	_	KIRDFDKIPIETLKPLQIKIKEAYF VLYEE		ATTEMACULTA AGUULTI ACAATTA AAAT CAAAGGUTTA
		ALUKAMQEKGSDNAEKNPDVKLPED YCKQTALESMLETTDTFQASCIAIALKS	246	GAACACACACATTCCAAGCAAGCTGCATCGCTATCGCT
		ANNEIT		CACAATCCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
	-	A ENIKSEIKKLENQLIETTTRLLTSYOIFLN NARDSANNQITANKTESLEALNQAKTS		AMICAAATCAGGGTAACAAACCGAAAGCTTTTAACGAGCTATC AATCAAATCA
		EFLMLLAYADGILDSKEKELFLINGVFL QIDNQDFNELYDNFERFN		TAACGAGCTTTATGACAATTTTGAACGCTTCAATG
		KKENFESLCQEIADHTHGEYTKRLKLV		AAGAAATCGCCGATCACACGCATGGGGAATACACCAAACGCC
	1 -	22 OTOTGAYMRLLKFLDIOKNALDNALRT		AAATTTTAGACATTCAAAAAAGGCTTTGGATAACGCCTTAAG ACAGCGAACAGCAAAATTTAGCCAAAGAGCTTCTCAATGAGCC
	_	UNASLKRLSFE		ATTGAGTTTTGAA
	T	50 NDEKIADALYLAKTFSMSAIGHESDFLI SDLVADLRASTPSNAMEILLPSSDEWI		GCCAAAACCTTCAACATGTCAGCTATTGGGCATGAGAGCGAT TCTACGCCTTCAAACGCGATGGAAATTTTACTCCCCAGCAGC GAAATTGCACCGCTCGTTTAAAACTTTACAAGAAATTAAAAAAAA
·				GATAAAATCCACGATAAAACCAAAAACGAAAGGGGCTT
	=	NKENIRACKENGIÓANVFSMLLKYPRK MGLFKRGKGGLKRND		3GGCTTATTAAAAGGGAAAAGGGGGGGCTTAAAACGAAACG
	S	FSYLKEVLVVMRTGGVSASGFKSLLI		AAAGAAGTGTTAGTGGTGATGCGCACCGGTGGGGTTAGCGC
		EIGEFNPKTLLYGWPAHPTLFVKKAN	· ·	HGCTTTATGGCGTAGTGCCAGCGCACCCCACGCTTTTGTC
	ш	58 SGDIIALLNSDDFYKDEFVVEKVVHEF		ATTTGGTGTTTGTGGTAAAAAGTGGTGGAAAAAGTGGTGCATGA ATCTGGTGTTTGTCAAACCTGATTGTTTAGAAAAAGTGGTGA

v	2
\circ	3
~	5

	2/066501		;	PCT/E
AMAGENGAMANTOMITOMITOMICANGGENAMORECTRAMOGENAMORECTRAMOGENAMORITOMICANGGENAMORECTRAMOGENAMOG	170 TSMRTNEGEVSATLNANTENIKSEIKKI ENGLIETTTRLLTSYGIFLNNARDSANN GITANKTESLEALNGAKTSANNEITANG TGALTNINEAKENANNGITENKTGAITN NEAKNQSLSKH	72 IDPPYNTONNEFIYADNFKRSSWLSMM ENRLELARKLLNDKGAMFVSIDDNEGA YLKVLMDEVFNGGGVITL	74 LMLHYAGELAKKRKEKGIKLNYYEAVA LISAHIMEEARAGKKTAAELMQEGRTL LKPÓDVMDGVASMIHEVGIEAMFDGT KLVTVHTPIEANGKLVPGELFLKNEDITI NEGKKAVSVKVKNVGDRPVQIGSHFH FFEVNRCLDFDREKTFGKRLDIASGTA VRFEPGEEKSVELIDIGGNRRIFGFNAL VDRQADNESKKIALHRAKERGFHGAK SDDNYVKTIKE	6 LEEGKDKSYKVVEEYPSSRTHIIVRĎI Ú GNERVLSNEEIGKLIKEEEAKIDNGTSK LVÓPNINGGSNEGSGFGLGSALGSAA GAILGSYIGNKLFNNPNYQQNAQRTYK SPQAYGRSQNSFSKSAPSASSMGGAS KGQSGFFGSSRPTSSPAVSSGTRGFN S
2473 C C C C C C C C C C C C C C C C C C C		24	247	247
HP1482 HP0073 HP0073	A469/HGGGCACCAACGAGGAAGTAAGTGCTTTTAAACGAGCTAACACGAAAACGTCAAAAGGGGAGATTAA AAAGCTAGAAAATCAATTGATAGAAACCACTACAAGGCTTTTAACGAGCTATCAAATTTTTAAACAAGGCGAAAGGGGA AAAGCTAACAATTCAATGAAACCACTACAAAGCCAAAGCCTTGAAGCGCTAAACCAAGCGCTAACAAGCAAG	2471 TATTGATCCGCCTTACAACACGCCAAAACAATGAATTTATTATGCGGATAATTTCAAGCGCTCCAGTTGGCTCTCTATGATGAAAACGCGTTCCAGTTGGCCTCTATGATGATGATAAAAGGTGCGATGTTTGAAAACGCTTGATGATGACAACGAAACGAAAAAAAA		· q q - q - q
	1484 284	HP1482	HP0073	

	Similar Control		
HP0073	7//25	Z417/CGACITITITICAAGITAGGGTICAAGGGGAAGIGAGTAATTIGACIATCCATAAGGTGAGGGCGCCATGCGTATTTTT	2478 TFLQVRVQGEVSNLTIHKVSGHAYFSL
	<u>, c</u>	COCI CANAGO ACEANTAGI COGI I A II PANI OCCI I CI I I I PANI OCCI I A II PANI OCCI I TANA I I COCI I I PANA I I CACI I PANA I I CACI I PANA I I CACI I PANA I I CACI I PANA I I CACI I PANA I PANI OCCI I PANA I PANI OCCI I PANA I PANI OCCI I PANI PANI OCCI I PANA I PANI OCCI I PANI PANI OCCI I PANI PANI OCCI I PANI PANI OCCI I PANI PANI PANI PANI PANI PANI PANI P	KUSUSVIKCVLFKGNANKLKFALKEGO
	<u> </u>	GAAGGGGGGGGGGAAG II II GGGGGGGTATAAAAAGAAAAAAAAAA	EVVVFGGISVYVPRGDYQINCFEIEPKD
		A REACCULATEGE I CALL MECH I I SEGULATION OF THE SECRET I SEGULATION	IGSL'I LALEQLKEKLR'I KGYFDEENKLP
-	<u>٠ </u>	GATEANGAAN AND TACCANACCECAT TICCTANACEA GECAGICATCACT TOTACANA TICAGCCCCTTEG	KPHFPKRVAVITSONSAAWADMKKIAS
	<u>ا ن</u>	GGGGACATGAAAAGATCGCTTCCAAACGATGGCCGATGTGGAATTAGTTTGTATCAACACCTTAATGCAAGGGGA	KRWPMCELVCINTLMGGEGCVQSVVE
	۱ <u>ت</u>	GGGC I CAAAGCG I GG I GGAAAGCA I CGTTTA I GCGGATAGT I TI CATGAAAAAAAAA GCTTTTGATGCGA	SIVYADSFHDTKNAFDAIVVARGGGSM
_	<u>- 1</u>	TIGTAGTGGCTAGGGGTGGGGGGAGCATGGAGGATTTGTATTCTTTCAATGATGAAAAATCGCTGATGCTCTGTAT	EDLYSFNDEKIADALYI.AKTFSMSAIGH
	<u>- '</u>	1166CCAAAACC11CASCA1GTCASCCA1TGGGCATGAGAGCGATTTATTGAGCGATTTAGG	ESDFLLSDLVADLRASTPSNAMEILLPS
	<u>. ن</u>		SDEWLORLDGFNVKL-IRSFKTLLHOK
	**	A BI BEAZATI TECACCECT CETT A BAZA CONTROL TO THE SECOND T	KAHLEHLVASLKRLSFIENKHHLNALKL
	<u>u 1</u>	AACGA I GAGATI I GAAAACGACCATI I AAACGCI I AAAACTAGAAAAATTAAAAATCGCCCTAGAAAATAAAAAC	EKLKIALENKTLEFLRFKKTLLEKISTQT
		CIAGAAIIIIIACGIIIAAAAAAACGCIIIIAGAAAAATCICIACICAAACATTAACAAGCCCTTTTTACAAACTA	LTSPFLQTKTERLN
HP1449	2479	2479 GAAGAAAAAAACCCTAATGGCATTCAAGCTAATTCCCCTACCCAAAAAGTGGGGGCTACTACCACCAATTCGTTCAAT	2480 EEKNPNGIOANSPTOKVGATTTNSFNK
	<u> </u>	AAAAACCCCCATTTAATGCGGATGTGGAGCTTAGATGATGTGTTTCAATCAA	NPHLMRMWSLDDVFNOSELOAWLORI
	<u> </u>	CATTTTAAAAGCCTATCCTAGTGCTTCGTTGTGTGTTCGCCCAAACTTGATGGGGTTTCGCTCAATCTTTTGTATCA	LKAYPSASFVCSPKLD 3VSLNLLYQHG
	₹	ACATGGCAAGCTAGTGAAGGCGACCACTAGGGGCAACGGCTTAGAGGAGAATTAGTTAG	KLVKATTRGNGLEGELVSANAKHIANIP
	₫.	ATCGCTAATATCCCCCACGCTATCGCTTATAATGGAGAAATAGAAATCAGGGGGGGG	HAIAYNGEIEIRGEVIISKKDFDALNQER
		TTTGACGCTTTGAATCAAGAGCGCTTAAACGCTAATGAACCCCTATTCGCTAACCCCCAGAAACGCCGCATCAGGGGG	LNANEPLFANPRNAASGSLRQLDSEIT
	<u>t-</u>	TTGAGGCAACTTGATAGCGAAATCACTAAAAAGCGTAAATTGCAATTCATTC	KKRKLQFIPWGVGKHSLNFLSFKECLD
_	≪_	AAATTITTAAGCTTTAAGGAGTGTTTGGATTTTATCGTCTCGTTAGGTTTTAGCGCCATTCAATACTTAAGCCTAAAC	FIVSLGFSAIQYLSLNKNHQEIEDNYHT
	<u> </u>	AAAAACCCACCAAGAAATAGAAGACAATTACCACACCCTAATTAGAGAAAGGGAGGG	LIREREGFFALLDGMVIVVNELNIQKEL
	<u>.</u>	CATGGTGATCGTTGTGAATGAATTAAATATTCAAAAGGAGCTAGGCTACACGCAAAAATCGCCTAAATTCGCTTGCGCT	GYTQKSPKFACAYKFPALEKHTKIVGVI
	<u>-</u>	TATAAATTCCCGGCTTTAGAAAAACACACCAAAATTGTAGGAGTCATTAACCAAGTGGGGGGGG	NQVGRSGAITPVALLEPVEIAGAMINRA
	<u>.</u>	CACCGGTCGCTCTTTAGAGCCTGTGGAAATTGCTGGAGCTATGATTAATAGAGCGACCTTACACAATTATTCTGAAA	TLHNYSEIEKKNIMLSD: ZVVVIRSGDVI
	<u>-</u>	TGAAAAAAAGAATATCATGCTCAGTGATAGGGTCGTTGTCATTAGAAGCGGCGATGTGATCCCTAAAATCATCAAGC	PKIIKPLESYRDGSQHKIERPKVCPICS
	<u>u</u> _	CTTTAGAATCTTATA	HELLCEEIFTYCQNLNC:PARLKESLIHF
			ASKDALNIOGLGDKVIEQLFEEKLIFNA
	117070	OTO ATTO ATTO ATTO ATTO ATTO ATTO ATTO	LDLYALKLEULMKLDKFKIK
HF1449	74017		2482 VIDGAUKIKV IIPGSNKE YSA I LVG I DS
	<u>، د</u>	CCATTO COMPANIENCE OF THE CONTROL OF	ESDLAVIRITKUNLPTIK FSDSNDISVGD
	<u>C</u>	ACACIONE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CO TOTAL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE C	CALANGINE GOVES COLONO COLON COLON C
	<u>- 4</u>	AAATTOGGGGGGGGTTTAATTGATGACGGTGGGGTTAGTGGGGATTAATACCGGTATTATTATCTCTAAAACTGGGG	SINGLENT CHARACTERIST SINGLES IN COLORS
	<u>. </u>	SCAACCACGGCATTGGCTTTGCCTTCTAAAGTTAAAGATACTGTAAACCCAACTCATCAAAACCGGTAAG	VKDTVTOLIKTGKIERGYLGVGLODI S
	<u> </u>	ATTGAAAGAGGTTACTTGGGCGTGGGCTTGCAAGATTTGAGTGGCGATTTGCAAAATTCTTATGACAAAGGAGG	GDLQNSYDNKEGAVVISVEKDSPAKKA
	<u>១</u>	GGCGGTAGTCATTAGCGTAGAAAAAGACTCTCCGGCTAAAAAAGCAGGGATTTFGGTGTGGGATTTGATCACCGAA	GILVWDLITEVNGKKVKNTNELRNLIGS
	<u> </u>	GTCAATGGGAAAAAGGTTAAAAACACGAATGAGTTAAGAATCTAATCGGCTCCATGCTACCCAATCAAAGAGTAAC	MLPNQRVTLKVIRDKKE:RAFTLTLAER
	<u>ပ</u>	CTTAAAAGTCATTAGAGACAAAAAGAACGCGCTTTCACCCTCACTCTAGCTGAAAGGAAAAACCCTAACAAAAAGA	KNPNKKETISAQNGAQSQLNGLQVED
	<u> </u>	AACCATTICTGCTCAAAACGGCGCGCAAGGCCCAATTGAACGGGCTTCAAGTAGAAGATTTAACTCAAGAAACCAAAA	LTOETKRSMRLSDDVQGVLVSQVNEN
	<u>o (</u>	GET ET TE GEGET TE GAGE GATE GET CAN GAGE GAA TE COOK AGE CON GAGE TO COOK AGE CON GAGE TO COOK AGE CON GAGE TO COOK AGE TO CO	SPAEQAGFROGNITKIEEVEVKSVADF
	<u>o</u> (GGATTTAGGCAAGGTAACATTATCACAAAATTGAAGAGGTTGAAGTTAAAAGCGTTGCGGATTTTAACCATGCTTTA	NHALEKYKGKPKRFLVI.DLNQGYRIILV
	9	GAAAAGIAIAAAGGCAAAACCC	X

	ı	K	
	٠	•	
•	,	•	•
•	۰	,	١

02/066501		PCT/EP01/15428
2484 EDL GSFFEDAFGFGARGSKROKSSIAP DYLQTLELSFKEAVFGCKKTIKVQYQS VCESCDGTGAKDKALETCKQCNGQG QVFMRQGFMSFAQTCGACQGKGKIVK TPCQACKGKTYILKDEEIDAIIPEGIDDO NRMVLKNKGNEYEKGKRGDLYLEAQV KEDEHFK 2486 YYEFFIFPKERELFESFLLDATHLALE ESSLENLKAFDDKETIGFISGSNWHYF ATHDPLKKDLKENLKEKPPHLKNFVILR SQKDLNNSLIPALEAFCLNLKQNLQSE FDFFYLSRNLASKDWLEAYKQAILPVQ CTKFYHPSWHQKPSHVYTNDCIMIDP ALAFGSGHESTSMCLELLSDIDLKRK NALDVGCGSGILSIALKKGGVSALVAC DTDSLAVEETLKNFSLNQIPLLVQDKVI	EFVRLCNHTLILSGILETHLNSVLQIYYN GFEVLEQRQRNEWVALKLLKKQPIN 2488 DKENAREYLFA	2490 IQGGAGTSTNMINMEVIANILEYMĞ HQKGEYQFCHPNDHVINRSQSTNDAY PSALKIAYERLSNLVAPMIKALRDAFAQ KAKEFAHVIKMGRTQLQDAVPMTLGQ EFETYAHVIKMGRTQLQDAVPMTLGQ EFETYAHVIKMGRTQLQDAVPMTLGQ EFETYAHVIKMGRTQLQDAVPMTLGQ ULGTYALMYDIEQVLDARINWVREL NLGGTAIGTGINSHPDYRSLIEKKIQEY TGRPPYMANINLEATQSTGAYVQVSG VLKRIAVKLSKVCNDLRLLSSGPRAGL NEINLPKMQPGSSIMPGKVNPVIPEVV NQVCFAVIGNDLSVALAAEGGQLQLINV FEPVIAYKLFHSFVILGRAIETTTTKCVE GITANEKICHDYVFNSIGIVTALNPHIGY EKSAMIAKEALKSDRSIYDIALEKKILTK EQLDDIFKFENMLSPHAFKKHKD
2483	2487	2489
HP1449 HP1202	HP1322	HP1322

Ć	-	۲	١
ė	•	•	٠
٠	•	٠	•

2/066501			
2492 DVWQAAKSQATLAKE IYKRVQDLYDN GVASLQKRDEAYAAYE:STKYNESAAY QKYKMALGGASSESKI AAKAKESAALG QVNEVESYLKDVKATA PIDGEVSNVLL SGGELSPKGFPVV 2494 LELALGYQLISLADMK(3GGDLLERIRGI RKKIASDYGFLMPQIRIRDNLQLPPTHY EIKLKGIVIGEGMVMPCIKFLAMNTGFV NKEIEGIPTKEPAFGMI)ALWIETKNKE	2496 LTREGVYDLSFEPILALNANASKPHALP SAKDFLKAEHSILLDMGIKYERYCSDRT RTAFFDPKDFVFKRECSFKDKERGKIY DIVKEAQEKAISGIRAGMTGKEADSLA RGVISDYGYGOYFTHS	2498 EEVLEYIGSLSVLELSELVKMFEKKFGV SATPTVVAGAAVAGGAAESEEKTEF NVILADSGAEKKVIKVVREITGLGLKEA KDATEKTPHVLKEGVNKEEAETIKKKL EEVG	2500 VFKDGKPFSLEFKDGWINNLVTITFSQA EINPTIANEIFVFKPKDENIDIVRQ
2491 GACGTTTGGCAAGCCAAATCCCAAGCCACTTTAGCCAAGGAGTTATAAGCGCGTTCAAGATTTGTATGATAA TGGCGTGCGAGGCCAAAAGCGCGATGAAGCCCTATGCAAAGCCCCTATGAAAGCCCTAAGGCGCGCGGGGCGCGTTCCAAAAGGCGCGGGGCGCGCTTAGGGCGAAGCTAAAAGGCCCTAAGGCCTAAAGGCGCGGGCGG	2495 TTGACTAGAGAGGGGGTTTATGATCTGAGCCTTTGAGCCTATTTTAGATGCGAATGCGAACGCGAGCAAGCCCATGC TTTGCCTAGTGCGAAGGATTTTTTAAAAGCGGAGCACGCATTCTTTTGGATAGGGGATCAAATACGAACGCTATTG CTCTGATAGGACTCGCACGGCTTTTTTTGACCCTAAAGATTTTGTCTTTAAAAGAGGAGAGTTTCAAGGATAAAGA GCGTCAAAAGATTTATGACATTGTGAAAGAAGCGCAAAAAGGCTATTTCAGGCATTAGAGGGTATGTGAAAGAAGGAAG	2497 GAAGAAGTGTTAGAGTATATTGGTTCATTGAGCGTTTTAGAGCTTTCTGAATTGGTTAAAATGTTTGAGAAAAAATTTGGGAAAAAA	2499 GTTTTTAAAGACGGCAAGCCTTTTTCATTGGAATTTAAAGATGGAATCTTGTAACGATCTTGTAACGATCACTTTTTAAAGACGGCAAGGCGCAAGGCGCAATGGTTTTAATGATCATTGCAAAGTTTAAAGAAAATTATGAGCCCAATGGCGCCAATGGAAATTTTAATGATTCATTGCACCCAATGGTAGCCAAAGTTGAAAATTATGGCGCCAATGGATTTTTAATCATTCAATTCTTGCGCACCAGATAGCATGCAAAAATAAGCGAAAAAATAATGGCGCCCAATGGAATTACGCTCCAGCTTTAAAGCTTTTGAAAAAAAA
HP1322 HP0113	HP1200	HP1200	HP1563

3	⋍	-
(3	١
ė	÷	٠
¢	٠	1

250 HITTAGARAMANIAGEGCCATAGARGCATTGATTAGARGAGTTTATATAGARGAGGTTTGAARGGGTTTTGAARGGGGTTTGAARGGGGTTTGAARGAGGGGTTTGAARGGGGGGGTTTGAARGGGGGGGTTGAARGGGGGGTTTGAARGGGGGGTTTGAARGGGGGGTTTGAARGGGGGGTTTGAARGGGGGTTTGAARGGGGGTTTGAARGGGGGTTTGCAARGGGGGTTTGCAARGGGGGTTTGAAGGGGGTTTGAAGGGGGTTTGCAAGGAGGGTTTGCAAGGAGGTTTGCAAGGAGGTTTGCAAGGAGGTTTGCAAGGAGGGTTTGCAAGGAGGGTTTGCAAGGAGGATTGAAGGGGGTTTTGAAGGGGGTTTTGAAGGGGGTTTTGAAGGGGGTTTGAAGGGGGTTTGAAGGGGGTTTGAAGGGGGTTTGAAGGGGGTTTGAAGGGGGTTTAGTTTTAGAAGGAGG	2/066501		F
AND THE TARGET AND THE CONTRIVERS OF THE TRANSPARATION TO THE CONTRIVERS OF THE CONT	502 ILOKIDAMNGFEFEEYSKIFFTSKGFEV SITOKSGDYGADLIEKDGIKWAVOVKR YSHKVSPKAIQEVVSSKAYYACEKACV ITNSYFTQAAQKLAQANEVLLIDRDEW VRFLNEKR	504 KAKKIL	106 AYMATRTLQNYNERLITLFVIGFMSCSA RLPIYVLFVGSFFPSSSAGFVLFCIYILG AVVALVMAKILIKLSVFKGQTESFIMEM PKYRFPSWRMVYFSIYTKSLSYLKKAG TYILVGAILIWFMSQYPKSDAAMIKAYK GESLLVNKDTTLSSEAKEEKLKELKTEL DKKNLKNSIVGRAGAYLEKVFSPMDFD WRLSVSLVTGFMAKEVVNSTLGVLFSL GDONEKSDAFRGILKKEVSVPSGIAFIV FVMFYIPCFAATITFGREAGGIKFVAYL FIFTTVVAYAFSLIAFYATQILV
2501			52
HP0800 HP0800	2501 ATTITACAAAAATAGACGCCATGAACGGCTTTGAATTTGAAGATATTCCAAAATCTTTTCAAAGGGTTTTG AAGTGACATCAAAAAAAGGGGTTTTG AAGTGACATCACGCAAAAAAGCGGCGATTATGGAGCGGGATTTGATAGAAAAAGGGCTTCTAAAAGTCATTTACGCTTG AAGTGACCTCACCCAAAAGGTTTCGCCCAAAGCCATTCAAAAACTCTAAAAGCTTTTTAAAAGTTTTACGCTTCTTCTAAAGCTTTTTACGCTTCTTTTAAAAGTTTTTCACGCCCAAAAGCGCTCAAAAACTGGCTCAAGCAAG	2503 AAGGCAAAAAGATCCTTTGAAACGCCCTACTATGCCCTTATTATAGAGAGCTTAGAAAAGGCTTAGCAAGTGTTTAGAAGTGTTTAGAAGAGATTATAGAAAATAGAAATGTGAAATGTGAAATTGCGATGCTTAGCAAGAGATTTAGCAAGAGATTTATATTGCGATGCTTAAAAAAGCTGTCAGAATTTTAGCAACAAAGAGAGATTTATTT	2505 GGCTTACATGGCGACAAGAACCTTACAAAACTATAACGAACG
	HP1563	HP0800	HP0800

HP0800	2507	2507 CATT CAAGGGGCATT AGAT ACT AGGGGGGCTTT TAAAA GCCT ACCAAGA GGAAGCTTGCGAAAAAA AACTTTGAAAAACTTTTGAAAAAACTTTT	2508	250BIOGAI DTBEI I KANDEEACAKNEGAEC
		TTTGTGTGTTTGTGGGGGATTGTGAGAAAAGGGATAACATTCAAGGCTTGAGTTTTGATATTTATGAAGCGCTATTAA AGACTTGGTTTGAAAAATGGCACCATAAAGGGAAAGGATTTGGGTGTTAAAAAATGGCACAGGCCTGGGCGA AGACTTGATTGAAAAATGGCACCATAAAGGCATTTAGGAAAGAATAGAAAAATGGCACAGCCTGGGCGA TGTTTTGAAGAATTTTAAGCATAAGGCGTTTTGGAAATTGGGAAAAATGCCTTAGAACTATAGGAAA TTTATTGAAGATTTTAAGCGTAAAGGCGTTTTGGAAAATGCCATAATAAACGCATTTATGAAGAAA GAAGCCACCCTTTAAAAGGGGCTCCTATTTAGCTTAAAAAGGAGTTCAAATGCAAAGGATTTAGAAGGATTTGAAAAA GAAGCCACCCTTTAAAAGGGGTTTTATTACGAAATTGTAAAAGGGGTTTAATTGAAAAATTGAAAAATAGCGAAT ACTTGCTCAATCCTTTAGAATTTATTACGAAATTGTCGCTGATTAAGGCGATTAATTGAAAAATTGAAAAAT GTGCGAAGAAAAATGCTTACTACTACTGGTTTTGGAGGCCTTATGCGAATGACTATAAGAGATTAAAAAA GCACAGAAAAAAATGCTTCCTGGTTTTGGAGGCCTTATGGAGGCTTTAATTGAAAATATGTGCCTA ACTTGCTGAAAAAAGTGTTCCTGGTTTTTGGAGGCTTTTGATTTAATTGAAAAATATGTGCCTA ATTAGAAAAAAAGTGTTGCCCAAAAAAATGCTTTCGGGTAAGCCCTGGTAAGCCAAAAAGTGCTTAAAAAAGTGCTTAAAAAAATATGCGTGGTAAGCCAAAAAGTGAAAAAAGTGCTTAAAAAAATGCTTAAAAAAAA		VFVGIVRKEDNIGGLSFDIYEALLKTWF EKWHHKAKDLGVVLKMAHSLGDVLIG OSSFLCVSMGKNRKNALELYENFIEDF KHNAPIWKYDLIHNKRIYAKIERSHPLKG SGLLA
HP0800	2509	2509 GGTAGAAGTGCGATTTTTTGGACCCAŢAAAAGAAGAAATTTTTTCATCAAAGCGAATGATTTGAAGGAATTAAGAGC GATTTTACAAGAAAAAGGGGCTTAAAAGGGGTTGGGCGTTTGCGCGATAGCCCTTAATGATCATTTAATAGACAA GATTTTACAAGAAAAAGGGGCTTAAAAGGTGGTGGTTGGGCGGTTTGTGGGGGCCTAGGTGTTTAATAGACAT TTAAACGCGCCTTTAAAAGGTGTAATAAGTTTGTTGCCCCGGTTTGTGGGGCCTAGGGTTTTGGAAAATCAT TCAAGGGGCATTAGATACTAGGGAGCTTTTAAAAGCCTACCAAGAGGTTTTGAGGAAAAACTTTGGAGCGTTTT GTGTTTGTTTGTGGGAAAAAGGGAAAAGAGATTCAAGGCTTGAGTTTTATGAAGCCCTATTAAAAGA CTTGGTTTGAAAAATGGCACCATAAAGCCAAAAGATTTGGGCGTGGTTTAAAAATGGCCCACAGCCTGGGCGATGTT TTGATAGGACAAAAGCTCATTTTTATGCGTTTCAATGGGAAAAATGGCCCACAGCCTGGGCGATGTT TTG	2510	2510 VEVRFFGPIKEENFFIKANDI. KELRAILQ EKEGLKEWLGVCAIALNDHLIDNLNTPL KDGDVISLLPPVCGG
HP0800	2511	AAACGAGCAAAAACAGCAATTGATTGAAGGGGTTTCAGATTTGATGGTTAAGGTGCTGAATAAAAATAAGGCTTCTAT TGTGGTCATTATAGATGAGGTCGATTCTAATAATTATGGTCTTGGGGCGAGAGCGTCCATCATTTGAGGCCAAAAAA TGTAAAGAGTTTTTAAAATTCAAAGGTTGCGATAACATTTAGGCGTGCTTATTTCTACCCCCTAAAAACTATAAAC ACTAAAGAGTTTTAAACATGACAAGGCGTTTGAAAAGGGGAAGTTTTAGCCCTTTGCCATGCGTTTCATAAAGG GTAACTCACGTTAAACATGACAAGGCGTTTGAAAAGGGGAAGTGTTTAGCCCTTTGCCATGCGTTTCATAAAGG AATTCATCGCTAAAGGGATTTTCAAGCCCATTTCAAAGCCATTATGCCTATTGACATTCACACGGAACCCCAAAATTCA AAGGGATCTGGAAAAAACTCGTGTGCATTTTAAGCTTGATAAGGCAAAATGAAAAGCCACAAAATTCATGCCAAAAACCCAAAAATCAAGGGATCTGGAAAAAACCCAAAAATTCAAAGCCACAAAATTCATTAGCTTGAAAAGCCAAAAACCCAAAAATTCAAAAGCCAAAAATTCAAAAGCCAAAAACCCAAAAATTCAAAAGCCAAAAACCCAAAAATTCAAAAGCCAAAAACCAAAAACCCAAAAATTCAAAAAACCCAAAAAA	2512	2512 NEOKOQLIEGVSDLMVKVLNKNKASIV VIIDEVDSNNYGLGGESVHHLROKN
HP0800	2513	2513 GGATTTATGCGCCTATTTTAGCCGGGCTTGCCTCTAATAACAAATACTCTTTAATTGGCTCCGCAAGAGCGACGATCC 2513 GGATTTATGCGCCTATTTTAGCCGGGCTTGCCTCTAATAACAAATGGTGGTAGGATCGCTCTTTTAGTG AACTGCTCAGCTTTGAAGCGGTGGGTTTTTAGCCGTTCTGGCTTTAAGCAGCCTCTAGGGTTTGTTT	2514/1	2514 IYAPILAGIASNNKYSLIGSARATIQILS FEVVSTLTILAPLMVVGSLSLYEINHYQ SGGFLDWLVFKQPLAFVLFL/ASYAELN RTPFDLLEHEAEIVAGYCTEYSGLKWG MFFLAEYAHLFAFSFVISIVFFGGFNAW GFIPGGIAILIKAGFFVFLSMNVRATYP HVRPDQLMDMCWKIMLPLAI.LNIVLTGI

НР0800	2515 TGACGCCAAGGCTCAAGAAGTGGCGATGGCGTAGAGAGGGTAAAACCCTAAACGATAAGGGGGCGCTTGAAACGCCTTGAAACGCTTGAAACGCCTTGAAACGCCTTGAAACGCCCTGGTTTTGCAGAAACGCTTTTGCAGAAACGAGATATTCCAGAAGCTTTTAGAAACGAGCAAGACCTTTAGAAATCCCCCGAAGATTTTAAAAAAAA	2516 DAKAQEVAMCVAMGKTLNDKGRLKHS VHEFYIKSPEEMAKLFADIPEALENTOE IADKCVLEIDLKDDKKNPPTPPSFKTK AYAQNEGLNFEDDASYFAYKAREGLK ERLVLVPKEKHDQYKERLEKEIEVITNM KFPGYMLIVWDFIRYAKEMGI
HP0353	2517 THTGATTGATTGATTGAAAAAAACCGATGAGCTTTCAAGCCATTTAGTGAAATTGCAAATGCAGTTTGAAAAAGCCCATTTAGAATGCCAGTTTTGAAAAAGCCCATTTAGAAAAGCCCATTTGAAAATGCCATTTAGAAAAGCCCTTTAAAAATCGGCTTTTAAGATGAAAAAAAA	2518 LIDCLLKKTDELSSHLVKLGMGFEKAG EESKVLIENAKNDGYKIGFKEGEEKMR NELTHSVNEEKNGLLHAITLDEKMKK SEDHLMALEKELSAIAIDIAKEVILKEVE DNSGKVALALAEELLKNVLDATDIHLKV NPLDYPYLNERLGNASKIKLESNEAISK GGVMITSSNGSLDGNLMERFKTLKES
HP0353	2519 ATTICAGCCTTTAAAAATGAAAACATGTTTTTAAAAGACGCTTTAATCTCTATGCAAGAAGTCTATGAAGAAGATAAAAAAAA	2520 ISAFKNENMFLKDALISMÖEVYEEDKK TIDLLRDELNDAREEIEFMKRKYRLMW GKVADMSSVNKK
HP0353	2521 CCTAAAATCCTTAAAAAACCGCTTGAATCAGCATTTTGATCTATCGCCTTGGTGGGGGGTGAAAAAATCATGCC CAATATCGTTTATGCGGATGGTTTTAACCCGTCTGTGGGCGATGGGTGAAGAAAAGGCGATGGCGGAAT GCGTGGGAATGGTGGTGGTGGCAGAAAAGAGGCGGTTTGGTTTTACGCCCTTTAACTTTATGAGGGGGCGTAGGG TGGCGATAAGGTGCTTTTTAAAAGAGGGGTTGAATTTTCCTGTGGGCCGTATTTTAGGGAGGG	2522 LKSLKNRLNÖHFDLSPRYGSVKKIMPN IVYADGFNPSVGDVVKIEKSDGSECVG MVVVAEKEGFTPFNFIEGARAGDKV LFLKEGLNFPVGRNLLGRVLNPLGQVI DNKGALDYERLAPVITTPIAPLKRG
HP0801	2523 TAAGAATAAAAGCATTCCACAACATTGCCCTTGATATTGAAACCCTAAAAGCAAGAAGCCCTAAAAAAAA	2524 KNKAFHNIALDIETLNGEALKNTYDVSA ISFGLYPKIANDYALLPTATSFGNGYGP KLYKKKGVKLKKDFRVALSGEHTTNAL LFKIYYKHARITYMNFLDIEKAVLEEKVH AGVLIHESILDFHNELEVEKELWDVWK ELIEVDLPLPLGGMAIRRSIPLYRAILIKK
HP0801	2525 GGGCTAGGTGTTAAAAÁTCATTCAAGGGGCATTAGATACTAGGGAGCTTTTAAAAGCCTACCAAGAGGAGAGCTTGCGGCGCGGAAAGCGCTACCAAGAGGGAAGCTTGCGGCTTGCGGAAAAGGGGATACAAAAGGGATTGAAAAATGGCGAAAAAGGCCTAGAAAATGGCAAAAGCGCTGCGCCTATTAAAGCTTTGGTTTGGAAAATGGCCCCCCCC	2526 G

	GCATGGATAAATCATCAAGAAGACATTACAATCCATGCGTTATTGAACCAAACTAAAGACGCATTATTGCAAAAAGCC CTCAAACTCTACGCTCTTTAAAGCCTTTAGAATTGAATGGAGCATAGCCATAGCCTTTTCTAAAATAGGGAATTTGT TTGGTAGGGAATTAGAATCCTTTTGCGTGAAAATCCAGCCCAAAAACACCCGTGCTTTAAATAGTGAGAAACTTTATT	HQEDITIHALLNQTKDALI.QKALKLYAL
	TTGGTAGGGAATTAGAATCCTTTTGCGTGAAAATCCAGCCCAAAAACCCCGTGCTTTAAATAGTGAGAAACTTTATT	こうしょうこう こうこうこう こうりこう トレー・コート・コート・コート・コート・コート・コート・コート・コート・コート・コー
		CVKIOPKNTRALNSEKLYLKLFOKGVIA
	TAAAGCTTTTCCAAAAAGGCGTTATCGCAAGGATTTCATGCGAATTCGTGTGCTTTGAAGTCTTTAGCTTGAATGAA	RISCEFVCFEVFSLNEKDFEKIALVLEEI
	AAGATTTGAAAAATCGCTCTGGTTTTAGAAGAAATTCTTAATAAAGCTTAAAAATTCGCTATAATAAAATTTCTTTA	LNKA
	AACGCGCCATATCCCCCACAAAACGCTAGAGAATGATAGAAAACGACAGAACATCAATTTAAAGGAACTTAAAGAACTTAAAAAATGCATGTTATAGAATGCATTGCGTATGAAAAAAATTTGCCTAAAGGATGATTTCAAAAGTGA	
	2529 TAGCAT GCT A GT G G G G G TA G C C TT C CTT C TT A G A G C A T G A C C T G C C T A A T G G G G	2530 SMLVGVAASLIPFLEHDDANRALMGTN
	ACTAACATGCAGCGCCAAGCGGTGCCCTTATTAAGAAGCGACGCTCCCATTGTAGGCACGGGGATTGAAAAATTAT	MORQAVPLLRSDAPIVGTGIEKIIARDS
	TGCTAGGGATTCTTGGGGAGCGATCAAAGCCAATCGCGCAGGCGTTGTAGAAAAAATTGATTCTAAAAAATATTATAT	WGAIKANRAGWEKIDSKNIYILGESKE
	TTTAGECGAAAGCAAAGAAGAAGACTATATTGATGCGTATTCTTTGCAAAAAACTTGCGCACCAACAAAACACAG	EAYIDAYSLOKNLRTNONTSFNOVPIV
	THI I LOAN CAAGE CCCT AND ANGE GEGGGALAAAGE GEGGAGGCCGGGCAAA I CAAGAGTATAAAAAA CAAGAAAAAAAAAAAAAAAAAAA	NVGUNVGAGGIADGPOWIDKGELALG
	GAI AGAGGCGAA I GGCCA AGAGAAAAA I GI GCCGA GGCG I GCCA I GCAA I GCCA I AAAA GAAGAAAAAAAAAA	
	CGAICGIGGIGGIGGIGGA GCAICACH ANG A CAN THE CACHI CCACCCACATH IN GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	COURT OF THE CANODARE LANGUE IN THE CANODARE I
	GGGGGCT AAGCA GGTGT GGAAGAA ACCGC GATA CC GATGT GTGAAGGAAGAAGCCC CC CC CC CC CC	DIPUVNEEALATICUES NAVEL 1 VOA
		GMILVGKTSPKGEIKSTPEERLLRAIFG
	GATTAAAAGCACGCCTGAAGAGCGGCTTTTAAGGGGCTATTTTGGGGATAAAGCCGGGCATGTGGTCAATAAGAGTT	DKAGHWNKSLYCPPSLE:GTVIDVKVF
-	rgtattgccctcccagtttggaaggcacggtgattgatgtgaagtcttcactaaaaaggctatgagaagacgg	TKKGYEKDARVLSAYEEEKAKLDMEH
	CGAGTTTTGAGCGCGTATGAAGAAAAAAGCCAAGCTTGATATGGAGCATTTTGATCGCTTGACCATGCTCAATAG	FDRLTMLNREELLRVSSLLSQAILEEPF
	AGAAGAATTGTTGCGCGTTAGCTCGCTCCTTTCTCAAGCGATTTTAGAAGAGCCTTTCAGCCATAACGGCAAGGATT	SHNGKDYKEGDQIPKEEIASINRFTLAS
	ATAAAGAAGCGATCAAATCCCT	LVKKYSKEVQNHYEITKNVFLEQKKVL
		GEEHEEKLSILEKDDILPNGVIKKVKLYI AT
HP0806 25:	2531 GATTAAACGCCACCCAAGCCCTAGAACTCGCCTTCTTAATCGCTGACATGCTCAAAAAACAGCACGCTTAGTTAAAAAAAA	2532 LNATQALELAFLIADMLKKOHA
HP0928 25	25331 GAGTGGCTTTAAAAAGCGCGTATTTTCAAGGCGTTTGCGATGAATGA	2534 VALKSAYFQGVCDEMIVAQNIEFYSTC
_	CTTGCGAGCACCATTTGCTCCCTTTTTTGGGGAATATTAGCGTGGGATATATCCCTAAGGAAAAGATTGTAGGCATTA	EHHLLPFLGNISVGYIPKEKIVGISAIAKL
	GCGCGATCGCTAAACTCATTGAAATTTATAGCAGACGCCTACAAATCCAAGAAAGGCTGACCATTGAAATTGCAGAA	IEIYSRRLQIQERLTIQIAETFDEIIEPRG
	ACCITTGATGAAATCATAGAGCCAAGGGGCGIGAITCGIGGIIIGGAAGCCAAGCAITGGGGAAGCAIGAGCAIGAGCAIGAGCAIGAGCAIGAGCAIGAGCAIGAGCAI	VIVVCEARTICIMSMUGVCRUIVININININININININININININININININININI
	GGG GCAAAAGCAAAA GCGA CAA AAAACAAAC	VENGET NADON INVELING
-	CGAGCGTTTTGAAAAGCTTTTTAAAAAACCATCATTTTACACCTTGAAAAGCTTCCACCCTTATTTGGAAAAAGCCTTTTTT	
-	GAAATGGTGCTTAATGGAGGCAAAAGGTT	

1	Ģ	ľ
(7	١
1	•	٦

HP0928	2535/6	2535 GCAAAAAGACGCTTGCGGGTTCATCTATGAGATCAGCGAGTTCATGAAAGCCTATACCGCATTGCTAAAAAAAA	2536 LVVDA COEIVEIGE ENVAYORAL I MAGAETA
	<u> </u>	GACCGATACGTCTATTTATTGAGGTATCTCCCCTCTAGGTATTGGGCCAGCATTTTAACGACTGCCCTTTATGTCAAA	2330 RNDACGFI EISEFMRAY I ALLKKUDKY VYLLRYLPSRYWASILTTALYVKYPDFD
	<u>- 0</u>	INCOCTION IN GENERAL INGENIALIS OF THE GOVERNMENT OF THE CARREST OF THE CARGAGE AND THE CARREST OF THE CARREST	ALKKLLVSYYYQTWIAGGTITRIKQTSIN
	<u> </u>	TGAATAGCATCGACTCTTATAACACCTTTGATCAATACCTCTATAACTTATGGGATAGCTCTTCTGTTTATCATAGCA	III NI WOSSSYYHSKAAVEDYN EI ANY
	<u> </u>	AATGGGTGCGTCCTGTCTTAGCCCTAGCTAATTATTTCATGGCAGATGAAGAGAAACCCCATTTTATCGCTATGGATG	FMADEEKPHFIAMDAETQVEHILPQTP
	<u>ه ر</u>	COGRANCO AND SOLVE OF A STANTANT OF CONTRACTOR OF THE SOLVE OF THE SOL	KRGSQWNADFDKEKREEWVNNIANLT
	<u>(</u>	GGATITIGATGAAAAAGAAAAATTTATGGAGGCAAAAGACACGAAAGTGATTAGATTAGATTAGAAAAAAAA	LLKRKKNAHALNGDFDEKRKIYGGKDT
	<u> </u>	ATTGTATAGCAATTATAGGAAGTGGAATGAGAAGTCCCTCCAAGAGCGATACAAATCTTTGTATAACACTATCACGCC	RYKS! YNTITPV! HIEGOFODFED
	_	TGTTTACACATAGAGGGGCAAGAAGATGATTTTGAAGATGATTTTGATCTAGAATGATTAAAGATTGCCAAGCATCA	л 2011
	<u> </u>	AAACAACAAGGGGGGGGGGGCCCTATTCTTTTCTATACACAGATGTCAAAAGGATGTCAAAGGAAAGGATTTTTAAAGACTTCTTAAA AGAAGCCAAACAGCAACTCCCCTATTCTTTTCTATACAATAAAAAAGAAGATGATGAAAAGGAATTTTAAAAAAAA	
	9	GICTATGTGTT	
HP1204	2537 6	2537 GGATTTATGAGATTGAAGTCAAGCTTGGATCGGGGGTTGTGGGCGTGTTTAAAATTGATGTGGTGGCTGAGTAGAAA	2538 IYEIEVKLGSGVVGVFKIDVVAE
	₹ Ø	A I GLA GENERAL GALGA L'ENTRE GENERAL GENERAL GENERAL GAN L'ANDRA GAN CONTROL GENERAL	
HP1324	2539 Tr	2539 TGACGCTATGGAAAAAGTGGGTAAAGACGGCGTGATCACCGTTGAAGAAGCTAAGGGCCATTGAAGATGAACTAGAT	2540 DAMEKVGKDGVITVEEAKGIEDELDVV
	<u>) {</u>	GI I GI BERBAGGCA I GCAATTIGATAGAGGCTACCTCTCCCCTTATTTGTAACAAAAGGCTGAGAAAATGACGCTCAA	EGMOFDRGYLSPYFVTNAEKMTAOLD
		TEGANICACION INCATOR INTERPRETATION OF THE TOTAL OF THE T	NAYILLTDKKISSMKDILPLLEKTMKEGK
	<u>(</u>	ATTANGAGE CONTEST TO C	PLLIIAEDIEGEALTTLVVNKLRGVLNIAA
	<u>(</u>	ALLANGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	VKAPGFGDRRKEMLKDIAILTGGQVISE
	<u>.</u>	GGCAAAGCCGGAAAGCATTGTGAATTGAATTGAATTGAA	ELGLSLENAEVEFLGKAGRIVIDKDNTT
	7	ACCA ANGEST CONTROLL OF SATING ANATONIA CALLANGA INCALLANGA INCALA	IVDGKGHSHDVKDRVAQIKTQIASTTS
	<u> </u>	Treason to the property of the	DYDKEKLOERLAKLSGGVAVIKVGAAS
	<u>¥</u>	ACCGGGTTGATGATGATGATGATGATAAAAGAGAGTTTAAAAAA	EVEMKEKKDRVDDALSATKAAVEEGIV
	<u> </u>	TCATTCGCGCGCCCCAAAAGTGCATT GAATTTGCACGATGATGATGATAAAAAAGTGGGCTTAATAAAAAAAA	IGGGAALIKAAUKVHLNLHDDEKVGYEI
	<u>A</u>	ATTAAAGCCCCCATTAGCTCAAATCGCTATCAATGCCGGTTATGATGGCGGTGTCGTCGTCAATGAACTAGAAAAAA	IIIIIININAINAINAINAINAINAINAINAINAINAINA
	<u>ಕ</u>	CGAAGGCCATTITGGTITTAACGCTAGCAATGGCAAGTATGTGGATATGTTTAAAGAAGGCATTATTGACCCTTAAA	KVERIAI ONAVSVSELI TTEATVHEIK
1,700	A N	AGTAGAAAGGATCGCTTTACAAAAT	EEKAAPAMPDMGGMGGMGGMGGMM
erio44	₹ 1 8 67	2341 AACUGUGAUAAUUAUGUAAGAUGGGGGTAACGATCACCACTACCTATAATAATAACAAAGCCACCGTCAAATTTGACA TCACCCAATAACGCTGAACAGCTGTTAAATCAAGCGGCAAAACATCAAGCATCAAAGTAATAATAAGAAATAAAT	2542 TATTTQDGVTITTYNNNKATVKFDITN
	<u> </u>	<u> GTTCCACGAATAACGAAACACTCCAGGGGGTTGATCAACCATTGAGGTTTAAACCACATTGAGGAATAACGAACATGAGCAATAACAACAACAATGAGGAAACAACAACAAACA</u>	MENTOCOCOMING STOCKSTN
	ົວ	CTTCCAACAAGAATTTAGCCAGGTTACTAGCATGATCAAAAAGGCCCCAAGAAATAATCGC	FSOVTSMIKNADEII
HP0115	2543 TT	11GAAA1GCTTTATGAAGGGATTTTGAGAATTTTCTTCGCAAGCCCAAACGCTGTATTGAAAATGAAGACATTGAAAAAAA	2544 EMLYEGILRFSSQAKRCIENEDIEKKIY
	<u>8 6</u>	GATTATATATAGGGGGGGTTATACGGGGGATCAAATCAA	YINRVTDIFTELLNILDYEKGGEVAVYLT
	<u>છ</u>	GATTGATTTGGTGTTGAATGTGGCCTAGAGGGTTATTAGAAGCATGGAGGGAAATCCATTCAGATGAACTCGCCTAAC	ARGII FAWREIHSOFI'A
	TA 2A	ATTITATI AGANTA AND AND AND AND AND AND AND AND AND AN	
	₹ ₹	ASANGGAAAAGAAGCATTGGATTACAATTGCGCTTTTAGAGAGCTTCAAAAT AAAAGAAAAAGAAGAACTGCAATTACAAATGCATAAGGCTAAGAAGATTCAAAAAT	

066501				PC	T/EP01/15428
2546		LEANTANDER OF THE SET WINNER THE LEANTANDER ALTHRIKOTSIN HIKNYKSNKSVETIKELILINSIDSYNTFDQ YLYNLWDSSSVYHSKWVRPVLALANY FMADEEKPHFIAMDAET QVEHILPQTP KRGSQWNADFDKEKREEWVNNIANLT LLKRKKNAHALNGDFDEKRKIYGGKDT SKVISCYDITKELYSNYRKWNEKSLQ	·	2554 NLKSQFADAKALLICDYKGLSVKKLEAL RNKARNGGIKVQVIKNTLAHIAMKETG YSDLDLKETNVFLWGGIXQIALSKLVFD FQKEHKDHFVLKG	CSSS VERUSARDACIST EISETWING THELD KYDDRYVYLLRYLPSRYVASILTTALYV KYDFDALKKLLVSYY-TJWIAGGTITR IKQTSINIIKNYKSNKSVETIKELILNSIDS YNTFDYLYNLWDSSS/YHSKWVRPV ILALANYFMADEEKPHFIJMDAETQVEH ILPQTPKRGSQWNADFIJKEREEWVN NIANLTLLKRKKNAHALNGDFDEKRKIY GGKDTSKVISCYDITKELYSNYR
2545		2549 GCAAAAAGACGCTTGCGGGTTCATCTAT GACCGATACGTCTATTTATTGAGGTATCTC TACCCTGATTTTGACGCTTTGAAAAAGCTT CGCATCAAGCAACCAGTATCAACATTATG TTGAATAGCATCGACTCTTATAACACCTTT AATGGGTGCGTCCTGTCTTAGCCCTAGCT CCGAAACCCAAGTGGAGCATATTTGCCA AAAAGAAGAATGATGGAAAAAATTATGG GGATTTTGATGAAAAAAAA		2553 TAACTTAAAGTCGCAATTTGCAGATGCCAAGAGCAATCAAGAATAAGGAATTGAATTGAATTTGGAATTTGAATTTGAATTTGAATTTGAATAAGAGAGATAAAAAA	2555
HP0115	1334 944	HP1334	HP0002	HP0002	HP0002

١	¢	,
¢	э	١
ř	÷	'n

/066501	4					
2558 QNFIEIKAKTLEEALIGASIALNCPIINLO YEVIOTPSKGFLSIGKKEAIILAGVKESV KEIKEESVKETNTKEIHOSAEEKKÖKLE TETPOEEIITPKPSKKNPKEESHSGDKL HEIKOELKDLFSHLPYKINKVEVSLYEP GVLLIDIDGEDSALLIGEKGYRYKALSY LLFNWIHPTYGYSIRLEISTFLQNOEKV	MD I O 2560 AYYVNISYSKEHDFKVGDKINEKEIKM STEELAGIYAVOSTPTIVLSDKTGKTIYE LPGYMPSTQFLAVLEFIGDGKYQDTKD DEDLTKKLKAYIKYKTNLSKSKSN	2562 KKDACGFIYEISEFMKAYTALLKKQDRY	2564 PLDKWNDIIFHASKKLSKKELERLLÊLL ALLETFIEKEDLEEKFESFAKALRIDEEL QQKIESRKTD	2566 DPPYNISVKNNFPTLKSAKROGIDFGE WDKNFKLLEWIARYAPLVNPNGCMVIF CSYRFISYIADFLEENGFVVKDFIQWVK NNPMPRNIHRRY	2568 TKSLEČGEIGIVSLGLKSVTDIAVGDTLT DAKNPTSKPIEGFMPAKPFVFAGLYPIE TDRFEDLREALLKLQLNDCALNFEPES SVALGFGFRVGFLGLLHMEVIKEŘLEŘ EFGLNLIATAPTV	2570 KSGSHFDLPIALLIALGKÖELAFKEWFA FGELGLDGKIKPNPNIFPMLLDIAIKHPH AKIIAPKANEELFSLIPNLQCFFVGHFKE ALEI
		25	25		25	255
255/ I ISCAAVATITIATIGAAATCAAAGCCTTAGAAGCCTCATTCAAGCCTTCTATCAAGCCTTGAATTGCCCCAAAACCTTAGAAGAGCCCTTCATCAAACCTTGCAATTGCCCCCAAACCAAAGCCTTAAAGCAAAGCAAAGCAAAGCAAAGCCTTAAAGCAAAGCAAAGCAAAGCAAAGCAAAGCAAAGCAAAGCAAAGCAAAGCAAAGCAAAGCAAAGCAAAGCGTTAAAGCAAAGCAAAGCAAAGCCTTAAAGCAAAAAAAA	2559 GCGCTTACTATGTCAATATCAGCTACTCCAAAGAGCATGATTTAAAGTCGGCGATAAATAA	2581 GCAAAAAAGGCGTTGCGGGTTCATGAGATCAGCGAGTTCATGAAAAGCCTATACCGCATTGCTAAAAAAAA	2563 ACCCCTTAGACAAGGGAATGATATTTTTCATGCGAGTAAAAAGCTTTCTAAAAAAGGGCTAGAAAGGCTTTTAG AGCTTTTAGCTCTTGGAAACTTTTATAGAAAAAGAAGACTTAGAAAAGAAAG	2565 GGACCCTCCTTATAACATTTCGGTTAAAAACAATTTTCCCACCCTAAAGAGGCTAAAAGGCAAGGCATGGTTTTGGGGATGGGTTTTGGGTTTTGGATTCGGGTTTTGGATTGGGTTTTGGATTGGGTTGGGTTTTTGGATTCGGGTTGGGTTGGGTTGGGTTTTTTGGGGTTTATGGGTTTATAAGGTTTATAAGGTTATTGGGTTAGAAGGGTTTATGGGGTTTATGGGGTTAAAAGGTTTATGGGGGTTAAGGGGTTTAAAAATAAGGTTAAGGGGTTTATGGGGTTTATGGGGTTAAAAATAAT	2567 CCACCAAAAGTTTAGAATGCGGCGAGATTGGGCATTGTGAGTTTAGGGCTAAAAAGCGTTACGGATATTGCGGGTGGGT	2569 TAAATCCGGGGGGTCATTTTGATTTGCCTATCGCTCTTTTAATCGCTTTTGCAAAAACAGGGTTGGCTTTTAAAGGGTTGCGTTTGCGGGGGTTGCTTTTGCGGGGGTTGCGGGTTGCGGGTTTTGCGGGGGTTTTGGGGGG
HP0002	HP0124	HP0124	HP0242	HP0001	HP0001	HP0001

ļ,	_		
ľ	-	<u>.</u>	,
4	Ç	,	١

HP0249 CAAAGGACCCTTGAAAGCGTTTATCGCTTG TTTAGCGAGCCTTGAAATTTTTACCCATTGGTTGGAACATTTTACCCATGGTGGT TCATTTGTTTGAACAATTTTTACCCATTGGTGGT GGCTCTAGTGAT TCATTTGTTTGAACAATTTTTACCCTTGGT GCCTCTAGTGAT TGAGGCGATTTTGGAACAATTTTTAGAAAAA TGGCCCCCAGTTTGGAACAACCGCTTTGG HP0249 2583 GCGCGCAGTTTGCAATTCTTGGAAAAA TGGCCTCTTAAAAATGCTTAGGGGGTTTCTGGTTTTGGAAACCGTTGGGTTTTTGGAAACCGTTTGGGAACCTTGGGTTTTGCAACCGGTTTTGGAAACCGGTTTTGCAACCGGTTTTGGAAACCGGTTTTGGAAACCGGTTTTGGAAACCGGTTTTGGAAACCGGTTTTGGAAACCGGTTTTGGAAACCGGTTTTGGAAACCGGTTTTGGAAACCGGTTTGGAAACCGGTTTTGGAAACCGGTTTTGGAAACCGGTTTTGGAAAACCGTTTTGGAAAAACTTTAGAAAAACTTTAGAAAAACCTTTTGGAATTTTAGAAAAACCTTTTGGAAAAACCTTTTGGAATTTTAGAAAAACCTTTTGGAAAAAACCTTTTGGAAAAAACCTTTTGGAATTTTAGAAAAACCTTTTGGATTTTTGGATTTTTTTT		
2583 2583 2583 10 2583 10 10 10 10 10 10 10 10 10 10 10 10 10	AACGAGCGCTTGAAAGCGTTTATCGCTTCTTTACCCTTTAAGCTCACAGCGGATCAACAAAGCGCATTAAAGAAATC CAAAACGATCTCACTAGCTCCATAGCGTGCAAGCGTTTGATTATAGGCGATGTGGGGGTGCGGGAAAACGATGGTGA	ERLKAFIASLPFKLTRDQQNAIKEIQNCO LTSSIACKRLIIGDVGCGKTMVILASMV
2581	TTTTAGGGAGCGTGAATTTTAACTTACCGAAATAAAACCCTTTTAATGGCGCCCACTTCCATTCTGGCAATTTAATAACAACATTAAAAATTTTTAAAAATTTTTGAAATTGCGCGAAATGGAAATTAAAAAAAA	TYPNKTLLMAPTSILAKOLYNEALKFLIO
2583	AATCACGCATGTGGTTATCGGCACGCAAGCGTTGTTTGTT	GTGALLFOKROLNEFALV GGALLFOKROLNEFALV GOALLFOKROLNEFALV
2583	2581 GAGAGCGAGTCTCTTTTCAGCCTTTTTACCCCAAAACAGAAAAACCCAATCGCCCTCAAAGGTTTGCGCATGTTTCTA GCGCCCCAGTTTGGAATTTTAGAAAATTAGTGATCCGCTATCTTTTAGAAGAAGAAGAGCGC TGGGCTATATCCATAGTGGGGTATTCTTGCATAAAAAAGAAGAATT	2582 ERVSFQPFYRKTEKPNRPQRFAHVSS APSLEFLEKLVIRYLLEDRSLLDLAVGYI
2585	2583 GCGCGAATAAGAGTTTGCAAGACAAACCTATCGCAGAAATTTATAAGAGCGTGCCTAAAGGCCACCAACGAAGTGATG	2584 ANKSI OOKPIAEIYKSVPKATNEVMAII
2585	GCTATTTTAGAMAACGGCTCTAAAGCGACTTTAGAATACTTAGATCCCTTTAGCCATAAGGAAAATTTTTTAGCCGTTG	ENGSKATLEYLDPFSHKENFLAVETFK
2585	AAACOTTIAAAATAGOTAGAAAACAGAAAGTAAGAAGAAAAATOTTAATTGAATGATGATGATGATTAATAATGAAAAAGACAA GGTCTATGAGCAAGTAGGCTCGGTGCGTTTTGTGGTGATCATAGCGAAGCCAATCATGATGTTAGCCTTGATTATA	MLGKTESKONLNWMIALIIEKDKVYEQ
2585		SORI FAVORTI CHEEKI I NIOANOGI
2585	CCAATTCTAGCGGTATTAAATTGATTGAAGCGAAATCCAATGACGAGTTAGGCCGCATGCAAA	KLIEAKSNDELGRMOTAINKNILOTÓKI
2585		MAEDROAVADTIKVVSDVKAGNFAVRI
2585		TAEPASPDLKELRDALNGIMDYLGESV
2585	AAI GEGALICA I GGATTATTI GCAAGAAAGCGTAGGGACTCACATGCCAAGCATTTTCAAAATC	GTHMPSIFKIFESYSGLDFRGRICHAS
2585	I CAVACCI I I I I I I I I I I I I I I I I I I	GRVELVTNALGQEIQKMLETSSNFAKD
2585	I NEGOCIANOS AN I COMMANA I ECI AGAMACI I CELCANI I I GECCANAGATI TAGECGANTA GECCECANITA	LANDSANLKECVONLEKASNSOHKSL
2585	AAAATATCACCACTTCCAAAAA I I IAGAAAAAGCI I CAAACI CCCAACAAAAGCI I GATGGAAACTTCCAAAACGATAGA AAATATCACCACTTCCATTCAAGGCGTGAGCTCTCAAAGTGAAGCCATGATTGAACAAGGGCAAGACATTAAAAGCA TTGTAGAAATCATTAG	METSKTIENITTSIQGVSSQSEAMIEQG QDIKSIVEIIRDIADQT
O O	302C TITLE AND AND AND AND AND AND AND AND AND AND	
TTGCAACCCTAATGCTAACGCC CCCCATGTTAGGGATTTTTCT TTAGTGCCTTTGTCGGTGCGTG GCGCTTACACGCCAGAGGGT CAAATCGTTTGCAGGGGTT	ATGATTICECATTITITICCTATCTITITICCTTAATCCCTATTITITITI	2586 FFKNTMSLDIASMIFNHOSYONLLKOH
TTAGTGCCTTTGCGGTGCGTGCTGCTGCTGCTGCTGCTGCTGC		TLMLTHYFFIFKEKEC
GCGCTTACACGCCAGAGGTT CAAATCGTCTTTGCAAGCTTAGT	GTGCGTGGGCTTTGAGGGTTTGTAGGGCGCGATTTTTACCCACTTTAGAAATTTTCAAAC	
CAAAICGICTTIGCAAGCTTAGT	NGAGGGTTTTATCATTGCTTGCTTGTGCAATTGTTTTAGGGGTGTGCGCGTCTGTCT	
	CAAAICGICTITIGCAAGCTIAGIGTITIGCAACCGATAGCATCAGCTTTTCTATGGGGCTTACGATGGCGAGCGCGTA	
TCGTTCCACCATCAAATCATTTGTTTGTTTGTTG	ATCATTTTGTTTGTGGGATCACAGCTTAAAAGCCGTCCTTTAGGGCAATT	

_		
•	J	١
٠	2	١

HP0249	2587 ICCGAAATCACTTCTAACACCGCCACCGCCTTTTTTACCGGTGATTGGAGGGGGTTGCGATGGGCTTGGTTA TGAAAACCATCAGAGCTTGTTATTGACCATTCCTGTAGTGCGCGTTGCGCGTTCATGCTCCTGTGGTCA TGAAAACCATCAGAGCTTGTTATTGACCATTCCTGTAGTTGATTAAAAGCCGCGTTTGTGCTTAAT CCCCACCGATTGTTTTAAGCAAAAATTTTAAGCTTTTTTTT	GCCGCATTTTTACCGGTGATTGGAGGGGTTGCGATGGGCATGGGTTA TCCTGTAGCCTTGAGTGCGCTTCATGCTCCCTGTGGTCAT TCCTGTAGAAATAAAGGCGACTTGCGCGTTCATGCTCCCTGTGGTCA GGGTATGTTAAAATAACGGACATGATTAAATGGTTTGTGGCAAAAAAGTGA ACATTACAGGGTTGTTTTAATCATTGATTGATTAAGGAAAAAAGTGA ACATTACAGGGTTGTTTTAATCATTGAAGCGTTAATGATTATTCCA ACGGGGGATTTATGCGTTATCAAAAGCGCACCATAGCGATTATTCCA TTTAGTGTTGTCATGGTGAAAAGCGCACCATAGCGAGCCATTTTAC GCGCTTTTTGGGGGCGCGTTTTTAGCGCACAAACCCCTTTCAGC GGGGCGTTTTTGGGCAAAACCCCTTTCAGCGCCCCCTTTTACGCCGCCCCCTTTTTGGCCCCCCCC	2588	2588 EITSNTATAAAFLPVIGGVAMGMGYENG HQSLLLTIPVALSATCAFMLPVVTPPNIO IAYGSGYVKITDMIKAGLWLNLVGVVL:0 STFSYFLVSLIFN
HP0249	SATCATGGAAGTGA AGTAAAATCGTGCT TGTTAGATCGTATT TTTCTGTCTTTTTAC TTCTATGTGGGGTGC CGTTAGTTACGAATACGAATACGAATA	ATATGGATTITGTGTTAAACAAAATCAGCAAGGTTTTGCCTTTCACAAC AGCTTTGACGATTTTAGCCTTATTGCTGGGTTTAAGGAAGTTGATCAC TTTGAAATCATGCAGCGCAATAAAAAAATGCATGTCAATGTGCAAAAG SCCCTATTTAGTTGCGAGTGGCTTTAGATTTTCTACTACTACCTAACG SCCCGGTGTATATCATGCTTTTAGATATTTTCTACTACCCTAACG SCCCGGTGTATATCATGCTTTTAGCATGGTTAGTGATAGCGCTTTTTAATGGCTACCAAAGAAGGAGCGCAATTTTAGAAAAGAAGTGATCAACTTG	2590	2590 LPKNLIMEVNMDFVI.NKISKVLPFTTHS LQVSKIVLALTILGLIGLKKUTMLALL LDRIFEIMQRNKMFVNNQKSIVSPVS VFLALFSCDVALDIFYYPNASPPKVSM WVGAVYIMLLAWLVIALFKGYGEALVT NMATKSTHNFRKEV.NLILKVVYFL
HP0249	2591 TGCCACTATTAACGCCACTAATGTTGATGCGGACAAAATAGCTAGC	GGACAAAATAGCTAGCGATAATCCTATTTATGCTTCCATAGAGCCTGA CATTAAGGATAAGAATTTAGAAATTAGCTAAGGCTTTAGGTGG CATTAAGGATAAGAATTTAGAAGCTAAAGTTAGGTAGGTGG TAAAAAATCCACAGCAGAAAGAGCTAAAGCTTAAGGTTGG TAAAAAATCCACAGCAGAAAAAGAAGAGAGTGGGGAATTTGTAG STGAAATCGCTCTTAAGAAAAAAAAAAAAAAAAAAAAAAA	2592	2592 ATINATNYDADKIASIONPIYASIEPDIAK QYETEKTIKDKNLEAKLAKALGGNKKD DDKEKSKKSTAEAKLAKALGGNKKD DDKEKSKKSTAEAKLENNKIDKDVAET AKNISEIALKNKKEKSGEFYDENGNPID DKKKAEKODETSPVKQAFIGKSDPTFV LAQYTPIEITLTSKYDATLTGIVSGVVAK DVWNNMNGTMILLDKGTKVYGNYGSVK GGTPIMTRLMIVFTKAITPDGVIIPLANA QAAGMLGEAGVDGYVNNHFMKRIGFA VIASVVNSFLQTAPIIALDKLIGLGKGRS ERTPEFNYALGQAINGSMQSSAQ
HP0249	2593 GGGTAGAGCAAGTGTTAGCCGATCTCAAAAACTTCTCAAAGGAGCAATTGGCTCAACAAGATGAAAATGAAGTTAT TTCAATACTGGAAAAAATTCTGAACTATACCAATCCGTTAAGAATTGGGTTAAAAAACCCCTAGTCGGTAATGGGTTAT TTCAATACTGGAATAGGACTCTCGCCAAAATTTTTCGGATATCAAGAAATTGAAATTAAAAATTTCA ATAACAATAATAATAGGCTCAAAAACAGCACAGAACCCATTTATGCTAAAGTTAATAAAAAAGAAAATTGACAAGTAGGAA ATAACAATAATAATAGGCTCAAAAACAGCACAGAACCCATTTATGCTAAAATTGACAAAAAGGAAAATTGACCGAATCAATC	ACTTCTCAAAAGGAGCAATTGGCTCAACAAGCTCAAAAAAATGAAGATAAAATGAAGATAAAACCCTAGTCGGTAATGGGTTAT AATCCGTTAAGAATGAGAATGAAAAACCCTAGTCGGTAATGGGTTAT AATTTTCGGATATCAAGAAAGAAATGAAAAGGAAATTTCA AGAACCCATTTATGCTAAAGTTAATAAAAAGAAAAACGGACAAGTAG TGCTAAAAAGGTAAATGCAAAAATTGACCGACTCCATCAATAGCAA GGCTTCCCTTTGAAAAGGCATGATAAAGTTGACCATCAGTAAGGT CGCTACGATTGATGATCTCGGCGGACCTTTCCCTTTGAAAAGGCATG GGTTCCCTTTGAAAAGGCATGATAAAGTTGACAATCAATC	2594	2594 VEQVLADLKNESKECLAGGAGKNEDF NTGKNSELYGSVKNSVNKTLVGNGLS GIEATALAKNFSDIK-ELNEFKNFNNN NNGLKNSTEPIYAKVNKKKTGQVASPE- EPIYTQVAKKVNAKICRLNGIASGLGGV- GQAAGFPLKRHDKVDDLSKVGLSASP- EPIYATIDDLGGPFPLKRHDKVDDLSKVG GRSRNGELAGKIDNI.NQAVSEAKAGF- FGNLEQTIDKLKDSTKKNVMNLYVESP- KKVPASLSAKLDNYAINSHTRINSNIGNE GAINEKATGMLTQK

•	-
•	_
e	-
	·

HP0249	2595,	2595 ATAAACTCATTICTTGGCTGGGTCCGCAGGATTTGAGCGTTTTAGTGAATATCGCTTTAAATAGCATCACTAACCGTA GTAAAGAGCTGACTGACCTAACCCTA	2596/KLISWLGPQI LTSTISSIGE	2596 KLISWLGPQDLSVLVNIALNSITNPSK LTSTISSIGEKALNDLLGDG
HP0249	2597	TCACCGAATTAGAGCCAACAGGCCTAACCCTCCCCTATCATGAAGCGTTTTACCATAAAAGGGCGATTTTGATTCAGGGGCTAAGGCGAATTAGAAATTCAAGAAATTTTAGATTCAGGGCTAAGGCCTTAGGGGCTAAGGCGATCAGGGGTGCCCTTAGGGGCTTTAAGAAACCTTAGGGGCTTTAAGAAACCATCAACTTTATGATGGGGGTTGCATTGAAAATTTTAGGCGAACGATTAAAAACCATCAACAATTTAGGCGTTTGAAGAATTAGAAAACATCAAAAACATCAAAAACATAAAAAACAATAAAAAA	2598 TELEPTGLTLSP SYDMSYMYAGI SHYYSKTPMKD CHVYSKTPMKD EGWWQQNGNE EGWWQQNGNE LIILMASLNIISSI MGSSQKEIQKT VLAFLSMYLLSV LINLSLMDFTLTL	2598 TELEPTGLTLSPIMKRFTIKGDFDSGLS SYDMSYMYAGLQAISAIRRLPLGLYDS VHVYSKTPMKDIEILRNALKTINHHGKS EGWWQQNGNFSAMELEKRALFIVLS LIILMASLNIISSLLMVVMNRRKEIALLFU MGSSQKEIQKTFYLGNIIGLGGVALGV VLAFLSMYLLSVFPIISLPADVYGINTLP LINLSLMDFTLTLI
HP0249	25997	2599 ATTTAGCGAATGTTCTCAGTCAAGTGGCTATGGAAAAATCAAGCCGGCGGCGGCGGTTTAGGAAACTTTATAGAAAAC CSON ATTTAGCGAACTTTATAGAATTGCCCGCTAGCTTGCAAATGATGAACTTATAGAAATAAC TTAGATGATTTATTGAATAATAGCGGGGTCATGAATGCCAAATATTATCAGTAAAAACTAAGGCTTTTTGGTA ATTTGTTACCCCATCCATAGAAAACTACCTTGCTAAGCGTCTTTAAAAAGCATGCTAGACGATAATCCC AATTTATCGGTGGGTATATGAAACGCTTCTGCTAAGCGCTCTTTAAGCGTGGTTTTAAAAGGGCTTTT GAATTTTATCGGTGGGTATATGAACGCTTCTGAATTAAGTTCTATTTTAAGCGTGGTTTTTAAGAAAGA	2600 LANVLSQVAI SPLSKELPAS LLNNSGVMN IIENYLAKQSI NASELSSILS VANDLLNEFI NNIISQGGLS ALKENDLGTI	2600 LANVLSQVAMEKIKQAGGLGNFIENAL SPLSKELPASLQNETLGQLIGQNNLDD LLNNSGVMNAfQNIISKKLSIFGNFVTPS IIENYLAKQSLKSMLDDKGLLNFIGGYM NASELSSILSVVLKDITNPPTSLQKDIGV VANDLLNFFLGQDVIKKLESOGLVSNII NNIISQGGLSGVYNQGLGSVLPPSLQN ALKENDLGTLLSPRGLHDFWQKGYFN
HP0249	2601 C C C C C C C C C C C C C C C C C C C	TITAGAAGACATTGGCAAAATCACCGTITCCACTAATTTAGGGCATTTGCACATTAAGGATTTTGCGAAGTCATCAGGCCACGAAGACATTGCACAGAAGTCATCAGGCCACAGAAGATTGCACACAGAAGATTCATTAAAAGCCACAGAAGACCACAGAAGACTTGTTCTTTAAAAACCCCTTTTTAACAAACA	2602 LEDIGKITVST REILGYVTKDC KEITQYYQKI DRSEFTQKAI LGNLRASVAV LTUNLMSLGS AFEKLSANTK VSGVVIIIVFF QSIVYALLGT HSETFLTRFL	ZBOZ LEDIGKITVSTNI.GHLHIKDFAKVISQSR TRLGFVTKDGVGETTEGLVLSLKDANT KEITQVYÖKLEELKPFLPNGVSINVFY DRSEFTOKAIATVSKTLIEAVVLIITLFLF LGNLRASVAGVILPLSLSVAFIFIKFSD LTLNLMSLGGLVIAIGMLIDSAVVVVEN AFEKLSANTKTTKLHAYRSCKEIAVSV VSGVVIIIVFFVPILTLOGLEGKMFRPLA QSIVYALLGTLVLSTIIIPVVSSLVLKATP HSETFLTRFLNRIYAPLLEFFV

-	

0.2/066501			PCT/EP01/15428
2604 QĞYKĞPSAVSDIITAFĞEFSVSĞNYVIĞ ALIFSILVLVNLLVYTNGS.TRVTEVRARFĞ ALDAMPĞKQMAIDADLINSĞLIDDKEAKĞ KRRAALSQEADFYGAMDGASKFVKĞDĞ KRRAALSQEADFYGAMDGASKFVKĞDĞ KRRAALSQEADFYGAMDGASKFVKĞDĞ ASTFTILTIGDĞLVĞQIPALINTATĞIVA TRTTQNEEDFASKLITQLTNKSKTLVI VĞAILLLFATIPĞLPTFSIAFVĞTLFIA WLISREĞKDĞLLTKLENYLSQKFĞLDL SEKPHSSKIKPHTPTTRAKTQEELKRE EĞQAIDEVLKIEFLELALĞYQLISLADMK QĞĞDLLERIRĞIRKKIASDYĞELMPQIR İRDNLQLPPTHYEKLKĞIVIĞEĞMVMP DALWIETKNKEEAIIQĞYTIIDPSTVIATH TSELVKKYAEDFITKD	2606 YFLKAPILGFEHINEVRI,EKIDSLFSRLIS QTNSPMALDMVLVNPYCLREYSFVIPK YIELLLELDSHSKVEVY;CVVVLQKNLED SMVNFLAPLVFNSKNGFGAQVALSMM DYPDFGFRDPLKSFVIQERERA	2608 SSGTTCSGWLINLLGAIPTNGVSDTNN LINLLTEFIKTAGFIONNDSSVSTSLTSA FOAITSAISOGFOALONDISPNAILTLO EITSNTTTIQSFSQTLROLLGDKTFFMA QQKLIDAM	2610 MIFDVKAPILGFE I IHKIMKLUNDERFLY LINSTEENSVVSFILVNPFALRKYEFEV PTPLKILLELEGAKSVLVANIMVVQTPIE LSTVNYLAPLIFNLDKCILMGOVVLDSN KYPHYHLRENILSHTHE
2604	260	. 260	261
2603 CGCAAGGCTATAAAGGGCCTAGTGCGGTGAGCGATATTATCACGGCGTTTGGGGAATTTAGCGTGAGGGGGAATTA TGTGATTGGGGCGATTTCTTTAGTATTTTAGTGCTAGTGAATCTATTAGTGGCTCTACTAGGGTTACT TGTGATTGGGGCGCCGATTTGCTATTGCTATGCCGGAAATGGCGATTTAATGGCTCTACTAGGGTTACT TGTGATGGGGCGCCGCAAAAAACGGCGCGCCGCGGAAAGCCGAATTGATGCGGATTTTATGGCGCATTGGCGGATTTTATGGCGCTCAAAAGCGGCGCCGCTCTAACCCATTTATGGCGCAAATTCGCAAAAACGGCGCGCCCCTCTAACCCATTCAACGGGATTTTAGT GGCGCAAATTCGTCAAAGGCGATGCGAT	2605 ATTACTITITAAAAGCCCCTAITITAGGATTIGAGCATATTAACGAAGTGCGTTTGGAAAAAATTGATTCCTTATTCAG CGGATTAATTAGCCAAACCCAATTCCCCCATGGCGTTGGATATCGTTTTAGTGAAAAAATTGTTGAGGGAATACAG CCGATTAATTAGCCAAACCAATTCCCGCGTTGGAATTCCCATTCCAAAGTGGAGGTGTATTGCGTGGTCGT GTTGCCAAAAAAAATTTAGAAGATTCTTGGTTAATTCTTAGCCCCTTTAGTGCTTTGAAAAAATGGCTTTGGCGTCGT GTTGCAAAAAAAATTTAGCAGATTATCCGGATTTTTTTGGCTTTAGGGGGGGG	CACCAAACAA Z807 GTAGTAGTAGTACTTGCTCCGGTTGGCTTATCAACCTTTTAGGGGCCAATCCCCACCAATGGAGTGAGCGATACG Z807 GTAGTAGTTAATTAATTAATTACTGAATTCATTAAAACCGCCGGGTTTATCCAAAATAATTAAT	2609 TATGATTITTGATGTGAAAGCGCCTATTTTGGGGTTTGAAACCATTCATAAAATGCGTTTGCAAAAGATTGATGAAATC TITTTGCGTTTGAATAGCACAGAAGAAGAATTCCGTGGTGTCTTTCACGCTGGTCAATCCCTTTGCCTTTAGAAATAC TTTTTGCGTTTGAAGTGCCTACCCCTTTAAAAATCCTTTTAGAATTAGAGGGAGCCAAGAGCGTTCTAGTCGCTAATATCATG GAATTTGAAGCCCCATTGAGCTTTCCACCGTGAATTATTTAGCCCCTTTAATTTTCAATTTGGACAAGCAGCCACTCATG GGGCAAGTGGTTTTGGATTCTAACAAATACCCACACTACCATTTAAGAGAGAATATTCTAAGCCACACGCATGAATGA
HP0249	HP0249	HP0249	HP0249

	•
•	•
•	•
*	٠

VO 02/066501	11-1-60	4111		CT/EP01/15428_
2612 DACGFIYEISEFMKAYTALLKKODRYVYOLLIRYLPSRYWASILTTALYVKYPDFDALGOKKLLVSYYYOTWIAGGTITRIKOTSINIIKONKSNKSVYHSKWVRPVLALANYFNGADERPHFIAMDAETOVEHILPOTPKR GSOWNADFDKEKREEWVNNIANLTLKRKKNAHALNGDFDEKRKIYGGKDTSKYISCYDITKELYSNYRKWNEKSLQERYKSLYNTITPVLHIEGO	2614 LKNAFLQTALTLDAKTLATKALVRDSŇL ISAKAQAMPIVLQLHALYNEENNYTQYL LSVMLPCMWLIFIAIGMLNFIQKASNMR ELLISIVANVCVFSFWGMGMAFYFNLIG MEGHYAHL	2616 LCALFILEERIKANAKEVVQALQNKGLE LEILSGDNESSVKECAKKLGISNYHAHL TPEDKAQTISSYKGVCAMVGDGNNDA LALKQASVSLGFEKSALSKSACDILLE EDLSLLKKAFDNAQKVYQVVLQNIVLSL YNAILIPVAMLGYINPLIASLSMSASSLL	2618 KETNEKLSLÖMDEFLÖDLÖLSGERNÜD LEEVVGVNRPEEEKEEGNFSSRLÖVA GITGLOKSFIMRLIPNDYPLESYRRVSA AFNKRIHPILHVLHNHTGLDLSTAINTPV YASASGVVGLASKGWNGGYGNLIKVF HPFGFKYYAHLINKIVVKTGEFVKKGQ LIGYSGNTGMSTGPHLHYEVRFLDÖPI NPMSFTKWNMKDFEEVFNKERSIRWQ SLITIINRLMQKQDQRLSSLKAQK	2620 LIRIRVRYYLGGN
2811 AAGACGCTTGCGGGTTCATGAGATCAGCGAGTTCATGAAAGCCTATACCGCATTGCTAAAAAAAA	2813 GCTCAAAAACGCCTTTACAAACCGCTTTGACTTTAGACGCTAAAACCTTAGCCACCAAAGCTTTAGTGCGAGATTC CAATTTCAAAAACGCCTAAAGCCAAGCC	2815 CTTTATGCGCGTTATTCATTTTAGAAGGCGTTTGAAAGGCTAACGCTAAAGGAGTCGTTCAGGCTTTACAAAAAAAA	2617 AAAAGAGACGAATGAAAAGCTTTCCTTGCAAATGGATGAATTTTTAGACGATTTGCAGCCTTTCAGGGGAACGCATCAA CGATTTAGAAGAATGAAAAAAAAAA	2619 CCTCATTCGCATCAGAGTGCGTTATTACTTAGGGGGCAATTAAAAATGGAAATCACGCTTTTTGACCCCATAGACGC CCACTTGCATGTGCGAGAAACGCACTTTTAAAAGCGGTGTTAGGATATTCTAGCGAGCCTTTTAGTGCTGCAGTGA TCATGCCTAATCTCAGTAAGCCCTTGATTGACTCCAACCCCTTGAATACGAAGAAATTTTAAACCATTCTT CAAACTTCAAGCCTCTAATGAGTTTCAATGACTTCAATGGCTTGACTTTAGAAGAATTGCAATGCGCAAAAGAAAAG GCGTCAGGTTTTAAAGCTCTACCCCAAAGGCATGACCTGACTTTAGAAGGCGCATTTGTTGGGGTGAA AAAACTTTAGAGGTTTTAGAAAACGCCCAAAAGGCATAGGCTTTATTTTTGTTGGGTTTTGTTGGTGAA
HP0249	HP0249	HP0249	HP0249	HP0591

W	O	02/	О6	65	50:
	1_			S	m

Q 02/066501		PCT/EP01/15428
2622 INNLLYLHGNFNATNIFLTNIAFNYGNPN O AGGGATINFNADETLNADGLNYTNFQT 80 VALGLQTSASQHSWANFNSKLSMEIK O VALGLQTSASQHSWANFNSKLSMEIK O NSNFRDFTWGGFNFNSGRITFENTTFS GWTNINGATESGSSYVNMVANTDLIFS G NSILGGGRYDLKANNIFNNSYLSWFNA AINIGDSQTQTALENASSLSFYNNSVA AFNGTTAFNGVSYLNLNPNAQVSFNQ VNFNNNANVTFYGIPLFGKTPDFGNSAR LINFKGNTNFNOATLNLRAKNIHINFQG VSTFKQNSTMNLAESSQASFNALKYF GETNFNLNNSSLLNFNSDASFDLSNNS TLNFKGNTNFNSDASFDLSNNS TLNFKGNTNFNSDASFDLSNNS TNNFGSKGILNLSYMNLFGGBKKTS VYDVLQAQNIDGLMGNNGYEKIRFYGI QIDKADYSFOSKGILNLSYMNLFGGBKKTS VYDVLQAQNIDGLMGNNGYEKIRFYGI QIDKADYSFOSKGILNLSYMNLFGGBKKTS VYDVLQAQNIDGLMGNNGYEKIRFYGI QIDKADYSFOSKGILNLSYMNLFGTITETLHNNRLKVQISQNGVSNNKMFNL APSLYDYOKNPYNETENSDKV GTYYLTSNIKGFNONNKTPGTYNAON	QPLQA 2624 GAFAKMLLREIGIVCESGIIEIGGIKAKN YDFNHALKSEIFALDEEQEEAQKTAIQN AIKNHDSIGGVALIRARSIKTIVOKLPIGL GQGLYAKLDAKIAEAMMGLINGVKAVEI GKGVESSLLKGSEYNDLMDJKGFLSN RSGGVLGGMSNGEEINRVHFKPTPSI FQPQRTIDINGNECECLLKGRHDPCIAI RGSVVCESLLALVLADMVLLNLT 2626 RLKEKIANAKVLCAVSGGVÖSTVVÁTL	LHRAIKDNLIAVFVDHGLLRKNEKERVO AMFKDLKIPLNTIDAKEVF 2628 NNARERIKVGGLPTFKFGAKINAKEEO YKODERLNERLREFAETLIESVRKKLO KLGDYENIEKILDLEEALRRY'SSPISEL EFLKEIEKNESFF 6FLKEIEKNESFF 7725
ស៊ី	262	262
TAACGCTGGCGTGGGCGACGATTAATTTTAACGCTGTGATGAATTTAATTTTAATTTTAATTTCAACGCTTTGAACGCTTTCAACGCTTTCAACGCTTTCAACGCTTTCAACGCTTTCAACGCTTTCAACGCTTTCAACGCTTTCAACGCTTTCAACGCTTTCAACGCTTTCAACGCTTTCAACGCTTTCAACGCTTTCAACGCTTTCAACGCTTTCAATTTTAGCGGCTTTCAATTTTGAATTTCAATTTCAATTTCAATTTCAATTTTGAACGCTTTCAATTTTGAACGCTTTCAATTTTGAACGCTTTCAATTTTGAACGCTTTCAATTTTGAATTTCAATTTCAATTTTCAATTTCAATAATTTCAATAAT	2623 CTGGGGCGTTGCTAAAATGCTTTTAAGAGAAATCGGTATTGTTGTGAAAGCGGGATTATAGGAAATTGGGGGTATTA AAGCCAAAAATTATCATTTTAATCACGCCTTAAAAAGCGAGATTTTTGCCCCTAGATGAAGAACAAGAAGCGCAAA AAGCAGCCATTCAAAAACCACGCTTAGGCTAAGGGGGTGTGGCTTTGATTAGAGCGAGAGCGCAAA ACCAATCAAAAGCCTATCGAAAACCACGGATAGCGATAGGGGTGTGGCTTTGATTAGAGCGAGGGGAGCATAAA ACCAATCAAAAGCGCTTAGGTTAAGGCCATAGGCAAAATTAGAAAATCGCTGAAGCGATGAT GGGGTTAATGGGGTGAAAGGGGTTGAAATAGGCAAGGGGGTTTTATAAAAGGCTCAAAATGGCAAGAAA GGGGCTTAATGGAAAAGGGGTTTTTGAAGCCAAGCATTTTTCCAACCTCAACGGGGCATGAGAAAAAAAA	ABANAGGG I GCAAGCGATGATTAAGGACTTGAAAATCCCTTTAAACAGGAGGCTAAAGAAGTCTTT 2627 CTAACAATGGCGTGAGCGGGATTGCCCACTTTTAAATTTGGTGCTAAAAAAAA
	нРо591 НР0368	нР0368

_	-
7	Г
	>

VO 02/066501	-	•	Pe	CT/EP01/15428
2630 SAFKNLKLQLKRREIINRYVSQALGDLK O KGFRYAKVEHQILKIYFTHPSYLKAFKIE® EAYYTNHLKAHLKETGKTLKALDYPFD Ø FKTIQASVKKRAYGKPVVKKEKPPKSV Ø NVNCEGLSDFTKKGFLKLKRACNDNTL® RTPP	2632 DPYKAFLSAVKVMSKOLGVFGERPIAN TEYSGDYAORDDAKOLSAKIESMNLSA RCFNCLDKIGIKYVGELVLMSEEELKG VKNMGKKSYDEIAEKLNDLGYPVGTEL SPEQRESLKKRLEKLEDKGGND	2634 AYKNHRAYNTIELKDEVARLAKLALTK MMELS	2636 KOHRPIVFYTDNDCDGMLAGS 2638 ISDRAKNKMAKSNLRLVVSIAKRFTSR GLPFLDLIQEGNIGLMKAVDKFEHEKG FKFSTYATWWIKQAISRAIADQARTIRIP IHMIDTINRINKVMRKHIQENGKEPDLE VVAEEVGLSLDKVKNVIKVTKEP	V 21 22 V 21 13 720
2629 CGTCTGCGTTTAAAAAATTTAAAAACTTCCAACACATTTAAAAACGGTTTAAAAGGGTTTAGATACGCTAAAGAGGGTTTAGATACGCTAAAGAGGGTTTAGATACGCTATACACCCTTGATTTTAAGACTTTACACCCTTTGATTTTAAGACTTTCAAAAACCCCCTAAAAACCCCTTGAAAAACCCCTTGAAAAACCCCTGAAATAGTGAGCAGTCTACGCCGCCCCTCAGAGCTGAAAAACCCCTCAGAGCTTCAAAATTTTTCAAAATTTCTTAAAGACTTCAAAATTTTCAAAAATTTTCAAAAATTTCAAAAATTTTCAAAAATTTTCAAAAATTTTCAAAAATTTTCAAAAATTTTCAAAAATTTTTCAAAAAA		2633 GGCTTACAAAAACCACAGGGCTTACAATAC CTAAAATGATGGAGTTTT TTTGTTTGAAAGGGTGTTAGAAAAGATTTT TTTGTTTG	2637 GATITCCGATCCGCCCTATIGITICIATAGATAATGATTGTGATGGCATGTTAGCTGGCAGCGT 2637 GATITCCGATCGCAAAAAACAAATGGCTAAATGCAATTTAAGGTTGGTGAGCATCGCTAAACGATTCACGA GCAGAGGCTTACCATTCTTGGATTTCAACAGGCCAATATTGGCTTGATGAAAGCGGTGGATAAGTTTGACGAT GAAAAGGGCTTCAAGTTTTCTACCTATGCGACCTGGTGGATCAACAAGCTATCAGCAAAGGCCATAGCCGATCAGGC CCGCACTATCCGCATTCTACCTATGCGACCTTGGTTGATCAAAAACGCTATCAGCAAACAGCCATAGCCGATCAAGACGC AAACGGCACTATCCGCATTCACATGATGATTGATAATCGCATCAATAAAAGTCAAAAAGTCAAAAAGACCAAAAAAGACCAAAAAAGACCAAAAAAAA	
HP0368	110308	HP0368	HP0005	

vv		U2/			
	I.	<u> </u>	_ 1	တ	11

02/066501			PCT/EP01/15428
	2642 KRIISEIDKQPKAKKEAKFIELANKU ID PNSKNAQNGGDLGKFOKNUMAPDFS KAAFALTPGDYTKTPVKTEFGYHIYLIS KDSPVTYTYEQAKPTIKGMI.QEKLFQE RMNQRIEELRKHAKIVINK	2644 LYGGACANLLHKNSGI IIDI 35953 EC ALIEKGKIKDLISLDVGTIRIK EMFLDKDL EVKLAKAFIQKEVSKLPFKHKNAFGVG GTIRALSKVLMKRFCYPIDSLHGYEIDA HKNLAFIEKIVMLKEDQLRLLGVNEERL DSIRSGALILSVVLEHLKTSI MITSGVG VREGVFLSDLLRHHYHKFPPNINPSLIS LKDRFLPHEKHSQKVKKECVKLFALS PLHKIDEKYLFHLKIAGELASMGKILSVY LAHKHS	2646 I A I I I I I I I I I I I I I I I I I
2639 CTTACATGAGGACCGATAGCTTGAATATC GCAAAGACTATTTACCCCCTAAAGCCAAAA AGGCCCACTTCTATTATTTTAGAGCCCAAAC AGGCCCACTTCTATTATTTTAGAGCCCAAAC TTTACAAACGCTTTTTAGCTTCTCAAATGC GCGAGTTTAAAAGCGAGTGGGAGAAAGCCCC TGCTCCCCAATTTGAAAGAAAATGACCCC CACGCTATTCTGAAGCGAGCTTGATTAAA ATTCCCTTTTAGAAAGCGAGCTTGATTAAAA ATAGAAATTTTAGAAAAGCGACTTCGAGAA TCGCTCAAAATAAAAGGCGACTACCAGCAA AAAAAAAATGCCGTTATGGGGAGTTTATGCTT AAAATAGCCGTTATGGGGAGTTTATGCGT AAAATGCCGTTATGGGGAGTTTTAGCGAAA TTAGCTTGCAA			2645 AACCGCGACACCGCGAGAGACGCGTAACGATCACCACTATAATAATAATAAGAAAGCCGCGTCAAATTTGACAAATTTGACAAATTTGACGTCGTCGTTAATTTGACGCGCGTTAGTGCTTTAATTCGCGGCATGCCGTTTAGTGCTTCCCCGGCAATGCCTTTAGTGCGTTCCACGGAATACGAAAACACTCCAGGGGGTGGTCAACCATCGGGGATTTAGCCGCGTTTAGTGCTTTCCACACAACACACAC
HP0005	HP0005	HP0005	HP0005

١	•	>
e	=	Ś
ì	=	Ξ
-	v	Г

VO 02/066501	1 02 \$0~ _ ww. 4	>××	МΩ M X II
2648 KAVQTTLTFETPFNKTPKIMEVEGOKVJ O VLKNAKLDSKKTMDFKEASLNALEMFSØ YQNDIYLLSKKAKVELEIQASNSKDKKFØ LRFLFLPKGFHLAPPPNLKEKSQÖTNL SAKAKTOTNEQPQSPLNTLELKPPLNLSHAGE	2650 TNSFNKNPHLMRMWSLDDVFNQSELQ AWLQRILKAYPSASFVCSPKLDGVSLN LLYQHGKLVKATTRGNGLEGELVSANA KHIANIPHAIAYNGEIEIRGEVIISKKDFD ALNGERLMANEPLFANPRNAASGSLR QLDSEITKKRKLQFIPWGVGKHSLNFL SFKECLDFIVSLGFSAIQYLSLNKNHQE IEDNYHTLIREREGFFALLDGMVIVVNE LNIQKELGYTQKSPKFACAYKFPALEK HTKIVGVINQVGRSGAITPVALLEPVEIA	GAMINRATLHNYSEIEKKNIMI.SDRVVV IRSGDVIPKIIKPLESYRDGSQHKIERPK VCPICSHELLCEEIFTYCONLNCPARLK ESLIHFASKDALNIOGLGDKVIEQLFEE KLIFNALDLYALKLEDLMRLDKFKIKKA ONLLDAILKSKNPPLW	2652 TFRIEKGHIKHRKÄKELVFSVHLTDDLK RRDFSMNAJAYSPTKGLIDPFKGONAIE NOMIECVGEARLRFFEDALRILRSLRFS ATLGFKIAPNTKEAVFACKDLLKHLSKE RLOSELNKLLMGKNAYEVAKEYGEILE LVIOEKIENLGFLKNAPFNLELRLGFFK HOKSLESLRYPKKTTVLFSKAKECHKSF LNIHNKTELKFLLKNYDLEPFNLALDFY ALKNPKHALKIKGLLKEIFDSNEPFKKE HLALKGGALGSLGYQHOKIGEILNACL
26	26		26
2647 AAAAGCCGTGCAAACCACGCTCACTTTTGAAACGAAAACGCCTAAAATTTAAAGAAGCCTTTTGAAGGGCCAAA AGGTGATCGTCTTAAAAAACGCTAAACTGGATTCTAAAAAAAA	2649 CACCAATTCGTTCAATAAAAACCCCCATTTAAAAGCCTTTAAAAACCCTAGGGGGGGG	ACACAATTATTCTGAAATTGAAAAAAGAATATCATGCTGCTCAGTGATAGGGTCGTTGTCATTAGAAGGGGGGGCCTT CCCTAAAATCATCAGAGCTTTAGAATCTTATAGAGCGGCTCGCCAACATAAAATTGAAGGCCCCAAGGTTTGCCCTAT	2651 CAACTITTAGAATTGAAAGGGGCATATCAAACAGGAAGCCTAAAGGATTTTTAGCGTTCATTTAACAGGACGATTTAAAGAGGGATTAACAGGACGATTTAAAGATTGAATTAAGGTTTTTT
HP0005	HP0005		HP0005

•	٠
U	٦
-	-
•	

O 02/066501				PCT/EP01/15428
2654 STEDLQITLEFLKEYEDEAITRLKELLKS PNFTQNALEKVKTQML AALLGKESDFD YLAKLTLKQELFANTPLANAALGTKES) YLAKLTLKQELFANTPLANAALGTKES) QKIKLDDLKQQFAKVFIELNKLVVVLGG DLKIDQTLKRLNNALNF'LPQGKAYEEP YFETSDKKSEKVLYKD TEQAFVYFGAP FKIKDLKQDLAKSKVMIAFVLGGGFGS RLMEKIRVQEGLAYSVYIRSNFSKVAH FASGYLQTKLSTQTKSVALVKKIVKEFI EKGMTQQELDDAKKFILGSEPLRNETI SSRLNTTYNYFYLGLPINFNQTLLNQIQ KMSLKEINDFIKAHTEINDLTFAIVSNKK KDK	DETLIPSLROKLEILES JSFLEKANYO MIGMDHFAKSDNELYLALQKAEL	58 EENRFKDSGYLKEKLKEAKDLIDALNL RKATIYKIGLMLLEYQYDFFKGKELRPL KLLDLANEFNHSVSTISRAISNKYLACE RGVFPIKHFFSIALDNSETSNAVIKDYLL ELIKNEDKKEPLSDAK!' ELIEEKFHLKM VRRTITKYRQLLNIASSSERKRLYLMRA		2662 FSNAKDKESASEALNWARAEINTURT NNAKYLDKVVOSNPDYISTHSESALDL LKLLKKNOMNASAIEIAHLLNODDDLK AKEQALYDLGALYARIKDFKNAHLYNL QYLQDHAELDKASVVIRARDEKALFSN EGNTOEKAHYDKIIQNIFPNSNEALKAL ELKAQLLFENKRYAEVLSMQKNLPKDS PLIOKTLNVLAKTPLENIHRCEEALKYLS QITTFEFSPKEEIQAFDCLYFASLKEKA QIIALNAFKTAKAPSEKLIWLYRLGRNY YRLGDFKNS
265	22	2658	266	26
2653 CCAGCACAGAGGATTTGCAAATCACTTTAGAATTTTTAAAAGGAATACGAAGATGAAGGCCATTACGCCGCTTTAAAATCCCCTAAAAGGACCTTTAAAATCCCCTAAATTTCACCGCAAACCCTTTAGAAACCCCAAATGTTAGCCACTTTTACAAAAGAAAG	2655 GGGTTTTGAAACTGGATCCGGACCGATTAGCGGTGTTTAATTACGCGCATGTGCCTTGGGTGAAAAAACGATGTGCGT AAAATTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2657 GGAAGAAATCGCTTTAAGGGTAGCGGCTATTTAAAAGAAAATTAAAAGAGGCTAAAGGATTTGATTGA	2659 GTTTGGAAAAACCTGATTTGAAGGAGTTGGAGGAATACTACCATAAAAACAAGGTGTCTTATTTGGACAAAGAGGGGGGGAATTGCAGAAAAACAAAACCAAGAGGGGGGGG	2661 CTTTTCTAACGCCAAAGAGAGTGCGAGTGAAATCGCGCTTAATTGGGCTGAAGCAGAGATCAA AATTTTAATAACGCTAAATACCTCATTGAAAAAGGTGGTGGATCCAATCCAACCTGATTATTTTTACGCGTTGCTGCAATCAA AATTTTAATAACGCTAAATACCTCATTGAAAAAAAACCAGATGCAATCCAACCCTGATTGAGGTCGCTTGCTCCCTCAATC CCCTAGACTTGCTCAAAGCTAAAGAGCAGCGCTTTATGATTAGGAGCGTTGTATGCAGGACTTAAAA ACGCCCACCTTTACAATCTGCAATATTGCAGGACAAAAAATGCGCCAGTAAGAGCGTTAGGGCGCGGT GAAAAAGCCCTTTACCATGGAATATTGCAGGAAAAAAAAA
HP0005	HP0005	HP0005	HP0005	HP0005

D/	CIT	/FDA1	/15428

 _	P	CTA	EP0	1/15	428	
			_			
 ~					1	

O 02/066501———			PCT/EP01/1
2674 KGLLTKLKATAGRNNNGRITSRHKERGOAKKLYRIIDFKRNKYNIEGKVAAIEYDPYOAKKLYRIIDFKRNKYNIEGKVAAIEYDPYOBNARIALVVYPDGDKRYILQPSGLKVGONGSVIAAEGGLDIKVGFAMKLKNIPIGTV SOWINIEMHPGAGGQLARSAGMSAQIMGSOKNYTIIRMPSSEMRYILSECMASVGUNGSAMPYTIIRMPSSEMRYILSECMASVGUNGSAMPYTIIRMPSSEMRYILSECMASVGUNGSAMPYTIIRMPSSEMRYILSECMASVGUNGSAMPYDHPGGGEGKTGTSGHPVSPAKGYKTRKKKASDKLIISRKKKHK	2676 KKDACGFIYEISEFMKAYTALLKKQDRY VYLLRYLPSRYWASIL TALYVKYPDFD ALKKLLVSYYYQTWIAGGTITRIKQTSIN IIKNVKSNKSVETIKELII NSIDSYNTFDQ YLYNLWDSSSVYHSKWYRPVLALANY FMADEEKPHFIAMDAETQVEHILPQTP KRGSQWNADFDKEKREEWVNNIANLT LLKRKKNAHALNGDFDEKRKIYGGKDT SKVISCYDITKELYSNYRKW	ZGŤB IDTKALEAFGVNAGFLSJMPNALKKMN KEEEWKRLVKRFDVNYOFIPIIKNMLIE ASVPQEFLFLAMAESKI-SSRAYSRKKA VGIWQFMPSTAKELGLKVNHYIDERRD PIKSTQAAITYLKRLYKOTGEWYLVAM AYNYGLRKYQNAIKAAGTSDIKILDED KKYLPKETREYIRSILSIALKFNSLDNLK DKEYLLNRGARYSLVGVPFKRRASLV QVAKNLNLSLETLKSYNHQFRYNILPS KDTYTYIPYEKLALFKQRQIKQNKNIQ ASSKSPFITHVVLPKETLSSIAKRYQVSI SNIQLANDLKDSNIFIHGRLIIPTNKKLLA TREF	2680 KKIRFPESSGIGVKPISKEGTERLVRKAI EYAIDNDKPSVTFVHKGNIMKYTEGAF MKWGYALAQKEFNAQVIDKGPWCSLK NPKNGKEIIIKDMIADAFLQQILLRPSEY SVIATMNLNGDYISDALAAMVGGIGIAP GANLN
			0,4
2873 CAAAGGCTTACTCACTAAAGCAACAGCAGGAGAAACAATAACGGGCCGTTCACCAGCCGCCCCAAAGAG AGAGGGCTTACTCATCGCATTATTGATTTCAAGCGCATTAATTGAATATTGAATATTGAAGGGAAAGGCGACCAAAGGCGTT GAAGGGGCTTACAGAAATGCGCGTTATTGATTTCAAGCCCAATAATTGAAGGGCAAAAGGCTATATTTACAGCC AAGCGGTTTGAAAGGGCCGATAGCGTTATCGCTGCTGAAGGCGTTTGCGATTTAAAAGTGGGCCTTTGCGATGAAG TTAAAAAATATCCCCATAGGAACGGTGGTGCATAATATTGAAATGCATCCAGGGGCTTTGCGATGAAG TTAAAAATATCCCCATAGGAACGGTGGTGCATAATATTGAAATGCATCCAGGGGCTGGCGGCGCATTAGCCAGAAG CGCAGGAATGATCGTGGGTTGGCTGGTAAATAATACACCATTATTAGGATGCCCAAATGCCCTGAATGCCCCAAATGCCCCCAAATGCCCCCCAAACGCGCTGGTTGGCTGGTTGGCTGGTTGGCTGGTTGGCGTAGGCGATGGTTTTATACAATGTCTTATCGGTAAGGCATGGTAGGCCAAGGCGTAGAAGCCAAGGCGATGGTTGGCTCAAGCGCATGGTTAGAAACGCAAGGCACAAGCCGCATGGT GGGGGTGAGGGCTCAACCTCTTTCCAGAAGCATCATTGCCCTTAAAGGCTTAAAAGGATTAAAAGGCTAAAAACCGTTAAAAACCTTAAAAAAAA	2675 GCAAAAAAGACGCTTGCGGGGTTCATCATGAGATCAGCGAGTTCATGAAAAGCCTATACCGCATTGCTAAAAAACAAA GACCGATACGTCTATTTATGAGATCTCCCCTCTAGGTATTGGGCCAGCATTTTAACGACTGCCCTTTATGTCAAA TACCCTGATTTTGACGCTTTGAAAAAGCTTTTGGTGTCTATTATTACCAAACTTTGGATTGCAGGGGGCGGTCACG TACCCTGATTTTGACACCTTTTGGTGTTTTAAAAAGCATTATAGGAGCGTTGGAACCATCAAGGGTTATA TTGAATAGCATCGACTCTTATAACACCTTTGATCAATACCTCTATAACTTATGGGATGGCTTCTTTTTTTT	TGACACCAAAGCGCTAGAGGCTTTTGGGGTTAATGCGGGCTTTTTATCCCAAATGCCGAACGCTTTAAAAAAATGA ATAAAGAAGCAGAGCGTTTTGGGGGTTAATGCGGAGTTCATGCCCAATGCTTTAAAAAACATGC TCATAGAAGAAGAATGGAAGAATTTTTTTTTT	2679 TTAAAAAAATCCGCTTCCCTGAAAGCAGCGGCATAGGGGTAAAACCCCATCAGTAAAGAAGGCACAGAGAGGCCTAGT GAGAAAGGCGATTGAAATACGCAATTGATAACGACAAGCCAAGCGTGACTTTTGTGCATAAAGGTAACATGAAAT ACACCGAAGGGGCGTTCATGAAATGGGGCTATGCGCTCGCT
2673	2675 GCA GACC TACC TTGA TTGA AATG CCCGA AAAA AAA	2877 TGAC ATAA ATAA TCAT GGAV GGATG ACAT ACAT TCGC GTGC GGTC CTCAATG	2679 TTAA GAGA ACAC CCAT CAAA GGGG
HP0247	HP0247	HP0247	HP1411

	_
	_
Ξ	_
•	7
٠,	ď

/O 02/066	5501		PCT/EP01/15428
2682 OKEALALIIVDEEVSLEVLEELKNIPACL SVHYVVI	2684 DLKKVCEKIKSALPFGIISAFKPFKDAFY RDFNHNEGKLLIGAAKSGCIGSSADKL AQLKTRLLYWODKSVKVDWDKPILIKD FFKGNNYLYRRFCFLLGKHFMDRFLKN NAKASVKDFMSSKEFVAKYRYTPKQN TERAKKLQSYLENKRDFIGFVQALNSL KDNPQDPFLPNEETSFLVFANEPTIVF NLRDYLLVLAGIFNQAGYCESKCPIE LINASPGKDFNKTQDSFPDIKFSTPNQL EQSLNALKNKLAAFFSKH 2686 PEAAKNALMERFTLSEIQSKAILEMRLG	RLTGLERDKIKEEYGNILLELIDDINGILK SEDRLNGVVKTELLEVKEGFSSPRTE IGESYENIDIEDLIANEPMVVSMSYKGY VKRVDLKAYEKONRGGKGKLSGSTYE DDFIENFFVANTHDILLFITNKGGLYHLK VYKIPEASRIAMGKAIVNLISLAPDEKIM ATLSTKDFSDERSLAFFTKNGVVKRTN LSEFESNRSCGIRAIVLDEGDELVSAKV VDKNAKHLLIASHLGIFIKFPLEEVREIG RTTRGVIGIKLNENDFVVGAVVISDDGN KLLSVSENGLGKOTLAEAYR	2688 YLKASISLELSNEKLLNEVKVKÖTAIKOT IIEILSSKSVEEVVTNKGKNKLKDEIKSH LNSFLIDGFIKNVFFTDFIIQ
2881 GCAAAAAGAAGCCCTAGCACTCATTATTGTAGATGAAGAAGTTTCTTTGGAAGTTTTAGAAGAGCTTAAAAACATTCC TGCGTGCTTAAAGCGTTGTTTAAAGGTAGTTGTTTTAAAAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGA	2683 GCGATCTTAAAAAGGTGTGTGAGAAAATCAAAAGCGCACTACCCTTTGGGATCTCCAGCCTTTAAAAGCATCTAAAAGCATTCTAAAAGCGGTTGATTCTAAAGGCGTTGATTCTAAAGGCGTTGATTCTAAAGGCGGTTGATTCTAAAGGCGGTTGATTCTAAAGGCGGTTGATTCTAAAGGCGGTTGATTCTAAAGGCGGTTGATTAAAGGCGGTTGATTAAAGGCGGTTAAAAGGCGATTGATT	CGTT I I GCAACGC I I AACAGGCCTT GAAAGGGATAAGATCAAAGATACCAAAACTTGTTGGAGCTTATTGATGATGATGATGATGATGATGATGATGATGATGA	2687 CTACCTTAAGGCTTCTATTTCGTTAGAATTGAGTAATGAAAGCTTTTTGAATGAA
HP1411	HP1411		HP141

_
_
∀

VO 02/066501	T	PCT/EP01/15428
2690 SKSKGNVVSLDKLLKTHGSDVVRLWV AFNDYQNDLRVSQTFFTQTEQHYKKF RNTLKFLLANFSDMDLKNLERPHNFSP LDHFMLETLETISAGVN:SAFEEHDFVK GLNILMAFVTNELSGIYLDACKDSLYCD SKNNEKRQAIQMVLLATASKLCYFLAPI LTHTIEFVLEHSQALRIFLQAKDVFDLK DISVSEKLHLKEFKKPENFEAVLALRSA FNEELDRLK	2692 EKRIFMLLCAGRNETLK KAVPIGVGLIE SAINLTRMCLKNPDTESLIFIGSAGSYS PEMELLSVFESVCGYGIEESFSHLNYI TPLDNFHIETEEQALFERVRNNSNYI HTSEMFAKKMYOKGVLLENMEFFSVL SVAKAFSLKAKGIFCVSNYVGLNAYQE FKENHAKVKQILENIIDSLII	2694 GEVLEIVALIAYLNSLGNISRINANGNAK 2696 EVKTAFKIADVEYVKDSTKLNFNYLKDL KDENNOPLSONIL TONVARYYLIVYNG EIKKIGGSOADGGIKSTLAIYKDGGVKG RPNIRSFGVWYFLYHTILTGAKIEFYMI YOPNFETOVKGLFGFCAIKDASISYKLL EGACLTDYRNNSNDALPEWNVOEQG KD
		TI GEGAATTGTGGCTTTTGAATGCTTGGTAATTCCAGGATCAGCCCAATCAAAGGGATGGGTGAATTGTGGGTTTTTTACCATTCTTTTTACAAGGGATACTGGGTTTTTTACCATTCTTTTTACCATTCTTTTTACGGTTACTGGGTTTTTACCATTCTTTTTACGGTTACTGGTTTTTACCATTCTTTTTACGGTTACTGGTTTTTACGGTTACTGGTTTTTACGGTTACTGGTTTTTACGGATACTGGATACTGGATACTGGATACTGGATACTGGATACTGGATACTGGATACTGGATACTGGATACTGGATACTGGATACTGGATACTGGATACTGGATACTGGATACTGGATTTAAACGGAAATTTTAAACGGACAGCAAATTTTTAAACAGGAAATTTTAAAAAAATTCGCCGAAAATTTTTAAAAAAAA
HP1411	HP1411	HP0482

•	٧
•	_

HP0482	2897/AATACGCTGATCCTAGCACTTCTAAAAAGAGCCGATAAGGGGATTAAAAAAGGTGTGTTCAAAGGACAGCAAAAAAGACA	O SEGRIVANDSTSKKRANKEI KKVEKNSKKNA
	GCTTGCGGGTTCATCATGAGATCAGCGAGTTCATGAAAGCCTATACCGCATTGCTAAAAAAAA	CGEIVEISEEMKAYTALLKKODRYVYLL 0
		RYLPSRYWASILTTALYVKYPDFDALK
	GACGCTTTGAAAAAGCTTTTGGTGTCTTATTATTACCAAACTTGGATTGCAGGAGGCACGATCACGCGCATCAAGCA	KLLVSYYYQTWIAGGTITRIKOTSINIIKN
-	AACCAGTATCAACATTATCAAAAACGTTAAAAAGCAATAAGAGCGTTGAAACCATCAAAGAGGCTTATATTGAATAGCAT	VKSNKSVETIKELILNSIDSYNTFDOYLYS
	CGACTCTTATAACACCTTTGATCAATACCTCTATAACTTATGGGATAGCTCTTCTGTTTATCATAGCAAATGGGTGCGT	NLWDSSSVYHSKWVRPVLALANYFMA
	CCTGTCTTAGCCCTAGCTAATTATTCATGGCAGATGAAGAAACCCCATTTTATCGCTATGGATGCCGAAACCCAA	DEEKPHFIAMDAETQVEHILPQTPKRG
	GTGGAGCATATTTGCCACAAACGCCCAAAAGAGGCAGTCAATGGAACGCGGATTTTGACAAAAAAAA	SQWNADFDKEKREEWVNNIANLTLLK
	ATGGGTAAATAATAATGCGGAATTTAACCCTTTTAAAGCGTAAAAAGAACGCGCATGCTTTAAACGGGGGATTTTGATGA	RKKNAHALNGDFDEKRKIYGGKDTSK
	AAAAAGAAAAATTTATGGAGGCAAAGGCAAAGTGATTAGCTGTTATGACATCACTAAAGAATTGTATAGCAA	VISCYDITKELYSNYRKWNEKSLOERY
	TIATAGGAAGTGGAATGAGAAGTCCCTCCAAGAGCGATACAAATCTTTGTATAACACTATCACGCCTGTTTTACACAT	KSLYNTITPVLHIEGOEDDFEDDFD
	AGAGGGCAAGAAGATGATTTTGAAGATGATTTTGATCT	
HP0241	2699 CGAGCGTGAGCGAAGTGTTAGAATTGTGCGATGTTTTAAACCCCGCGCAACATTAAGGGGCGTTTGAATTTGATCGTG	2700 SVSEVLELCDVLNPRNIKGRLNLIVRM
	CGCATGGGTTCTAAGATGATTAAAGAGCGTTTGCCTAAACTTTTACAAGGGGGTGTTGGAAGAAAACGCCGTATTTTA	GSKMIKERLPKLLOGVLEEKRHILWSID
	TGGAGCATTGATCCCATGCCATGGCAACACGGTTAAAACCAGCTTGGGGGGTTAAAAACAAGGGCTFTTGATAGCGTGTT	PMHGNTVKTSLGVKTRAFDSVLDEVK
	AGATGAAGTGAAAAGCTTTTTGAAATCCATAGGGCTGAAGGGAGTTTGGCTTCAGGGGTTCATTTGGAAATGACAG	SFFEIHRAEGSLASGVHLEMTGENVTE
-	GTGAGAATGTTACAGAATGTACGGTGGCTCGCAAGCGATCACCGAAGAGGGGTTTGAGCTGCCATTACTACACGCA	CIGGSOAITEFG! SCHYYTOCOPRI NA
٠.	ATGCGATCCAAGATTAAACGCCCCAAGCCCTAGAACTCGCCTTCTTAATCGCTGACATGCTCAAAAAAACAGCACG	TOALFLAFIJADMI KKOHA
	CTTAGTTAAAAAGAGATTAAATCTTTTTTAACTCTTTTACTTTATAATTATCGTTGGCATTTTAATATTCAAAGGAGCTTG	
	AAATGAGAATTTCTCTTTTAGCTGTAATTTTAGCGTTTGTTT	-
	AAACGAAGCCGATAGCACCCCTTCAGAAAAACCATTTGGCAACCTGAACAAAAATAAAAATTGTAAAAATACTCAAA	
	GGCATTTTTAAAATAAACGCAATAAAAAAGCTAGTGGGTGATAGTTTTTGTAAAGCGATCTTAGGGTTGTAGGGGA	
	ATGATTTCAAAACACCCCCTAACTCTTATGAAGTTTATTATAAAACTAAAACAAAATTTAAAACAACAAGTTTTAAAA	
	GTGAGAGAATGGCTAAAAAATCTCAAATTAAAATGGGCGAAAGTTAGAAAGTTAAACTACAAAACTCTCTAAAACCTTTT	-
	GAGCATGGCCTTTCGCTTTGACATTGTAGAAACATTTTTCTAAAACGCCTTGCGTGTTGATAATGAAGGTGGAGCGG	
	ATAATCCCCA	

13			
_	r	٧	
		-	4

02/066501		PCT/E	P01/15428
2702 QQSDPTTANIANPCALSAQSTNGASSNONASNNAPIALSNNDESLMYAANDFNFS\(\)CONIYANGVVDFSKIKGSANIKNLYLYNN9\(\)CONIYANGVVDFSKIKGSANIKNLYLYNN9\(\)CONIYANGALTISNQAVLEKNASFYTNNL\(\)STEPLIQAEGINLNTTQ**PFMNVNNSMANTTYTLLKSSRYIDYNINPNSLQSYL\(\)NLYTLININGNHIEEKNGALTYLQDY\(\)UNTYTLININGNHIEEKNGALTYLQDY\(\)UNTYTLININGNHIEEKNGALTYLQDY\(\)UNTYTLININGNHIEEKNGALTYLQDY\(\)UNTYTLININGNHIEEKNGALTYLQDY\(\)UNTYTLININGNHIEEKNGALTYLQDY\(\)UNTYTLININGNHIEEKNGALTYLQUY\(\)UNTYNQYKMSCGDKAMLYTLELASYTQ\(\)OTSRLTKLSDFRSREGESDFSLLELKN\(\)KRFSDPNPEVFVKYSQLSKHPNNLWV\(\)QGVGGASFISGGNGTLYGLNAGYDRL\(\)KRNNILGGYVAYGYSDFNGNIMHSLGN\(\)NVDVGMYARAFLKRNE**TLSANETYG\(\)GNATSINSNSLLSVLNQRYNYNTWTT\(\)	SYNGN TG TU-MITICLS/UDEAL ZYNGN TG TU-MITICLS/UDEAL NLGASTKNLIGDKANSPAYQAVELAINA AVGLWNTIGYAVMCGNG)NGTESGPG SVIFNDOPGQDSTOITCHREESTOPG SWSIDEFKKLNEAYQIQ JALKNQSGFP ELGGNGTKVSVNYNYE/SRQTADINGG VYQFCKAKNGSSSSN/3GNGSSTQTT ATTQDGVTITTYNNNI(ATVKFDITNN ACQLLNQAANIMOYLNT QCPLVRSTNN ENTPGGGQPWGLSTSGNACSIFQQEF SQVTSMIKNAQEIIAQSKIVSENAQNQN NLDTGKPFNPYTDASFAQSMLKNAQA QAEMFNLSEQVKKNLEVMKNNNVNE KLAGFGKEEVMTNFVSAFLASCKDGG	AVIENEMHTFFTKLIDGNYPDYGKILPK EVISSFTLGKEEFKESIKI.CSSLSSTIKL TLEKNNALFESLDSEHSI:TAKTSVEIEK	NOTION OF THE STATE OF THE STAT
270	270	2706	2708
CONTRACTOR AND CONTRACTOR CONTRACTOR CONTRACT CONTRACT CONTRACTOR	2703 ITTGAACAACCTTTTAACGAGATACAGCACCCTAAACACCCCTTATCAAATTGTCCGCTGATCCGAGCGCAATTAATGC GGTGCGGGAAAATCTGGGCGCGAGCACGAAGAATTTGATCGGCGATAAAAGCCAACTCCCCGGCGTATCAAGCCGT GTTTTTAGCGATCAACGCGGCGGTAGGGTTGTGGAATACCATCGGCGAACTCCCCGGCGTATCAAGCCGT GTTTTTAGCGATCAACGCGGCGGTGGTGTTGTGGAATACCATCGGCTCATGCGGCAATTACTTGCAACGGGCAACTCCAGGGATCCAGGGAACGGGAACGGGCTATTGCAGGCGGAACGGGCTTTTGAATCAACGGCGGAACTGGCGGAACTGGTGATTACTTGCAGATTCCTGAATTCAAATTCAAATTACAATTACAAAATTACAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAAA	2705 TAGCGGTAATTGAAAACGAAATGCACACTTTTTTCACCAAACTCATTGATGGGAATTACCCTGATTATCAAAAAATCCT CCCTAAAGAATACATTTCTTCTTTCACTTTAGGCAAGGAATTTAAAGAGAGATTTAAAGATTGTGCAGTTCTTTAAGC TCCACCATTAAAACTCACTTTAGAAAAAAAAAA	2707 CGGTGGGCGATGTTTTTGGTGAAAACGGGCTTTTAAACGCGCTAGATCCTACGGAAAGAAA
HP0241	НР0241	HP0241	HP0241

_	•	
_	1	
	-	

WO 02/066501-

02/066501			PCT/EP01/15428_
2710 RFKVPLLKDMLEYLKKVFDKENLDEVL DEEKILHAFIAK	2712 F	2714 AKKPSKPKATPTAKINNKSHKIDFSDAR DFKGNDIYDDETDEILLFDLHEGDNFN KEEEEKEIRGNINDRVRVQRKNPWMN ESGIKRQSKKKRAFRNDNSGKVIQSTT AIPEEVRYYEFAQKANLNLADVI 2716 SSGTTCSGWLINLLGAIPTNGVSDTNN LINLLTEFIKTAGFIGNNDSSVSTSLTSA FQAITSAISQGFQALQNDISPNAILTLQ EITSNTTTIQSFSGTLRQL	2718 LLHAEDNGVFLSVGYQIĞEAVQKVKNA DKVQKLSDTYEQLSRLTNDNGTNSKTTA SAQAINQAVINILNERAKTLAGĞTINSFL AYQATLLARSVLGLWNSMGYAVICG GYTKSPGENINGKDFHYTBENGNGTTI NCGĞSTNSNGTHSSSGTINTLKADKNV SLSIEQYEKIHEAYÖILSKALKQAĞLAPL NSKGEKLEAHVTTS
CTIGGATGAGGATTTTGGAAAGGATATGTTAGAAAGGTTTTTGACAGGAGAATTTAGATGGGTGTTTTTTGACAGGAGAATTTAGATGGGTGTTTTTTTT	2711 TTTGAAACATTTAACCCCACTCACTCACCACCATCTTTAAAGCCTTATGGCTAGGCACAGCCTTAAGTGCACTTTAA GTTTAGCCGCAACAGAAAGCCCCACTAAAACAGACCATTAAAGGCCTTAAAGGGGTTAAAAACAAGCCCCAAATCGCC GTTACTAAAGTCATGAATGACCAATTGCGACAATTTAAAGCCTTAAGGGGTTAAAAACAAAAGCCGC CGTTACTAAAGTCCTAAAGAAAATTTAGGCTATGAAATGGCAGGCA	2713 AGCCAAAAACCCAGTAAGCCCAAAGCCACCCCCAAAAACAAAACAATTTTTTTT	2717 ÁTTGCTCCÁTGCTGAAGACAACGGCGTTTTTTTAAGCGTGGGTTATCAAATCGGTGAAGCGGTTCÁAAAGTGAAAAAAAAAA
HF0241	HP0241	HP0241 HP0241	HP0241

v	7
	-
7	۲

WO 02/066501	× × × × × × × × × × × × × × × × × × ×		PCT/EP01
2720 GTFWRYSIGTLKDMEQNNRIVFNGKN PMAKRYLSEVAEGRKSST FWDGSEVG YNLNGDAEIKQLFNGNKVFNNPKPEAL LORILEISTKENDLVLDFFAGS 2722 GANLSAEPKWYSKAYNKTNTOKGYLY GSGSATSKEASKQKALAD.VASISVVV NSQIHIQKSRYDNKLKSSDSQTINLKTD DLELNNVEIVNGEVQKGYTRVRINGN	GVERTANDATIVAL TO CHEST LIMPROCK GVERTANDATIVAL TO CHEST LIMPROCK GVERTANDATIVAL TO CHEST LIMPROCK GVERTANDATIVAL TO CHEST LIMPROCK SANDY GO CYLGGEN LELLAWEMY AQUI FOLGEN ACTORIANDATIVAL DANIE ALLAWEMY AQUI FOLGEN ACTORIANDATIVAL SINLAME L'ALLANGO SPOVED FRONDY ELLNILLE MIDIO CRAFHIEL GO MASKEN L'Y CATORIANDATIVA CHA TO CH	TNTLDIEDTOLIFIALEEHEEVDWVCSZ 2726 GEAWLKKTFLSMGEKHSLL TTNLEKY QNKILVFDEVKNANDYTLTELKKILKTY LEGKLPLIAGKMGTSYTHFSIRNNAKVL GSCSYHNRL SFALLLVCAQKEAIDYVII HELAHTIHKNHSKNFWRCVGJFCPNYR ALRERLKONTIFYAQLLKTLQP	2728 GLGISFLKHIERTKVLAFVLDASRLDLGI KGQYQRLRLELEKFSSALANKPFGVLL NKCDVVENIDEMTKDFCAFLNLGAQKL NEFGLEPYLGFLHPHLTNDFENNPNEQ SALFVLPLSAVSALNVHALKF·VLLEALP
	2724	2726	2728
2719 GCGGGACTITITGGCGTTATTCAATAGGCACATTAAAAGATATGGAACAAAATAATAGAATAGTTTTTAATGGTAAAAA TCCTATGGCAACCAACCCAATCGTAAAAGTTGCAAAAATTTTTTTT	2723 TGTTCAAAGTGGGTTTGCGTTGCGCGTATGCCATTAAAAAGGCTACGGGTTTGAAAAAGGCTTTGCAAAGTGGGTTTGGTTAAAAGGCGGGGGGGG	2725 CAAGAAGCTIGGCTAAAAAAAACCTITITAAGCATGCAAGAAAACCCTCGCTCTGCGCACTAACCTAGAAAATAT CAAAACAAATCCTTGTGATGAGGTGAAAAACGCCAACGATTACACCCTATGCGCACTAACCTTAAAAAATTTAAAA ACTTATTTGGAGCAGAAACTCCCTTTGATCGCTCAAAAAATGCAACTTCATACACCCATTTAGCATTAGGAACAC GCTAAAGTTTTGGGGAGTTGCTCTTATCATAACCGCTTGAGTTTTGCTCTTTTACTAGTTTTGCGCCAAAAAGGAACGC ATTGATTATGTCATCATCATGAGCTAGCCCACCGATTTAAAAAAAA	TTTAGGCATTAGAGCGTTCCAGGCTGG ATTTAGGCATTAGACGTTCCAGGCTGG ATTTAGGCATTAGAGCGTTCCAGGCTGG ATTTAGGCATTAGAGCGTTCCAGGCTTGAGGTTGGAAAATTTTCATCCGCTTTGGCCAATAAGCCTT TTGGGGTGTTGCTCAATAAATGCGATGTTGAAAACATTGATGAGATGATAAGCCTTTTTTTT
	2	2725	
HP0241 HP0241	HP1570	HP1570 HP0448	

WO 02/066501			PCT/EPC
2730 HVGKDNLPFYFKKVKEVLKRGGMFLL HSILCCFEGKTNAWVDKYIFPGGYLPS LREVMSVMSECDFHLLMAESLRIHYAK TLDIWRNNFNHNLDQVKRLSYDERFIR MWDLYLRTCASAFRVGSADLFQLLLTN SVDNTFPLTKEYIYQ	2732 EADKVIKATKETKETKKEAKRI KKEAK QROQIPDHKKPOYVSVDÖTKTÖALFÖI YDTLNVNDKSFGDWFGNSALKÖKTYL YAMÖLLDYNNYLSIENPIIKTRAMGTYA DLIITGSLEOVNGYYNILKALINKRNAKF VLKINENMPYAÖATFLRVPKRSÖPNAH TLDKGASIDENKLFEÖGKKMYFNYAND VICRPDDEVCSPLRDEMVAMPTSÖSV TÖKPNI	2734 RAIADGARTIRIPIHMIDTINRINKVMRK HIGENGKEPDLEVVAEEVGLSLDKVKN VIKVTKEPISLETPVGNDDDGKFGDFV EDKNIVSSIDHIMRE	2736 LENDLKÖTFTYLNEVDAÍGLPTPKSVKE SDLIIKLTKLGTLHLDEIFEUKRLHYWY LONAFKTFTHLKFHERLNAWLPPFFND LIALFDDEGKIKÖGANATLDALNESLNR LKKESVKIIHHYARSKELAPYLVDTÖSH LKHGYECLLLKSGFSGAIKGWYLERSA NGYFYLLPESAÖKAOKIAGIGNEIDCCI VEMCOTLSHSLÖKHLLFKFLKFEFÖF LDSLÇARLNFAKAYNLEFVMPSFTÖKK MILENFSHPILKEPKPLNLKFEKSMAV TGWNAGGKTMLLKSLLSAAFLSKHLIP MKINAHHSIIPYFKEIHAIINDPÖNSANNI STFAGRMKÖFSALLSKENMLLGVDEIE LGTDADEASSLYKTLLEKLLKONNÖJIIT THHKRLSVLMAENKEVELLAALYDEEK ERPTYTFLKGVIGK
2729 GCATGTGGGTAAGGATAATTTGCCCTTTT, CCACTCCATTTTATGCTGTTTTGAAGGCAA CTCTTTAAGAAGTGATGAGCGTGATGA CTCTTAGCGAAGTGACATTTGGCGAAAC GCTTATCCGCATGTGGGATCTGTATTA TTGCTTTTAACCAACACTCTGGCAAACTCT CTACAATCCCCATGATTTTAGCATCACT CTACAAAAATTTTAATAGAGCTGCCGT ATACACTAAAAATTTAATAGAGCTGTCCGC TCAATAGAACATTAATAGAGCTGTCCGC	2731 GTGAAGCCGATAAGGTCATTAAGGCCACTAAAGAAACTAAAGAAGGACCAAGAAGGAGCTAAAGGAAGAAGAAGAAGAAGAAAGA	2733 CAGAGCCATAGCCGATCAGGCCCGCATATCCGCATTCACATTCACATTGATACGATTAATCGCATCAGTAAGG TCATGCGCAAACACATTCAAGAAAACGGCAAAGAGCCTGATTTAGAAGTGGTGGCTGAAGAAGTGGGCTTTTCGTTA GATAAAGTGAAGAATGTGATTAAGGTGACTAAAGAGCCTATCAGTTTGGAAACCCCAGTCGGCAATGATGATGGTGG CAAGTTTGGGGAAGATAAGAATATCGTCAGTTGATCACTTGATCACATGATCATGGAAA	2735 ITTAGAAAACGATCTCAAGCAAACTTTCACTTATTTAAACGAGGGGTTGGGTTTGCCCACCCCTAAAAGCGTTGCAAAGCGTTGCCCACCCCTAAAAGCGTTGCAAAGCGTTTGCAAAGCGATCTTATTATCATCAAACTTTAAAAACTTTCACGCATTTAAAAATTTCATGAAATTTTGAAAGCGCTTAACGCTAACGCTAACGCTAACGCTAACGCTAACGCTAACGCTAACGCTAACGCTAACGCTTAAAAGCGCTTTGATTTGAAAGCGCTTTAAAAGCGCTTAAAAAAGAGGGCTTAAAAAAAGCGCTTTGAAAAAAAGAGGCGTTTAAAAAAAA
HP0448	HP0819	HP1537	HP1537

17
4

VO 02/066501		PCT/EP01/15428
DIVDSKKIDTAVLALFNGGYF EGGILEFHFDEKARIAGVEIK KYDGLKSCHRIAGVEIK ALKTALEGOGYYGSVVEVRT ALLIVFDVNRGDSIYIKQSIYE RINELESLSANKORDFMGWM KLRLDGLEYDSMRIQDVYMR RISDILIEIDNPVVFLKTLERAL FNIEHLRADAGIL (TETADKG PDLDKDEKNGLVKVIYRIEVG VIISGNORTSDRIIRRELLLGP KLRNSENSLRRLGFFSKVKI SLMDLLVSVEEGIRTGOLGF GGLMLNGSVSEFINLFGTGO IATGGGRSYPGMPKGAGRM FNPRIFDSWYSSTINLYADYR GGGFGVNVGRMLGNRTHV	2740 FLOKFAGNONAYAGSENLDELKHAKI SSLMFLARAYSKADVOMSIEILKGLLNR SLKDEEKIAVLDLLAKNYFSVGYLQKTK DTVKEILRFSPRNVGALLKLHAYELEK DYSKALETLECLEELEVVEIETIKNYLYL MHLIENKEDVAKILHVSKASI.DLKKIALN HLKSHDENLFWOEIDATKRI.ENVIDLL W 2742 NGVEIVGLEHLDKVIYLDQAPIGKTPRS NPATYTGVMDEIRILFAEGKIEAKILGYS ASRFSFNVKGGRCEKCQGDGDIKIEM HFLPDVLVQCDSCKGAKYNPOTLEIKV KGKSIADVLNMSVEEAYEFFAKFPKIAV	KLK I LMDVGLGYI I LG Z744 FFVLAFIDLAIKRROYTNSLKMTKGEVK DEYKQOEGNPEIKAKIRQMMLKNATNK MMQEIPKANVVVTNPTHYAVALKFDE HPVPVVVAKGTDYLAIRIKGIAREHDIEII, ENKTLARELYRDVKLNAAIPIELFEAVA IVFAQVAKLEGERGKGKIIKPL
Zi37 ATGAAATTGTAAAGATTCGTGTGGGCGATATTGTGGATTCTAAAAAATAGACGCCCTGTTTTGGCTTTGTTCAATC AAGGGTATTTTAAAGACTTTTGAAGGCGGCATATTAGAGTTTCATTTTGATGAAAAAGGC CCGGGGTAGAAATTGAGGCACTTTTGAAGGCGGCATTTAAAAACCGCTTTAGAGGGCGCAGGGTTTGTGGGGATCAAAAGGG CCGGGGTGGTGGAGGGTAATTAGAGGCACTGAAAAGGGCTTTAAAAACCGCTTTAGGGGGCAGGCTATTATG CGACCGTTTGATGAGCACAAAATTAGAGGGAAAAAGGGCTTTAGAGGGGCAGGCTTTTATGAGGGGGGGG		2743 TATTITIGICITIGGCITITATAGCGATCAACGCGCCGCCAATACACCATTAAAAATGACTAACAAGA AGTTAAGGAATACAAACAGCAGGAACCCAATGCCCGCCAATCCCCCAATGACCTAACAGGA AGTTAAGGAATACAAACAGCAAGAAGGGAACCCAATGCCGCCCAATCCCCCAATGCCTAACACACC AAATTGATGAAGAACACCCTGTGCTAAAGCCCAATGTCGTGGTTATTATACCCATTACGCCGTCGCTTC AAATTGATGAAGAACACCCTGTGGTAGTGGTAAAAGCCCAACCCCCATTAGGAATTAAACG CGCTAGAGAGCATGACATAGAAATTATAGAAAATAAAACGCTCCAAGAGAGTGTGAAATTAACG CTGCCATACCAGAAGAATTGTTTGAAAATTATAGAAATTAAGCCCTAAAATAGAGCAAGAACCCCAA AAACAAAAGATCCTTTAAAGCCGTGGCGATAGTCTTCGCTCAAAAAAAA
HP1537	HP1537	HP1537

1	D	c	כ
		_	
i		٠	

	2745 TCGCTAAAAACACCCAGATTGTTTGAATTA TGGATGGGTGATGAACGCTATCAGCGTCAT GGGGAGAGCCTACCGCAACGCGTCATTA GGGGAGAGCCTACCGCAACGCGTCATTA CTTTGAAACCCCTCAAAACTCCCCCTAAAAC CGATGAAAAGGGGTTTTTTCTCAAATCAGCAAGGGTTGAAAACTTTTTCACAAGGCTTGAAACTTTTTCACAAGGCTTTGGCAACAAGGGCTTTTTTTT	2747 ATTTAAAAGGCTTGAAAGATTCCAACCACATT, ATGGGGCGATGGCTGAGCCTTTAGAAATCCT GAGAAGTCATAGTCATGGGCGGCGCGGGGTTAT GATTCAAGCGAGCTTTAGCTTTGGCGTTAT	2749 CCGCCTCAAACAACGACCGAGCATGATTTA CGCGCCATTTCACCGGTAAAGCCCCTAACGA TTTTAGTCATTGTGGATGAAAGCCCATGTGAGT AGTGTTTTAGTGGAATATGGTTTTAGATTGCC AAAATTGCCAGTTCCTTTTTGTGTCCGCTACG AAATCAATCAGTTAGTGGTGGCTAGAGCTG GATGAAATATTAGTGCTGGATGCGGCTTGAAGC TCATCCGCTTTAAGGCTTAAAGAGATTGACAAGCGCTAATGACAAGCGCTAATGACGGATCAAGGCGAAATTGACAAGCGATAATGGAAGCGCAAACGCTAATGGCAAACGCTAATGGCAAGCAA	2751 CACCTATCAAGCCGTGAGTGGGGGCAGGGAAC GTTTGGAAAAGACCCCACTATTGATTTAAACC CGATCGCTCATATTGATACTTTTAAGGAGATT TCATGGGCGTCGATTTCCCTATCAGGGGGGCG TATCGCTTTTGAAAAGAATTCGATCTCAAAGA TGATCCCAGTCATAATCTTTACCCCACGCCCC AGGATTTGTTTGATAGAAACTTTGCATGCC AGGATTGTTTGATAGAAACTTTGAGACGCT TTAAGGATAAGGATCAATCTAGCCCAATCTCTA TAATTGCATTAAGGATGAAAAATAATAGGATTAAAATATAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATAGATTAGAAAATAGGATTAGATTAGATTAGATAGATAGATTAGATTAGATAGATAGATTAGATTAGATAGATAGATTAGATTAGATTAGATAGATTAGATTAGATTAGATAGATTAGATTAGATAGATTAGATAGATTA
2746 AKKHPDCIELRVH GWMNAISVIGDKV TASAVISDIIEIARK PLKPKEEIQCAYY. SAILAQNDISLININ, STHTTNEKSMLN, KMIRLEN MAGGASIEKIDSVE LALYFKGAKVTU ATGKAPNETPFC VDESHVSLPOGFG EYGFRYPSALDNR LFVSATPNKLELEL LLDPKFEVRDSDK RGERVLITLTKKN KARYMHSEIDARF GINLLREGLDLPEV RGERVLITLTKKN KARYMHSEIDARF GINLLREGLDLPEV RGERVLITLTKKN KARYMHSEIDARF GINLLREGLDLPEV RGERVLITLTKKN KARYMHSEIDARF GINLLREGLDLPEV RGERVLITLTKKN KARYMHSEIDARF GINLLREGLDLPEV RGERVLITLTKKN KARYMHSEIDARF RGERVLITLTKKN KARYMHSEIDARF GINLLREGLDLPEV RGERVLITLTKKN KARYMHSEIDARF GINLLREGLDLPEV RGERVLITLTKKN KARYMHSEIDARF FERMRLRDEIAQU DTFKENGYTKEEL PISATCVRVLKNAPSI PLKASHTÖSVFIGF FCVADQLRVGAAT	GAGTGCATCCAAGCATGATTAAAAACGAATGCATGCTCTTAAAG GGGGATAAGGTGGGGCGGGGC	TITTAGACACCAAAAAGGCCCTTTTAGCATGCGACACTAAAGGCG TITAAAGCCGCTCAAAAGACGCTTATTTTGAAAACA GAAAAGATTGACAGCGTTCGAACGATTAGCAATCTTTCTAGCGG ATTTTAAGGGAGCCAAAGTTACTTTGTAGCGG	AAATGATTAGCGCGACCGGTGTGTGAAGGGGCATTGAAAATTACG ACGCCTTTTGCTTGTTTGATTATTTAGGGATTTTTGAGGGAAA TGCCACAGTTTGGCGGGGATTTTTGAGGGAAA AGCGCTTTAGACAACCGCCCTTTAAAATTTGATGAATTTATCCATA CCAATAAGCTAGAATTAGAGCTTTCCAAAAAGAATTGCCTGAGC AATTTGAAGTGCGAGACAGCGTTTCCAAAAAGATGCAGGATTTGTTT AAGGGTGCTCATCACCAGCGTTAAAAAAATGGCAGAATTGCCTG AATTTGAAGGGATCAATTTTAAGAGAAGGCTTGAATTGCCTG AAGAAGGGTTTTTAAGGGAGGGCTGCATTCAAACCATG TTTTAATAGGCTAAAAAGTTCAAAAAGCCTT AAGAAGTTCAATAAAAGCTCATAAAAAGCCTT AAGAAGTTCAATAAAAACCACTAAAGAGCCTT AAGAAGTTCAATAAAAACCTCAAAAGCCTTAGGCTA	CACCTATCAAGCCGTGAGTGGGGCAGGGAACAAGGGCATAGAGAGTTTAAAAAATGAGAGTTAAAAAACCGCTTTAGAGTGTTAGAGTTTAGAGATTGAAAAAACGCCTTTTAGAGTTTCAATGGTTTGAAAAAAGGCCTTATCCGATCGCTTTCCATTCAATGGTTTGGAAAAAGGCCTTATCCGATCCGATCGCTTTCAATGGCGAAAAGCCCTCATAAAAAAAA
PSMIKNECM GETLYYGAG GETLYYGAG KSSLMLGFE ARLLVSDEK LOKELHSNI LKELENLOS SATGVCKGIE SATGVCKGIE SATGVCKGIE SATGVCKGIE SATGVCKGIE SATGVCKGIE SATGVCKGIE SATGVCKGIE SATGVCKGIE SATGVCKGIE SATGVCKGIE SATGVCKTA SATGV	2746 AKKHPDCIELRVHPSMIKNECMLSKVD O GVMNAISVIGDKVGETLYYGAGAGGEFY TASAVISDIEIARKKSSLMLGFETPQKL © PLKPKEEIQCAYYARLLVSDEKGVFSQIS SAILAQNDISLNNVLQKEILHSNKAKILF O STHTTNEKSMLNALKELENLQSVLDTP KMIRLEN	2748 LKRLKDSNHIILDTKNALLACDTKGDGA MAEPLEILFKAAQTLLKDAYFENREVIV MGGASIEKIDSVRTISNLSSGIQASALA LALYFKGAKVTLI	ALKÖRTEHDLEMISATGVCKGIENYAR HFTGKAPNETPFCLFDYLGIFEREFLVI VDESHVSLPQFGGMYAGDMSRKSVLV EYGFRLPSALDNRPLKFDEFIHKNCOF LFVSATPNKLELELSKKNVAGQIRPTG LLDPKFEVRDSDKQVQDLFDEIKLVVA RGERVLITTLTKKMAEELCKYYAEWGL KARYMHSEIDAIERNHIIRSLRLKFFDILL GINLLREGLDLPEVSLVAIMDADKEGFL RSETSLGTMGRAARNANGKYLLYAKK ITGSMQKAFEITSYRRAKGEEFNKIHNI TPKTVTRALEEELKLRDDEIRIAKALKK DKMPKSEREKIIKELDKKMRECTKNLD FFFAMRI RDFIAOLRT	

_PCT	EP01	15428
		13420

FKKQDGTL ON A CAN CAN CAN CAN CAN CAN CAN CAN CAN	LPSLENLL ILQDATPLT ILESLEHLR SEKVAEEL SHDAIAYA VLASGPRC KVINPTQCE ASQGNFE SMESFNIH VILVTALNP	KADEMRA INAGKHAK ILHVNERG FEHLNPHY FIGGNMMV FIGGNMMV INFOEHGL FILEWIHT MLLSDST FKEAGG
A STAKYLPSGSAAATIGLATERRFKKQDGTL O GEEVCFIDARLFGRTAEIANQYLSKGS 6 SVLIEGRLTYESWMDCTGKKNSRHTIT O ADSLQFMDKKSDNPQANAMQDSIMHES NSNNAYPANHNAPSQIDFNQAYAQN£YKKENLQAQPSKYQN\$VPEINIDEEEIPT F	2756 INDTFPTAMHIVSVLEITI-IRLLPSLENLL KTFKEKSQQFKEIVKIG 3THLQDATPLT LGGEFSGYASMLEHSKQQILESLEHLR ELAIGGTAVGTGLNAHKELSEKVAEEL SQFSGVKFVSAPNKFHALTSHDANAYA HGAFKALAANLMKIANIRWLASGPRC GLGELNIPENEPGSSIMPGKVINPTQCE AMTMVAVQVMGNDTAIGIAASQGNFE LNVFKPVIIYNFLQSLRLI.SDSMESFNIH CASGIEPNREKIDYYLHISLMLVTALNP HVGYENAAKIA	2758 MTDNNONNENHENSSE:NSKADEMRA GAFERFTNRKKRFRENAOKNAEYSNH GAFERTNRKKRFRENAOKNAEYSNH EASSHHKEHRPNKKPINNHHKOKHAK TRNYACIELDSNKVEGYTEILHVNERG TLGFHKELKKGVEANNKIQVEHLNPHY KMNLNSKASVKITPLGGLGGGGNMAV IETPKSAIVIDAGMSFPKEGLFGVDILIP DFSYLHOIKDKAGIIITAAHEDHIGATPY LFKELOFPLYGTPLSLGIJGSKFDEHGL KKYRSYFKIVEKRCPISVGEFIIEWIHIT HSIIDSSALAIOTKAGTIIHTGDFKIDHTP VDNLPTDLYRLAHYGEKGVMLLLSDST NSHKSGTTPSESTIAPAFOTLFKEAQG
54 KYLPSGS GEEVCFI SVLIEGR ADSLOFA NSNNAYE YAKENLC F	SG NDTFPTAMHIV KTFKEKSQDFI LGGEFSGYASI ELAIGGTAVGT SQFSGVKFVSI HGAFKALAANI GLGELNIPENE AMTMVAVQVM LNVFKPVIIYNFI CASGIEPNREK	B MTDNNON GAFERFT EASSHHK TRNYAGE TLGFHKEI KMLNSK IETPKSAN DFSYLHON LFKELQFF KKYRSYFI HSIIDSSAI VDNLPTDI NSHKSGT
2753 GAAATATTTGCCTAGGGGTTCGGCTGCGGCTACAATAGGTTTAGCCACAAGGCGGGCG	Z755 CAACGACACTTTCCCTACCGCAATGCACATTGTGAGCGTGCTAGAAATCACGGACAGACTGCTCCCTAGTTTGGAGA ATCTGTTAAAAACCTTTAAAAAAGCCAACAATTTAAAGAATTTAAGAGATGCTCCAGGACGCCCTTTAAAAAACCTTTAAAAAAAGCCAACAATTTTAAGAGA ATCTGTTAAAAACCTTTAACATTTAGGGCAACAATTTAGGGGTATGCGAGCATGCTAGAGCATTCTAAACAAATTTTAGAGA GTTTGGAGCATTTAAGAGAATTAGCGATTAGGGGGGTGAAATTCGTCTGCGCCTAAACGCTCATAAAGATTGAG GTAGCCATGACGCTTAGCCATTGAGCGGGGTGAAATTCGTCTGCGCCCAATAAGTTCCATGCGCTCA CTAGCCATGACGCTTATGCCCAGTTGGGGCTTTTAAGCGGCTTTAATGAAAATCGCTAACGAT ATTAGTCGCGGGAAAGCTGCGCGCCTGTGGTTTTGGGCGAGCTTAATATTAATGAAAACGAGCGGGCGTTCTA TATGCCCGGTAAAGTCAATCCCACGCGGTGTTGGTTCGAACGACTGAAAGCGGGCAGTTCTA ATAGATGGCATTGCGGCCAGTCGGGGTATTTGAATTGAA	2757 TATGACGGATAACAACCAATGAAAACCATGAAAACAGCAGTGAAAATTCAAAAGCTGATGAGATGCGGGCGG
HP1537	HF1537	HP1537
堂 [Ē	<u> </u>

P	C	\mathbf{T}	EP	01	/15	428
---	---	--------------	----	----	-----	-----

	AAGAGGTGGAAAAAGGCCATTATAGCATTCCAAAACGCTTTGAAAATGCAAAAGGTGGGGCGCTAGGGTA AAGAGGTGGAAAAAGGCTTATAGCATTACCAAAACGCTTTGAAAATGCAAAAGGTGGGGCGCATTAGGGTA GAAATGCTTGGCGTTATAGCAAGGCCCATTTAGGAGCTTTAGGAGCTTAGGGGTAGGGTAGGGTAGGGTAGGGAAAATCAGGAAAAATCAGGAAAATCAGGAAAAATCAGGAAAAATCAAAATTATAGAAAAATCAAAAATCAGGAAAAATCAGGAAAAATCAGAAAAATCAAAAAATCAGAAAAATCAAAAAATCAAAAAAAA	LGACHYKHFONALKMCKAGIARVETLEE VEKGHYKHFONALKMOKVGGIARVET LGACNAYDKAHIASVKAKDVLEVSGLS FNSILSSKDOLVPSSKLEIRTEKNLPDL SFFFSSTLNSYPULKTLENDIGISKENT KI GIAKEI POVSFFGSYIMKONNSVFF
· .	AGCAAAACAATTCGGTGTTTGAAGACATGATCCCTAGTTGGTTTGTGGGCGTGGCCGGGCCGCTTGCTT	α . α
·	TCATTGATGCGAGGAACACGCTTTCTTCTATCGTCGTGGAGCAAAAAGCGTGGCTTATAAATACATCGTTTCATTAG CGAATTTAATGGCGTTAAGCGATCATATTGATTTATTATGAATTTGTTTATAAGGGAAAAAATCATGTCAAATAGCA TGTTGGATAAAAAATAAAGCGATTCTTACAGGGGGTGGGGCTTTATTATTAGGGCTAATCGTGCTTTTTTATTAGCTTA	QKSVAYKYIVSLANLMALSDHIDLFYEF VY
HP1537 276	2761 CTCTCACAGGGTGATGGATAGATTATTGAGTGGGGATGTGGGGTTTTGGGAAAACAGAAGTGGCGATTGCGATTTTTTGCGCGTTTTTGCGCGTTTTTGAAAGTGGCGTTTAGTTGTGGCCTACCACTTTATTAGCGCACCACCACAAAAAAAA	2762 SHRVMÖRLLSGDVGFGKTEVAMHAIF CAFLNGFQSALVVPTTLLAHOHFETLR ARFENFGVKVARI DRYASFKNKI I KAV
	AAAGGCGGTGGAATTAGGGCAAGTTGATGCGCTAATAGGCACGCATTTTAGGCGCAAATTCAAAAACCTG GGCTTGGTGGTGGTGGTGAAGAGGCATAAATTTGGCGTGAAAAAAAA	ELGGVDALIGTHAILGAKFKNLGLVVVD EEHKFGVKÖKEALKELSKSVHFLSMSA TPIPRTLNMALSQIKGISSLKTPPTDRK DSSPTEI KENNDELI KEIIVREI RRNGOL
	TTATTTACAGAGAATTACGCCGTAACGGGCAAATTTTTTACATCCATAACCACATCGCTAGCATTTTAAAAAGTCAAAAC CAAGCTAGAAGATTTAATCCCTAAACTCAAAATCGCTATTTTGCATTCCCAGATTAACGCTAATGAGAGCGAAGAAAT CATGCTAGAGGTTTGCCAAGGGAAATTACAGGTTTTATTATACACTTCTATTGTGGAATCAGGGATTCATTTGCCTAA	FYIHNHIASILKVKTKLEDLIPKLKIAILHS QINANESEEIMLEFAKGNYQVLLCTSIV ESGIHLPNANTIIIDNAQNFGLADLHQL RGRYGRGKKEGFCYFLEDQKSLNEQ
2762	GAGGITTGGAAAAAATTCATATTTAGGCAGGAGGCAGGAGGCAGGAGGAGAAAAAAAA	ALKKLIALENNS TLOSGES
0071.44	GOGATGCAGGATAATTTAGTGAGCGTGATTGAAAAACAGACCAATAAAAAGGTGCGTATTTTAGAAATCAAACCTTTA AAATCTAGCCAGGATTTAAAAATGGTCGTTATTGAAAACAGACCAATAAAAAGGTGCGTATTTTAGAAATCAAAACCTTTA AAATGTAGCCAGGATTTAAAAATGGTCGTTATTGAAGATCCGGACACTAAATACAATATCCCGCTTGTGGTGGGAGGAAGG GATGGTAATTTAATCATAGGGCTTAGCAACATATTCTTTAGCAATAAAAAGCGATGATGACAATTAGTTGCAGAAAACC	2764 ASVLSALLLVGLGAAPKHSVSANDKKMI QDNLVSVIEKQTNKKVRILEIKPLKSSQ DLKMVVIEDPDTKYNIPLVVSKDGNLIIG II SNIFFSNKSDDVQI VAFTNOKVQALN
	AATCAAAAAGTTCAAGGCTCTTAACGCCACCAACAAATAGCGCGAAATTGAACGCTATTTTTAATGAAATACCGGCT GATTATGCGATAGAGTTGCCCTCTACTAACGCTGCAAATAAGGATAAAATCCTTTATATTGTCTCTGATCCATGTGC	ATOONSAKLNAIFNEIPADYAIELPSTN AANKOKIL YIVSDPMCPHCOKELTKLR
-	CCACATTECCAAAAAGAGCTCACTAAAACTTAGGGGGCTTTAATCCAAGAAAATGGCGAAAGCTAGGGCTAGGGGAGCGAGC	DHLKEN I VRMVV VGWLGVNSARAAL IQEEMAKARARGASVEDKISILEKIYS
HP1286 276	Z765 TCGGTGGCGTGGCCATAGGGGGGTGATGCTCCCATAAGCACGCAAAGCATGACCTTTAGCAAAACCGCTGATATTGA AAGCACTAAAAATCAAATTGACAGACTCAAACTCGCCGGGGCCGATTTAGTGAGGGTGGCGGTGACTAATGAAAAG	
	GACGOTGAGGOTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAG	KELKKVSPLPLADIHFTYKFALIAAUSV Z DAIRINPGNIGSKEKIKAVVDACKEKNIP Z IRIGVNAGSLEKOFDOKYĞPTPKGMVE Z

	-	

1000	-010		'O
9821.44		AGAGGGTTATCGCGTATTTTTTTTTTTTTTTTTTTTTTT	2768 RPSYVDSDYEVFSETII-LQNMVYQPTE O ERDSFAQLTKDENDSI:NPETSVILLNE N PSDSDTKNPPLNQNE:NTNTANNDTK 90 NPFLYKPKRKTKDPKLIEYSQQNFYPL 99 KDGDIMMSKEGDQWLIEKSKALK
HP1286	2769	2769 CAGGCGGGGGGGCCAAGCTTGTATTTCAATAACCCTATTTTAATCAGCGTTTTTAGAGCATTTTTATCGCCAAAAAATCC CTTTATGTGTAGAGAGAATGGTTCTATTTTTTTTTT	2770 GGEPSLYFNNPILISVLEHFYRQKIPLC VESNGSIFFEFSPILKELHFTLSVKLSFS LEEESKRIHL
HP1286	7777	ACAACATTAAAAACGCCAAAGACTCCGCTCAAAAACGGCTCTCGCTCAAAAAACAGAAGCTTTAACGC ACAACATTAAAGAACACCCAAAGACTTAACGCCAAAGGCGAGTGAAGAATTAAAAAGCGTCATTAAAGGAAGTTTAAAGGAATTAAAGGAATTAAAGGAATTAAAGGAATTAAAGGAATTAAAGGAATTAAAGGAATTAAAGGAATTAAAGGAATTAAAGGAATTAAAGGAATTAAAGGGAATTAAAGGGAATAAT	2772 WKELSKNAKDSAQKQALAQKTEALTH NIKDTRERLTTLQHKASEELKSVIKEVN SLGSQIAEINKRIKEVE NINKSLKHANEL RDKRDELEFHLRELLGGNVFKSSIKTH SLTDKDSADFDESYNLNIGHGFNIIDGS IFHPLVVKESENKGGLINQVYFQSDDFK VTNTDKLNQGRVGALLNVYNDGSNGT LKGKLQDYIDLLDSFAKGLIESTNAIYA QSASHYIEGEPVEFNS DEAFKDTNYNI KNGSFDLIAYNTDGKEIARKTIAITPITT MNDIIQAINANTDDNQDNNTEN
HP1286	2773 773 740 740 740 740 740 740 740 740 740 740	CTCTGAGGGGACTITAGGCTTTATTTCAAGCGTGGAATTAGAATGCGTGAAAGGACTACGCTTATAAAACTTGCGCGTT ATTGTTTTATGAAAATTTAGAGCGATGTGCCAAAGCCTCAAATTCTAGCCGCCTTAAAAGCCAAACCAACC	2774 SEGTLGFISSVELECVKDYAYKTGALLF YENLERCAKAAQILAALKAKQPEMISSA ELMDYACLKSVKGLEG MPSVVLEIKEP NACLLIQSESDDPLILENSMQTILNALS AIPVVLDSQISSDPSIYQSWWKIRKGIF PIAASKRKSQSSVIIEDICFSQEDFVEG AKAIEGLLKKHGFKDNGIIFGHALSGNL HFVVTPILENEAERKAFENLVSEMFLM VSKSSGSIKAEHGTGRMVAPFVEMEW GEKAYKIHKQIKELFDPNGILNPDVIITN

с	٠	ı
		i
٠		٠
*	٠	۰

02/066501				P01/15428
2776 ATRSEVAMTGELTLSGEVLPIGGLKEK CHAAFKAGIKTALIPVKNYERDLDEIPAE SON VRENLNIVAVKNIAEVLEKTLL CONTRACTOR CONTRACTO	2778 IE'L GVKSMKIYVALEGACKTČSSSKIT LKNVIERQLKMDIHPNLEVVCLENAKEF DKL	2780 DSFGIÁRLYSNPALLDLDNHGIPNDIND NEEAPKNTPLKKYAKNLSALAGDNALD PVIGREEEILRVIEILGRKKKNNPLLIGE AGVGKTSIAEALALKIAČKEVPEFLÖEY EVYSLDLALMVAGAKYRGDFEKRLKKT LKEIQONGRIILFIDEIHTLLGTGSSNAG		2784 ÓKEÁLÁLIIVDEEVSLÉVLEELKŃIPÁCL SVHYVVI
21	277	278	2762	278
2775 GGGCTACAAGAAGCGAAGTGACGGGCGAATTGACTTTGAGCGGGGAAGTTTTACCCATAGGAGGGTTGAA AGAAAAGTTGATCGTGCTTTTAAAGCCGGCATTAAAACCGCTCAATTCCTGTCAAAAATTACGAAAGGGATTTAGA AGAAAAGTTGATCGCTGCTTTTAAAGCTGGTTGCGGTGAAAACATCGCTGAAAGTGTTAGAAAAACATT CGAGATCCCTGCTGAAGCAGGAAATTTAAAACATCGTTGCGGTGAAAAACATTGCGTTGCAAG AATGGGGGCGTTTTAAAAGCATTATGGCATTATGGTTTTGCTTTGCTTTGCGTTTGCGCTTGCAAG AATGGGGGCGTTTTAAAAGCGTTATAGGCTTTGATCATAACGCTTTTGCTTTGCTTTGCTTTGCGTTTTGCGCTTTGCGCTTTGCGCTTTGCGCTTTGCGCTTTGCGCTTTGCGCTTTGCGCTTTGCGCTTTGCGCTTTGCGCTTTGCGCTTTGCTTTGCTTTGGAATCATTCGGCGCCCTTATTGAAAAAAATGACCTTTTTGAAAAAAATGACCTTTTGAAAAAAAGCGCGCTAAAAAGCGCGCCATTTTTTTGCCCTAAAGCGCTTAAGGGGCCTTTATGAATGCCTTAAGGGGCCTTTAAAGGGGCCTTTAAGGGGGCTTTAAGGGGGCTTTTATGGCCATTGTGCGTTTAAGGGGGCTTTTATGAAAAAAGCGCTTAAGAAAAGCGCTTAAAAAAAGAATCATTTTAAGCGTTAAGAAAAATGAAAAGAATTTTAAGCGGTTAAAAAAGCGCTTAAAAAAGCGCTTAAAAAAAGCGCGGTTAAAAAAGAATGATTTTAAGCGGGGCTTTAAAAAAGAAATGATTTTTAAGCGGGGCTTTAAAGCGCTTTAAAGGAATGATTTTAAGCGGGGCTTTAAAAAAGAAAAAGGAAAAAAAA	2777 ATATTGAAGTGCTAGGGGTGAAAAGCATGAAAATTTATGTGGCTTTAGAGGGGAGCGTGCAAGACTTGCTCTAGCAGT AAAATCACTTTAAAAAATGTCATTGAAAGGCAGCTTAAAATGGATATTCACCCCCAATTTAGAAGTGGTGTGCTTAGAAA ACGCTAAGGAGTTTGATAAGGATTATAGGCATGCAAAAGTTGATTTGAATTTAAAAAGCGCGCGTTGAT TAAAGATGGCTTTTAGCGTTCAAACAAGCGCTTATCAGCCTTACGCTTACGCTTACGCTTTTTTTT	2779 GGATAGTITTGGCATCGCTCGTTTGTAATCCTGCTTTATTGGATTTGGATAACCATGGTATTCCTAATGACAT TAATGATAATGAAGAAGAAGAAAAACACTCCCTTAAAAAAATACGCTAAAAAATTTGAGCCCTTTAGCCCAAGACAA TAATGATCAAGAAGAAGAAGAAGAAGAAGAAGAATATTAAGAAATTTTAGGCGCAGAAAAAAAA	CCAAGGGGGTTATGGGGTTTTATTTGAAGGTTTAGGCGATAACGCTTTAATCTTACAGGCACCTCCAGCAAAAAAAA	2783 GCAAAAAGAAGCCCTAGCACTCATTATTGTAGATGAAGAGTTTTGGAAGTTTTAGAAGAGCTTAAAAAAACATTCC TGCGTGCTTAAGCGTTCATTATGTGGTTATTTAAGGTAGTTGGATGCGAGCATTTTTAAAAAAGCATGAT GAATTAAAAATCATTGACGCCCCCTTGAAGTGGATTTAGAAATCGCTCATCTAGCCTATATAGAAGAGAAAAACCT AATGGGGGCAAAGCCCTTTTATTCACGCAACCCATAAGAAAAGAGCATGACCAGATCAAAAACCTTTTGGCAAAGCCTGT TTTAATGAAGCCTTTTGACGCAACCCCATAAGAAAAGAGCATGACCAGATCAAAAACCTTTTGGCATGCCTGT
	စ္	_		<u> </u>
HP1286	HP1286	HP1411	HP1411	MP1411

~	٦
c	V

Q 02/066501	· · · · · · · · · · · · · · · · · · ·		CT/EP01/15428_
2786 (NNETKNIVEVGIDSSIEE:SYLAYSMSVII O GRALPDARDGLKPVHFIRILYAMHELGL TSKVAYKKSARIVGDVIGKYHPHGDNA O VYDALVRMAQDFSMRI ELVDGQGNFGS SIDGDNAAAMRYTEARMTKASEEILRDIC DKDTIDFVPNYDDTLKEPDILPSRLPNL LVNGANGIAVGMATSIPPHRMDEIIDAL VHVLENPNAGLDEILEFVKGPDFPTGGI IYGKAGIIEAYKTGRGRVKVRAKVHVEK TKNKEINLDEMPFQTNKAKLVEGISDL AREKOIEGISEVRDESCIREGIRVNIELK RDAMSEIVLNHLYKLTIMETTIF	CLEANANAMILLE OLIVILLIANDEINALIN STASPEAARNALIMERFTLSEIGSKAILE MRLQRLTGLERDKIKEIEYONLLELIDD NGILKSEDRLNGVVKTEILLEVKEGFS PRRTEIGESYENIDIEDI JANEPMVSM SYKGYVKRVDLKAYEKQNRGGKKILS GSTYEDDFIENFVANTHDILLFITNKG OLYHLKVYKIPEASRIAIAGKAIVNLISLA PDEKIMATLSTKDFSDERSLAFFTKNG VVKRTNLSEFESNRSCGIRAIVLDEGD ELVSAKVVDKNAKHLLIASHLGIFIKFPL EEVREIGRTTRGVIGIKLNENDFVVGAV VISDDGNKI I SVSFNGIKCOTI AFAYR	2788 VNLVSQNGRRYLKASISIELSNEKLLN EVKVKDTAIKDTIIEILSSKSVEEVVTNK GKNKLKDEIKSHLNSFLIDGFIKNVFFT DFIIQ	2790 RLMELGAPEIIVRNEKRMLGEAVDVLF DNGRSTNAVKGANKRFLKSLSEIIKGK GGRFRQNLLGKRVDFS GRSVIVVGPN LKMDECGLPKNMALEL "KPHLLSKLEE RGYATTLKOAKRMIEQI(SNEVWECLQ EITEGYPVLLNRAPTLH!QSIQAFHPKLI DGKAIQLHPLVCSAFNADFDGDQMAV HVPLSGEAIAECKVLMLSSMNILLPASG
210		272	275
2785 CAGTCAATGAAACAAAAATATTGTAGAAGTGGGGATTGATT		2787 GGTGAATCTGGTCTCTCAAAATGGCAGACGCTACCTTAAGGGTTTTCGTTAGAATTGAGTAATGAAAAGCTTTTTGGTTATTGGTTAGAATTGGTGAAGAGAGAG	2789 ACCCTTANTGGAGCTTGGAGCGCCAGAATCATTGTGCCAAAAAAGGATGTGCAAGAAGGATGTGCAAGAAGCCGTGGATGTG CTTTTGATAACGGCCGCAGCAGCATTAAAGGGGCTAACAAAACGCCCTTTAAAATCGCTCAGTGAAATCAT TAAAGGCAAGCAGGGCGTTTCAGGCAAAACCTTTTAGGTAAAACGGCGTGGATTTTTGTA TAAAGGCAAACTCTCAAAATGGATGAATGCGGGTTGCAAAAAACATGGCGTTAGAACTCTTCAAAATGGATTGTTA TCCAAGCTTGAAGAGGGGCTATGCCACCACCACCGCTCAAACGCGTTGAACGCATGAAGT ATGGGGGTTCCATGCAAGAAATCACAGAGGGGTATCCGGTGCTACTCAACCCCGTTAGTGTGTTCACCACACACA
HP1411		HP1411	HP1411

4
Č
4

HP1411 ZP9 GGZTSTICATICAGGGGTTAGGGGGTTAGGGGGTTAGGGGGTTAGGGGGGTTAGGGGGG	VO 02/066501	3		EP01/15428
TIPLI GCGTGTT GANTIGGATTTT AGGAGTGT AGANGTT CACANTATCTGTATICAAAAGGAGTATTTTATICATTTTATICATTATICATTATICATTTATICATTTATICATATICATATI	92 RVELDFRSVKMQVSGYLYQNVQSIWG DCISHPFVQGIGRGTLERDKFRFYIIQD YLFLLEYAKVFALGVVKACDEAVMREF SNAIGDILNNEMSIHNHYIRGLQITQKEI GNARPTLANKSYTSYMLAEGFKGSIKE VAAAVLSCGWSYLVIAGNLSQIPNALE HAFYGHWIKGYSSKEFQACVNWNINL DSLTLTSSKQEIEKLKDIFITTSEYEYL WDMAYQS	94 DLKKVCEKIKSALPFGIISAFKPFKDAFY RDFNHNEQKLLIGAAKSGCIQSSADKL AQLKTRLLYWQDKSVKVDWDKPILKD FFKGNNYLYRRFCFLLGKHFMDRFLKN NAKASVKDFMSSKEFVAKYRYTPKQN TERAKKLQSYLENKRDFIGFVQALNSL KDNPQDPFLPNEETSFLVFANEPTIVF NLRDYLLVLAQIFNQAICYCESKCPIE LINASPGKDFNKTQDSFPDIKFSTPNQL EQSLNALKNKLAAFFSKHPDKHNGME FNEIAKTQI	BÉ LLCAGRNETLKKAVPIGVGLIESAINLTR MCLKNPDTESLIFIGSAGSYSPEMELLS VFESVCGYQIEESFSHLNSYTPLDNFIH IETEEQALFERVRYNSSNYIHTSEMFAK KMYQKGVLLENMEFFSVLSVAKAFSLK AKGIFCVSNYVGLNAYQEFKENHAKVK QILENIIDSLII	BB IIKGGFIALSQMGDANASIPTPGPVYYR EMFAHHGKAKYDANITFVSQAAYDKGI KEELGLERQVLPVKNCRNITKKDMGFN DTTAHIEVNPETYHVFVDGKEVTSKPA NKVSLAQLFSIF
17.279 GCGTGTTGAATTGGAATTTTAGGAGTGTAAAAAGGCTTCGTTCG	, ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	27.6	276	279
1411	2791 GCGTGTTGAATTGGAATTTTAGGAGTGTAAAAATGCCAAGTTTCACAATATCTGTATCCAAAATGTGCAATCTATTTGGGGGGGG	2793 GCGATCTTAAAAAGGTGTGTGAGAAAATCAAAAGGTTACCCTTTTGGGATCATCTCAGCCTTTAAACCCTTTAAAGGACGATTTTACAGAGAATTTACAGAGAAAGTTAATGAGCAAAAGGTTACTGATAAAGGGGGCAGCTAAAAGGGGGTTGCATTCAATCTAAAAAGGGGGCAGCTAAAAGGGGGTTGCATTCAATCTAAAAAGGGCAAAAAAAGTTAAAAAAGGGGATTAAAAAAAA	2795 IGCTGCTTGCGCAGGAATGAGACTTTAAAAAAAGCGGTGCCTATTGGTGGGTTTGATAGAGAGGCGCGATT AATCTAACGAGAATGTGTTTAAAAAACCCTGATACAGAAAGCCTTATTTTTATAGGAGGCGCGGGAGTTATAGCCCA AATCTAACGAGATTTAAACGTGTTTGAAAACCGTTTGCGGCTTTTTTTT	2797 GATCATCAAAGGCGGGTTCATTGCGTTGAGTCAAATGGGTGACGCGAACGCTTCTATCCCTACCCCACAACCATTT ATTACAGAAATGTTCGCTCATCATGGTAAAGCCAAATACGATGCAAACATCACTTTTGTGTCTCCAAGCGGCTTATG ACAAAGGCATTAAAGAAATTAGGGCTTGAAAGACAAGTGTTGCCGGTAAAAAATTGCAGAAACATCACTAAAAAAA GACATGCAATTCAACGACACTACCGCTTGAAGTCAATCCAATCCATGGTTACCATTGCAGAAGACATAAAAAAA AGTAACTTCTAAACCAGCCAATAAAGTGAGCTTGCGCAACCTTTTAGCATTTCTAGGATTTTTTAGGAGCAACGCT CCTTAAATCC
	HP1411	HP1411	1411	HP0935

	3GA 2802 EGTKELGAVGFAQLLECKAISLNVDTS AGA TEDLOITLEFLKEYEDEAITRLKELLKSP AGA AN LOKESDEDY							ATA 2804 RGFIPPKDLLKQLEKISASLSKUVVARKU CAC VEKLELSYALIDNIQHNTLDDTLDFTFIV CAT GDSLSVQSLYVTFDLVIDMDRPMSEQF	
2799 GCGGACTAATAAAGCCTTGTATCAATTCATTTTGAGAATAGCTCAAAAAGACAATTTTGCTTCAGCGTATCTAACAACAGTC AAATTAGAATACCCACAAGACACGAAGTCTTAACACGCGTTATTGAAAAAGAGACAATTTTGAATAAAAAGAAGAGAAGAGAGGGCGTAGAGGGCGAAGAGGCGCAAAGAGGCGCAAAGAAGAAGAAAAAA		I ACCASCACATTAGCCGCAAAACGCTTTAGAAAAGGCTTTAGAAAAAGCCGTTTAGAAAAGGCGAAATGCTAGCGCGCACTTTAGCAAAAAAAA	TTAGGCACTAAAGAGAGCATTCAAAAATCAAGCTAGACGATTTGAAACAGCATTTGC AAGATTGCTTAATTTCTT	ANGO I COLOGO DE LOS DE CONTRO DE LA CONTRO DEL CONTRO DE LA CONTRO DEL CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DEL CONTRO DEL CONTRO DE LA CONTRO DEL CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DE LA CONTRO DELIGIO DEL CONTRO DELA	CIGAGCAGGCITICGISION STATEMENT CONTROLL STATES AND CARACAGE TO CAGG STATEMENT TO CAGG G STATEMENT TO CAGG CONTROLL STATEMENT C	GIGIAIAI CCGC TCCAA TAGAAATTCCTTAAGGAATTTATAGAAAAAGGCTGACGCAACAAGAATTAGACGCT AAAAGCGTTGAATTAAAATTCCTTAAGGAATTGAAACGATCTTAGCCGCTTGAACACACTAGAACTTATTTT	AAAAAGITTTGCCTTTAAATTTTAACCAAACGCTGCTCAATCAAATCCAAAAAATGAGTTTGAAAGAAA	CATTAAAGUCUA 2803 CGTGGTTTTATCCCGCCTAAAGACTTGTTAAAGCAATTAGAAAAATCAGCGCTTCTCTTTCTAAAGACATCGTAATA GCGATAAAGCAAGTAGAAAAATTAGAGCTTAGCTT	GCTTGATTTTACCTTTATTGTTGGGGATTCTTTGGGGAATTGG
2799 GCGG AAATT AGATT AGATT CATAT TTTT GATG GCTA	2801 ACGA	GCTT	TTAG	900 900 900 900 900 900 900 900 900 900	TGAT	AAAA	ATTT	2803 CGTC GCGA	. GCTT GATA
HP0935	HP0935							HP1530	

25

0 02/000301	PC1/EP01/1542
氏口≥をは口のの下っぱっぱっぱん ≧	8 10 1 0 0 8 2 0 0 0 1 2 5 1 5 10 8 0 8 8
にのひまにひんののコンキロをおくから	・ はっこうしゅん ロウスススススとにことしょく ー

W	/Q 译	02/ 02/	06¢ ₹ ≅	65(2)1 	စ္တ	တ္သ	×	z	ટ	z	ည		<u> </u>	<u> </u>		_	_]	S	S	ō	_	_	0	K	<u>~</u>	(1)	_	<u></u>	I,	ξ.	 > i		<u>.</u>		P(≤	CT	Œ.	P0: ∝	1/1
	SGKTLI	SIWTSL	SIFSG	NATIV	ONSYFI	FSNSF	TNSTNL	VSVGTS	ELOGD	ATINĎY/	NITTSL	NSSLDF	SPITFHO	/LDLKN			ESFKU	<u>۲</u>	EINNRV	SSKNA	VWMGR	EVNFR	GTLÖLW	KPSNT	VINPPN		MAHLH	TGNIT	NFEFK	NLKV0	SGVTGK	VK	ארבונ	PITION	OFSNI 1	ATLNVG	MKINSA	SLGTWS	MDICK	2
	(SIDFY)	IVFGAK	OKIVIT	OGILL	SANIGA	MALNLD	KNAISF	NSNES	SNHST	INSVI	VNFNSA	JEN SN	NAFSO	PNNSS/	טרנאטר	TAINE T	INALKII	YNIGSE	ILIDNFL	JASEGIT	KLMĞN	TSKVTG	SNKTHI	KOKPKO	UNSNI	FAGGK	CASLTT	ILLVEN!	LAGSS/	SLGRF	NTLDF	FNINE		CACCT	VANDVS	3660	SFY ÒPL	IGYGÑV	NNNN	SMVN
	TIYYYDI	GONSA	GHYEA	LNFNG	MNFISN	PNFSF	VFKFNA	KSVLFC	NASINA	JUNOST	NFNGA	VSLGG	AFNFYD	SGNLLN		SNWY		SIKNT	FNAKN	STALTIC	LASNSV	SYSTIN	NOAGIIA	PEGGYI	ŹNSAQ	ŻVIDGP	₹ \GGY	AASGR	VGGYA	TENNO	IGNGG	VAVK	SEUIGS		TI GON	TINATA	VÖSAT	LLKAKI	ERLAL	FAIGN
	2806 NLGNANNTIYYYDKSIDFYASGKTLFTKO	AEFSQTFTGQNSAIVFGAKSIWTSLSD 70	OCIGE!	GGGAS	AGTOSSSMNFISNSANIQAQNSYFIDD	TAQNGGNPNFSFNALNLDFSNSSFRG	YVGKTQSVFKFNAKNAISFTNSTNLSS	GLYQMQAKSVLFDNSNLŚVSVGTSSIK	ANAINLSQNASINASNHSTLELQGDLN	VNDTSSLNLNOSTINVSNNATINDYASI	IASNGSHLNFNGAVNFNSANITTSLNN	SSIVFKGAVSLGGOFNLSNNSSLDFQG	SSAITSNIAFNFYDNAFSOSPITFHOAL	DIKAPLSLGGNLLNPNNSSVLDLKNSQ	LVFGDGGSCN(ANIDLE, SDLNDNKNKV	Y NII CADMINSNWY Y EKISF FGMHINDGIY	DAKNO! YSF I NPLNNALKITESFKUNG	ILSVTLSQIPGIKNTLYNIGSEIF	RTTRV	GAGRKASSTVLTLOASEGITSSKNAEIS	LYDGATLNLASNSVKLMĠNVWMGRLQ	YVGAYLAPSYSTINTSKVTGEVNFNHL	TVGDHNAAQAGIIASNKTHIGTLDLWQ	SAGLNIIAPPEGGYKDKPKDKPSNTTO	NNANNNQÓNSAQNNSNTQVINPPNSA	OKTEIOPTÓVIDGPFAGGKDTVVNIDRI	NTNADGTIKVGGYKASLTTNAAHLHIG	KGGINLSNOASGRTLLVENLTGNITVD	GPLRVNNQVGGYALAGSSANFEFKAG	TDTKNGTATFNNDISLGRFVNLKVDAH	TANFKGIDTGNGGFNTLDFSGVTGKVN	INKLITASTNVAVKNFNINELVVKTNGV	SVGEY I AFSEDIGSUSKIN I VKLETGT PSIESOCY/KEKSOEKTVIDEEXXSDIAN	KSITSGGVARKSGERLVIDER I SEVVI VEDABNIKNVEITBKEASSTBENDWGT	SKI MENNI TI GONAVMOYSOFSNI TIO	GDFINNOGTINYLVRGGOVATLNVGNA	AAMFFSNNVDSATGFYOPLMKINSAQ	DLIKNKEHVLLKAKIIGYGNVSLGTNSIS	NVNLIEOFKERLALYNNNNRMDICVVR	NTDDIKACGTAIGNOSMVNNPDN
	2806 NL	A A	Z	SS	¥	<u>+</u>	<u> </u>	<u>ಠ</u>	¥	<u>\$</u>	<u>¥</u>	SS	SS	<u> </u>	<u>.</u>	Z :	<u>\$</u> :	S.	2808/AD	& ∶	<u>-</u>	<u>\$</u>	<u> </u>	SA	Z	ğ	토	<u>X</u>	g	2	<u> </u>	Ž	200	2 2	- X	9	₹	급	₹!	Ξ
			_																••																					
	ICTAT	GACG	CGGT	стп	BAACA	TTGA	AATG	SAT	[AATG	MAGC	ATTT	21993				,		1	GTGT	¥	GTGG	GGGA	CATA	AACCT	CACT	CTGG	AAG	ည္သည္ဟင္သ	GTTAT	ATA ATA	₩.				-					7
	<u>ACTATTACGACAAGAGCATTGATTTTTATGCGAGCGGGAAAACTCTA1</u>	I CACI AAAGGGGAATI II TOTCAAACATTCACCGGGCAAAACAGCGGGGATCGTTTTTGGGGGCTAAAAGCATATGGACG AGCTTAAGCGATGCACCGCAGTCTAACACCATCATTCGCTTTGGGGGAGAATAAGGGAGCAGGAGAAAAAAAA	GGCTTTATTACAGGGCATTATGAAGCGCAAAAGATTTACATCACCGGT	CGGTGGGGGGGGCGTTAATTTTAACGGGCTTCAAGGCATTCTTT	<u>AACGAACGCGACTITGTATAACCGCGCCGCTGGCACGCAAAGCTCGTCTATGAATTTTATCTCTAACAGCGCGAACA</u>	I I CAGECI CAAAACI CCIAII II AI AGACGAI ACCGCACAAAA TGGCGGTAACCCTAATTI CAGTITI CAACGCTTTGA	CCAAG	CONTENSITION CANCER CACCE OF THE PROPERTY OF T	AGIA HAAAGCCAATGCGATCAATCTTTCTCAAAATGCCTCTATTAATG	CERCEMICATION AND LABORATION AND AND AND AND AND AND AND AND AND AN	ACGAGGGGGGGTTAATTCAATTCAACGCGAATATTAACAACGAATTAAAATTAAAATTAAAATTGCGAGTGTGTGAATTAATT	TOTATA GEORGE CAST. CASCEGATION CASCEGATOR CAST. CONTRACTOR CONTRACTOR CAST. CONTRACTOR CAST. CA						*	ATAAT	ANTECESA ATTICITE ATTACK OF THE STATE OF THE	ACGUICAATTIGGUTICAAACAGCGTTAAATTAATGGGTAATGTGTG	1116GCCCCT	NI CACAACGCCGCTCAAGCAGGCATTATCGCTAGTAACAAGACTCATA	I I GECACACI I GENERAL I I GENERAL GENERAL GENERAL MANAGATTA TO COCOCOTOCA GAAGGC GOTTA TA A GGATA A A COTOCA GA GA COTOCA GA GA GA GA GA GA GA GA GA GA GA GA GA	AATGCTAACAACAACAACAGCGCTCAAAACAATAGTAACACT	TO SEE LA TRANCESCECE AND ASSESSED TO THE SECOND ASSESSED TO THE SEC	CTTCTTACCACCACTOR IN STREET STATES TO THE ST	ACCOUNTY TO CHANGE CONTROLL OF THE CANAGE CONTROLL CANDER CANDER CONTROLL OF THE CANDER CON	ATCACCETTER TO THE GEOCETT AND A GARDEN AND AND A GEOGRAPH AT CAME TO GEOGRAPH AT CAME	CGATHTAGTTTGGGAAGATTTGTGAATTAAAAAAGGGGGGGG	TANG TOOM TOOM TACKED TO THE TAKE OF THE TOOM TOOM TOOM TOOM TOOM TOOM TOOM TOO					٠.				
	99909	AAAAG	ATTTA	TTCAA	CTAAC/	GTTC	TCAATG	этстс	VATGCC	AACCT	CTCTC	AA							AAATCA	ATTACT	ATGGG	AAAAGI	GTAAC/	TTATAA	AACA	<u> </u>	IGGGA(AAGCG	CAAGT	AGCCA	4 5	•						•		
	TGCGA	GGGCT AGCAG	CAAAAC	၁၅၅၅၁	TTATCT	ATTTC	TAAT	AAAGC	CTCA	CGCTC	AATGG TOOTO	9							TTTAG	AAGGG	WATTA	ACTTC	CGCTA	99099	SCTCA	ATTGA	TAAAG	CAATC	AATAAT	GGCAC	5		_	٠.						
	A LE	AAGGG	AAGCG	ATTT	IGAATT	ACCCTA	1011	AGCTA	ATCTT	CCAGC	CGAGT	2						31.5	TAATT	CAG	CCG11	ATAAAC	CATTAT	CAGAA	ACAGO	SAGTO	ACGAI	TCTGT	GAGTG	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	<u> </u>					. •	- - - -			
٠.	SATTGA	GATCG	ATTATG	CCTTA	GTCTA.	CGGTA	SCAATC	ATGCA	GATCA	CGACA	GATTE	<u> </u>							AATTG/	SCAAGO	SAACA	GCACG	GCAGG	CCCTC	ACAAA	CACGC	3A166(A C	8 (1)	A ACC			•	•			· ·			
	4AGAG	:AGCGC	\GGGC/	3CGAG(AGCTC	AATGG(AAAACC	IATCA	AATGC	GTGAA	GAGCI	₹					٠					AIACA	CTCAA	ATCGC	AACC	CAAC	1000	30000		のとなった		. •		:,			•	:	٠.	
	ACGAC.	CARAAC	ATTACA	ည်၅၅၅	ACGCA	CACAA	16666	911199	MAGCC	TGAAT	AIGG	9			,				ASSA S	A	A LI		ອວວອວ	AACATI	AACAA	GAAAT	2 CAC	SCAPA CAPA	45 LO	95-75	ָ פַּרָי					•				
٠	CTATT)CGGGG	SCTIT	SGTGC	TGGC	TACCG	CIAIG		GIAIL	GCGAT	ACGA								ACGC!			200	CACA	GACTA	AIGCI	AAAAC 1		D		0 F C C C C C C C C C C C C C C C C C C	5						• • • • • • • • • • • • • • • • • • • •			
	CATTT/	ATTCAC	SCATAC	CTAGG	ည်သည်	AGACG/	AGAGG		AAGCA	TCAAG		5							A 10 10 10 10 10 10 10 10 10 10 10 10 10			¥ 600	SCGA	99999	AAAA	SCC AND COMPANY OF THE PARTY OF	541CG		\$ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	5 K 5 K 5 K 5 K 5 K 5 K 5 K 5 K 5 K 5 K	-				٠.				-	
	AACAC	CAAAC AGTCT	GCAAT	GCATT	ACCGC	TAT		ACGA	SSSAC	GAACI	\$2051 11000							0010	AG GG) (F 4 ()	541 GC	966A6	5	CAAAG	CACCO CACO CACO CACCO CACCO CACCO CACCO CACCO CACCO CACCO CACCO CACO CACCO CACCO CACCO CACCO CACCO CACO CACO CACCO CACO CACCO CACCO CACO CACCO CACO CO CACO CO CACO CACO CACO CACO CACO CACO CACO CACO CACO CACO CACO CACO CAC CAC	900 H			54	וליביל בינות בינות בינות בינות בינות בינות בינות בינות בינות בינות בינות בינות בינות בינות בינות בינות בינות בינות בינות	5				:				· ;-	
	SCAAAC	I CACI AAAGCGGAAI II I CI CAAACATI CA AGCTTAAGCGATGCACCGCAGTCTAACAC	GCGGCCATTGCTGGAATTTGCAATGCATA	AGCATTGAAAGCGGGAATCGCATTTCTAG	TGTAT/	CCIA		WCAG	CCAALLIAAGCGIIICAGIGGGGACAAGC			֝֝֞֝֝֝֝֓֓֝֝֝֓֓֝֝֝֓֓֝֝֡֝֝֓֓֓֓֡֝֝֡֓֓֓֓֓֡֝֡֝֓֡֡֝֡֡֝	-				٠	0.00	ACGAGG	AATGCGGAAATTCTCTTTATCATCCCAGC		A OTTO A TITTA A CONTO SECTOR	AGIGAAIIIAACCAICICACIGIGGGCGA	99191	AAGGATAACCIAGIAACACCACGCAAAT	₹ ()		ACCCTTTTACTORA A ATCTA ACCOCATA		GGATATTAGTTTGGGAAGATTGTGAATTT	; [:									
	GGAAT	CGGAA	recte(AGCGG	GACTI	A A A A C		֓֞֞֜֞֜֞֜֞֜֞֜֜֞֜֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֓֓֓֓֓֡֓֜֝֡֓֡֓֡֓֡֓֡֓֡֓֡	1	4 C		יייי									7			166A1					ر ا ا	֓֞֜֜֜֜֜֜֜֜֜֜֜֓֓֓֓֓֓֜֜֜֓֓֓֓֓֓֓֓֓֓֡֓֓֓֓֓֡֓֜֜֓֡֓֡֓֡֓֓֡֓	ACAC									
	TTTAG	TAAGC	GGCAT	4TTGA	SAACGC		- KO C					CTTTAGGAGGGCAGTT						710		מילים מילים מילים			- 6	SACA SACA SACA SACA SACA SACA SACA SACA		7				ATTAGE	GGTGGTTTCAACACCTT	.						·.		
	2805 ATAATTTAGGGAATGCAAACAACACCATT	80 C	<u> ၅</u>	AGC	¥ (2 5	֓֞֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	\$ { } } !	3 5	¥ (A 4 6 6 6	Į Į	<u>-</u>					1227	2807 PECCT CHILD COCACCACGAGAGI GGAI I I CAACGCI AAAAA I A ICTI AA I IGATAATI ITTI AGAAATCAATAATCGTGT	AATO	5 C	9 (2 6	9 6	2 6	9 (ع <u>د</u>	۲ <u>۲</u>	CATA	GGTG		_							
	28						-	•		•			•					186	707							•				-										
	26							-					_					1	<u>-</u>	_	_	_					_						_					_	_	-
	HP0797																	10000	2010																					

IJ

2810 SFLVSFLVAENAHEPEEIKÄKVÄYVKIP O QLEDLENNPVYIGQIIGVTYDLLLFDAE © FLEAKIKDGLDKTQIELLNRMPKWKKV SEELFRATYYYKIKGIKAIIFSLEVSAFS NKDKYIDHSIAPKYTLQYTJJSKNPRYAGN NVMAKDLQVLQYKTKDYDDKNNILVM E EIAFKEATWEDFHIKEAIKGIFDNASLN QIIKAKEGSVFYYCVLPKTIQNLSFDYF	2812 CPWLSNGGAGNVAGGNSIWAGIDKG DGSACGIFKNEISAIQDMIKNAEIAVEQ SKIVTANAQNQHNLDTGKAFNPYKDAN FAQSMFANARAQAEILNRAQAVVKDFE RIPAAFVKOSL GVCHEKGE DGNLRGTP SGTVTSNTWGAGCAYVGETVTNLKNS IAHFGDQAERIHNARNIAYTLANFSGQ YKKLGEHYDSITAALSSLPUAQSLQNV VSKKTNPNSPQGIQDNY	2814 YAQGINQRNAQFRIYLDWYLHHIGLFN PYKARIAEHVFKTTLAHDGIYYKLNYPP TTKYHGNSFTECAHFYLKNIYQQDLDD KSIEKLREQLGFIQKSEEFRRDSKIINLY RLSTPNVCSACCDDYDIKERSFLSLPL YQITQNPDSYYTEIHDFFRCINQRIRCF SKSC	2816 LALEVIRHSCAHLLAGSLKAYPDAKFF VGPVVEEGFYYDFKTSSKISEEDLPKIE AKMKEFAKLKLAITKETLTRICALERFK GDELKHAVMSKIGGDAFGVYQQGEFE DLCKGPHLPNTRFLNHFKI.TKLAGAYL GGDENNEMLIRIYGIAFATKIEGLKDYLF OIEEAKKRDHRKLGVELGLFSFDDEIG AGLPLWLPKGARLRKREDLLSOAIII	RGYEPVKGPEIL 2818 YGGSCPHGGGAFSGKDPSKVDRSAA YAARYVAKNLVASGVCDKATVQLAYAI OG GVIEPVSIYVNTHNTSKYSSAELEKCVKL SVFKLTPKGIIESLDLLRPIYSLTSAYGHT FGRELEEFTWEKTNKAEEIKAFFKR 61 75
2809 AAGTTTTTGGTAAGCTTTTTGGTTGCTGAAAACGCTCATGAGGCCAGAAGAAATCAAGGCTAAAGTGGCTTATGTGTGAAAAACCAATTATTGCTGAAATTATTGCTGAAATTATTGGGCTTATTGTTTTTGGAAAACCAAATTATTGCTGAATTATTGCTGAAATTATTGCTGAAATTATTGCTGAAAAAAAA	AGIN AND COCATIGGT TIGAGT GGT GGT GGC AGGC AT THE TIGG GCC GGA AT TAGE AT THE TIGG GCC GGA AT TAGE AT THE TIGG GCC GGA AT TAGE AT THE TIGG GCC AGG AT THE TIGG GCC AGG AT THE TIGG GCC AGG AT THE TIGG GCC AGG AT TO AGG GCC AGG AGC AT TO AGG GCC AGG GCC TO AGG AT THE TIGG GCC AGG AGG	2813 ATACGCGCAAGGCATTAACCAACGGAAACGCTCAATTCAGGATTTATTT	2815 CTTTGGCTTTAGAGGTGATTAGGCATTCATGCGCGAAAGCTTGAAAGCCTTGAAAAGCCTTTATCCGGACGCGAAAGCTTGAAAAGCCTTTATCCGGACGCGAAAATCAGCGAAGAGGGTTATTACGATTTCAAGAAGCTTCTCAAAAATCAGCGAAGAGGGTTTAATTACGATTTCAAGAACTTCTCAAAAATCAGCGAAGAGGATTTGCGAAGAGTTTGAAAAATTGAAGAAATTGAAGAAATTGAAGAA	2817 CTTATGGGGGGGGTTGCCCGCATGGCGGGGGGGCGTTTAGCGGGGAAGGCCCTAGCAAGTGGCTGGAGATTTA GCTATGCGGCCCGCTATGTGGCTAAAAATTTGGTAGCGGGGAAGACGCCTAGCAAAGTGGATAGGAGCGCG GCTTATGCGGCCGCTATGGCTAAAAATTTGGTAGCGGGGTTTGCGATAAAGCCGCTGCAAGTGGATAGGAGCGCG ATGCGATTGGGAATCGGTTTTCAAACTCACGCCAAAAGGCATAATGAAAGCTTGGATTTTAAGGCGCTGAGTTG GAAAAATGCGTTATGGCGCATTTTGGCGCGCAAAAGGCATTATTGAAAGCTTGGATTTAAAGCGCTGAGTTG ATTAAAGCGTTAAAGCGTTAAAAAAAATATTTTAAGGGATATTTTTAAAAAAAA
HP0797	11.0953	HP0933	HP0933	HP0933

•	•
r	
÷	٠

O_02/066501			PCT/EP01/15428
2820 ASVLSALLLVGLGAAPKHSVSANDKRM QDNLVSVIEKQTNKKVRILEIKPLKSSQ DLKMVVIEDPOTKYNIPLVVSKDGNLIIG LSNIFFSNKSDDVQLVAETNQKVQALN ATQONSAKLNAIFNEIPADYAIELPSTN AANKDKILYIVSDPMCPHCOKELTKLR DHLKENTVRMVVVGWLGVNSAKKAAL	2822 GGIACANLLHKNSGITIDIGGGSTECALI EKGKIKDLISLDVGTIRIKEMFLDKDLEV KLAKAFIQKEVSKLPFKHKNAFGVGGTI RALSKVLMKRFCYPIDSLHGYFIDAHK NLAFIEKIVMLKEDOLRLLGVNEFRLDS IRSGALILSVVLEHLKTSLMITSGVGVR EGVFLSDLLRHHYHKFPPNINPSLISLK DRFLPHEKHSQKVKKECVKLFEALSPL	2824 PEDNSIELSPSÖSAWRTNLVVRTNKAL YÖFILRIAGKONFASAYLTVKLEYPÖRH EVSSVIEEELKKREEAKRÖKELIKÖENL NTTAYINRVWIMASNEGIINKEKIREEKÖ KIILDOAKALETÖYVHNALKEKIREEKÖ KIILDOAKALETÖYVHNALKENPVPRNY NYYQAPEKRSKHIMPSEIFÜÖGTFTYF GFKNITLQPAIFVOYOPÖGKLSMTDAAIÖ PNMTNSGLRWYRVNEIAEKFKLIKÖKA LVTVINKGYGKNPLTKNYNIKNYGELER VIKKLPLVRÖK	2826 ÖKNHVYTPVYNELIEKYSEIPLNDKLKD TPFMVÓVKLPNYKDYLLDNKÓVVLTFK LVHHSKKITLIGDANKILGYKNYFGANG ARSDIDFYLQPTLNGKGVVMIASNYND NPNSKEKPQTFDVLQGSQPMLGANTK NLHGYDVSGANNKQVINEVAREKAĞL EKINQYYKTLLÖDKEQEYTTRKNNGRE ILETLSNRAGYQMRĞNVISSEIFKNGNL NMQAKEEEVREKLQEERENEYLRNGI RSLLSGK
2819 GAGCGAGTGTTGAGCGCGTTACTTCTTGTAGGCGCCAGCCCCCTAAACATTCAGTTTCAGCTAATGACAAA GGGATGCAGGATAATTTAGTGAGCGTGATTGAAAACGGCCCATAAAAAAGGCGTGCGT		2823 CCCTGAGGATAACTCCATAGAATTATCTCCTAGCGATAGCGCTTGGAGAACTAATCTTGTGCGGACTAATAAGCCCTGAGGATACCCGAGAATAAGCATAGAATAGCAATAGCAATAGCAATAGCAATACCCAAAGGAAACAGCGAAAGAACAATTTGCTTCAGCGTATCTAACAATTAGAATTAGAATAGCCAAAAAAGGAAGAAGAAGAAGAAGAAGAAGAAGAAATTAGAAATTAGAAATTAGAAAAATTAGAAGA	2825 AACAAAAGAACCATGTTATACGCCTGTGTATAATGAACTGATAGAGAAGTATAGTGAGATACCCTTAAATGAACAAACA
HP0933	HP0933	HP0933	НР0933

O 02/066501		PCT/EP01/1
2828 IIHSSLFHTDADSKDIWSQVRKGFDFIP GKTPVCVGVCYJAPYKNODLIGSSAFA WSLNFGATVGTLL(SSAQEKANNNG GSIWFGKNNLLYLHGNFNATNIFLTNN FNVGNPNAGGGATINFNADETLNADG LNYTNFQTVALGLQTSASQHSWANFN SKLSMEIKNSNFRDFTWGGFNFNSGRI TFENTTFSGWTNINGATESGSSYVNM VANTDLIFSNSILGGCIRYDLKANNIFN NSQMVIDVSKNYNQDSSLNGNVTFNNS RLSVKPNAAINIGDSQTQTALENASSL FYNNSVANFNGTTAFNGVSYLNLNPN AQVSFNQVNFNNANVTFYGIPLGKTP DFGNSARLINFKGNTNFNOATLNLRAK NIHINFQGVSTFKQNSTRNILGENGS FNALVSFYANNSCALNINGALNLSYMNLF GGDKKTSVYDVLQACINIDGLMGNNGY EKIRFYGIQIDKADYSFDNGVHSWRFT NPLNTTETITETLHNNRLKVQISQNGVS NNKMFNLAPSLYDYCIKNPYNETENSY NYTSDKVGTYYLTSNIKGFNQNNKTPG TYNAQNOPLQALHIYNQAITKQDLNMIA SLGKEFLPKINNLLSSGALDNLNSPNSF ETLFGIFEKYGITLNQENWKSLLKINNF SN	2830 GYRKSGEPYIVHPICI/ASLVAFCGGDE AMVCAALLHDVVEDTPCKIETIEGEFG ADVANLVDALTKITEIRKEELGVSSADP RMVVSALTFRKILISAIQDPRALVVKISD RLHNMLTLDALPHDKQVRISKETLAVY APIASRLGMSSIKNE	2832 FFYKNKEVAVLGGGLTAVEEAIYLANIC KKYYLIHRRDGFRCAPTLEHAKNNDKI EFLTPYVVEEIKGDASGVSSLSIKNTAT NEKRELVVPGFFIFVGYDVNNAVLKÖE DNSMLCKCDEYGSIVVDFSMKTNVQG LFAAGDIRIFAPKQVVCAASDGATAALS VISYLEHH
782	283	283
2827 CTATCCATTCTTCGCTTTTCCACAGACGCTGATTCTAAGGATATTTGGAGTCAAGACAATTTGATTTCACAGAGCAATTTGATTTCACAGAGCAATTTGGATTTTGGAGTCTATAAAAATCAAGACCTTATTGGAGTCTATAAAAATCAAGACCTTATTGGATTTTGCATGCGGAGCTTATTTGGAGTCGAGAGCCTTATTAGGAGAGCCTTATTTGGATTTTGCATGCGAATTTTGGATTAGTTAG	2829 GCAATACAGAAAAAGCGGCGGAGCCTTATATTGTCCATCCTATTTGCGTGGCAAGCTTGGTAGCGTTTTTGTGGGGGGC GATGAGGCGATGGTGTGCTGCTGCTGCTGATGTGGTGGTGGAAGACGCTTGTAAGATTGAAACGATTGAGC AAGAATTTGGGCAAGATGTGGCTTTTGCATGATGGTGGTGAAATCACTGAAATCAGGAAAGAAGAATTAGGC AAGAATTTGGGCAACATGTGGTGGTTTCAGTGCGCTCACTTACACAAATCAGGAAAGAAGAATTAGGCGCATACAGATTAGCGCCTTACAGAAGAATCAGTGGTTTTCAGAAAGATTTTCAGAAAGATTCCAAGATTCCAAGAAGATCC AAGAGCCTTAGTGGTAAAGATTAGCGACAGGTTGCACAACATGCTCACCTTAGACGCTTGCCTCATGACAAGCAAG	2831 GCTTCTTTTATAAAATAAAGAAGTAGCGGTGCTTGGTGGAGGCGATACCGCCGTAGAAGAGGCGATTTATTT
НР0933	HP0933	HP0933

C	,
Ē	`
_	
V	Г.

O 02/066501		DCT/ED04/45 404	D
2834 MFMCADAVIISKADMVEVFNFRVSQVFO EDMQKLKPEAPIFLMSSKDPKSLEDFKN NFLLEKKRENYQSTHSF	2836 ŚMLVGVAASLIPFLEHDDANRALMGTN MGRQAVPLLRSDAPIVGTGIEKIIARDS WGAIKANRAGVVEKIDSKNIYILGESKE EAYIDAYSLQKNLRTNGNTSFNGVPIV KVGDKVGAGQIIADGPSMDRGELALG KNVRVAFMPWNGYNFEDAIVVSECITK DDIFTSTHIYEKEVDARELKHGVEEFTA DIPDVKEEALAHLDESGIVKVGTYVSA GMILVGKTSPKGEIKSTPEERLRAIFG DKAGHVVNKSLYCPPSLEGTVIDVKVF TKKGYEKOARVLSAYEEEKAKLDMEH FDR.TMLNREELLRVSSLLSGAILEEPF SHNGKDYKEGDQIPKEEIASINRFTLAS LVKKYSKEVQNHYEITKNNFLEQKKVL	2838 EEFALKOVAKQATSSLLYRLGKTIILAS VCVEREPVSEDFLPLWOFLEKSYAAG KIPGGFWKREGRAODFEILTSRLIDRTL RPLFPKDYRYPTOITLMWLSHDIENDLC VSALNAASAALFLAHIAPIKSVSACRIAR MDNEFIINPSASLLNGSSLDLFVSGTKE SLNMIEMRSLGGKLNALEEPLMLEALE LAGKSLEETCTLYEEIFTPHONELFFKE AGGI	•
2833 GATGITICATGECGCGGATGGTTATCAGTAAAGCCGGATATGGTTGAGGTGTTTAATTTTCAGGGTTTCTCCAAGGTTCCCCAAAGGAGCATCCAAAGAGCGCTATTTTTTAATGAGGTTTTTTTAATGAGGTTTTGGAAGGTTTGGAAGGTTTGGAAGGTTTGGAAGGTTTGGAAGGTTTTGGAAGGTTTTGGAAGGTTTTGGAAGGTTTTGGAAGGTTTTGGAAGGTTTTGGAAGGTTTTGGAAGGTTTTAAAAGATTTAAAAAA	2835	2837 ČĞAAĞAĞİTCĞÇİÇİTÇAAACAÁĞITĞĞCÇAAAĞAĞGCÇĞÇĞCTÜÇTİTİTATAÇÇĞATİTAĞĞAAAAĞÇATİTİTTA AGGAGAAĞATÇIT AGGAGAGATÇITİTİT AGGAGAGAÇÇATİTİTİT AGGAGAGAÇÇATİTİTİT AGGAGAĞĞ ÇÖĞAĞĞ ÇÖĞ ÇAĞ TİTİTAĞĞAAATÇIT AGÇAGAĞĞ ÇÖĞ ÇAĞ GÖĞ ÇAĞ ÇAĞ ÇÜLTİTA GÖĞ ÇÜLÇÜN AĞĞA ÇÖĞ ÇÜLÇÜN AĞĞA ÇÖĞ ÇÜLÇÜN AĞĞA ÇÖĞ ÇÜLÇÜN AĞĞA ÇÖĞ ÇÜLÇÜN AĞĞA ÇÖĞ ÇÜLÇÜN AĞĞA ÇÖĞ ÇÜLÇÜN AĞĞA ÇÖĞ ÇÜLÇÜN AĞĞA ÇÖĞ ÇÜLÇÜN AĞĞA ÇÖĞ ÇÜLÇÜN AĞĞA ÇÖĞ ÇÜLÇÜN AĞĞA ÇÖĞ ÇÜLÜN AĞĞA ÇÖĞ ÇÜLÜN AĞĞA ÇÖĞ ÇÜLÜN AĞĞA ÇÖĞ ÇÜLÜN AĞĞA ÇÖĞ ÇÜLÜN AĞĞA ÇÖĞ ÇÜLÜN AĞĞA ÇÜLÜN AĞA ÇÜLÜN AĞA ÇÜLÜN AĞA ÇÜLÜN AĞA ÇÜLÜN AĞA ÇÜLÜN ÇÜLÜN AĞA ÇÜLÜN ÇÜLÜN AĞĞA ÇÜLÜN AĞA ÇÜLÜN ÇÜN AĞA ÇÜLÜN ÇÜN AĞA ÇÜLÜN ÇÜN AĞA ÇÜLÜN AĞA ÇÜLÜN ÇÜN AĞA ÇÜLÜN ÇÜN AĞĞ ÇÜLÜN AĞĞA ÇÜLÜN ÇÜN AĞA ÇÜLÜN ÇÜN AĞA ÇÜLÜN ÇÜN AĞA ÇÜLÜN ÇÜN AĞA ÇÜLÜN ÇÜN ÇÜN ÇÜN AĞA ÇÜLÜN ÇÜN ÇÜN AĞA ÇÜLÜN ÇÜN AĞA ÇÜLÜN ÇÜN ÇÜN AĞA ÇÜLÜN ÇÜN ÇÜN AĞA ÇÜLÜN ÇÜN ÇÜN ÇÜN ÇÜN ÇÜN ÇÜN ÇÜN ÇÜN ÇÜN Ç	
HP0933	HP0933	HP09933	

PCT	/EP01	/15428

1000		TO SET TO	
HP0933	2839	2839 GTGTTTTTGATGCAAGGGTTTTAAGAAGCUCTTTTTAAAAGAAGGGTTTGATATAGGCAAA	KGVLKEALELKKDRYFI.KEGFDIGKVE
	_	GAAAAGGGCGTTTTAAAAGAAGACGCTTGAAATTACAAAAAAAA	KVKDKAFFISLAKNYPKDPLIKNLPPSF
		GTTGAAAAAGTAAAAGATAAAGGCGTTTTTTAAAATGAAAAAGCCCGATAGCTTTTTTAAAGCC	KTDALILCQIECSKKRPIAFFKAALLNADS
		CCCCATCTTTAAAACAGACGCTTTGATTTAAAAAAAAAA	HTMIAYLAKKNNQIVAII2FKEPFKKPVS O
		CGCTCTTTTAAATGCAGATCACACGATGATGATGTTAGTTGGTAAAAAAAA	LKHSQKSLLELPRHCVVKIDTKKREISE
		GAGCCTTTTAAAAAACCTGTTTCTTTAAAGCACAGCCAAAACCTTTAAAAAACCTTTGTTG	LGALEDPLIDENLSLSLFDRVKDFSKDC
		ATTGATACTAAAAAGCGTGAAATCAGCGAGAATTAAAAGCGTAAAATAAAGCGGGAACTTAAAGCGGAGC	LNLAQHYAQLKASDFKDRINYSHIPFITI
		AGCCTTTTTGACAGGGTGAAGGATTTTGACCATGAAGACGATGA	DPKDAKDFDDAIFYDQEKRVLFVAVAD
	•	GATTITIAAAGACAGGATCAATATTOOCATTOOCATTOOTAATTOOTAGAAATTTOTAGAAAATTOOCAAAAATTOOCAAAAATTOOCAAAAATTOOCAAAAATTOOCAAAAATTOOCAAAAATTOOCAAAAATTOOCAAAAATTOOCAAAAATTOOCAAAAAAAA	VSEFVPKHSSLDKEARVRGFSVYFPNS
		CGATTTTTATGACCAAGAAAGAGAGAAAGAAGAGAAGAAAGA	VYPMLPLSLSQGACSLKAFEKRLALVY
	•	GTTTGGATAAAGAAGCIAGGGIIAGGGGTTTGAAAAACGCCTGGCTTTAGTGTATGAAATCCCTTTAGATATTTGA	EIPLDNLKN
			IONICAL STATE
	2007	AAAAAU	2842 EILVGESAKROAVINPEKITSIKRIMGL
HP0938	707	TCATACATTTAATGTTTAATGTAAGGTAAAGGCTAAAGAAGCCGAAAAGCGCTTGCCTTATAAGATTGTGGATAGGAATT	MFNEUKAKEAERKLF I NIVURINGAUNI
		<u> </u>	EISGENT I PUEISANICIMINENCIONES E
	- 2	SUPPLIED TO THE STATE OF THE SUPPLIED TO THE S	GESVIEAVII VPAYFNIJSURKAI NEAG
		SANCE CONTRACTOR TO A CONTRACT OF THE CASE	TIAGENVERINEP SAVICAT GEORGES
		ACATE SOCIETIES TA BABAGAGAGA A A A A A A A A A A A A A A	KIMVYDLGGG1FDV1VLE1GD1VVLVL
		SCATTATA CANA CASE CONTROLL OF THE TOTAL OF THE TABLE CONTROL OF THE TABLE OF THE T	ATGGDAFLGGDUFUNKVIDTLASETNA MINAKKEI ON WI
		ACCELT RESEARCH SECOND OF THE	ETGIEIKNOVMALCIRITIEAAEIVANDELS
		IGACA I COLOR I CANTO COCOCOCO A COLOR DE CANTO COLOR DE CANTO COLOR DE CANTO CANTO COLOR DE CANTO CAN	SAMETEINLPFITADATGPKHLVKKLIK
		B) I BCAACGCC PARAGONIC CONTROL OF THE TOTAL AND THE CONTROL OF THE GAAGE CTICACTAGGGCTAAATTTGAAAGCTTGAAAAAACTCACTAAGGGCTAAAATTTGAAAAGCTTGAAAAAAACTCACTAAGGGCTAAAATTTGAAAAACTTGAAAAAAAA	AKFESLTEDLMKETISKIESVIKUAGLIN
		CCTTTATCACCGCGGGGCTAACCGAACACTTCAAAACGTGGTGGTGGGGGGGG	NEISEVVMVGGSTRIPKVQEKVKAFINK
		GAGGAICICALGAAAGAAACGATCTTAATTAAGTCCTAAAGTCCAAGAAGGGTGAAAGGCGTTTATTAATAAAGATTT	DLNKSVNPDEVVAVGASIUGGVLNGD
			VKDVLLLDV1PLSLGIE: ILGGVM I NVID
		0000	RGTTIPAKKSOVFS AEDNOPAVSIMV
		GAAAGAT	LOGERELARDNKSLGAFDLUGIAFAFR
			GVPQIEVTFUIDANGIL I VSAQUNA I GN
	•		SUEINIS STATES AND SEVENDE
HP0938	2843	2843 CAGACGCTAAGAGCGTGGAATTAGAGGATTTGTATCACGAATTCAGTGAAGATAAGCGTTCTATTTCTATTTTGCCC CCACAAACGCCCACAAAGACATGCTCAAAGCGGTGGATTTTTTCAAAGAAAAAGGTCATACGGCTTATTTAGATGAG	2844 DAKSVELEDLYHEFSEDKSITTERT NAHKDMLKAVDFFKEKGHTAYLDEVR IVSTDFKDEI YEI HII
		GTGAGGGTCAGCACTGATGAAAAAGATTTTCTTTATGAATTGCACAIIAIIIAAAGGCIIGIIIGAAAGIIIAIIIAAAGIIIAAAAGACTAGAAGTAGAAGTAGAAGTA	
		AAACCATGGGTTGTGAAAAAAAAAAAAAAAAAAAAAAAA	·
		TCAGAAATCGGTCAATTCGCTAAAATCAAAAACCCCAACGCCAAAATCGGGGTTTGCGGGTGCACTGCAAGCCAACA	
		GGGAGCGGATATTTGAAAA	

wo

•	`
•	7

WO 02/066501	15		P	
2846 AKNSFKITPPTTIKEPNKILNCNNSGTT MRLYSGLLSAOKGLFVLSGDNSLNAR PMKRIIEPLKAFGAKILGREDNHFAPLV LGSPLKACHYESPIASAOVKSAFILSAL OAGGASTYKESELSRNHTEIMLKSLGA DIHNODGVLKISPLEKPLEAFDFTIAND PSSAFFFALACATPKSRLLLKNVLLNP TRIEAFEVLKKMGASIEYAGSKDLEM GDIYVEHAPLKAINIDGNIASLIÜEBPALS IAMLFAKGKSMVKNAKDLRAKESDRIK AVVSNFKALGIEGEEFDGFYVEGLEDI SPLKORFSRIKPPLIKSFNÜHMANSFA VLTLALPLEIDNI FCANISFPOFKHI I N	QFKKGSLNGN 2848 IKTSEGGTHEAGFKMGLSKAILÖYIGNN IKTKESRPISEDIKEGLIAVSLKMSEPL FEGGTKSRLGSSYARALVSKLYYDKIH QFLEENPNEAKIIANKALLAAKAREASK	2850 NGVEIVGLEHLDKVIYLDGAPIGKTPRS NPATYTGVMDEIRILFAEOKEAKILGYS ASRFSFNVKGGRCEKCGGDGDIKIEM HFLPDVLVGCDSCKGAKYNPOTLEIKV KGKSIADVLNMSVEEAYEFFAKFPKIAV KLKTLMÖVGLGYITLGONATTLSGGEA ORIKLAKELSKKDTGKTLYILDEPTTGL HFEDVNHLLÖVLHSLVALGNSMLVIEM NLDIIKNADYIIDMGPDGGDKGGKVIAS GTPLEVAONCEKTÖSYTGKFLAL	2852 YHLFGFTGTPIFAANCDKNINPLGTTEG KFGKCLHOYTIIDAIRDKINLPFRVEYH NTIKAKEDIKDNKVRAVDEKNALLDTRR IKEITKCILERFNÖATKNIKKFNSILACSSI EALKKYYÖAFKEEKHDLKIAAIFSYSAN EEIDTLEDENNESACRLDKSSRDFLEG AIADYNGMFĞVSFÖTSDQKFÖSYYKD	
2845 CGCCAAAAATTCTTTTAAAATCACACCCCCAACAACTATAAAGGAGCCTAACAAGATTTTAAATTGCAACAATTCTGGC ACAACCATGCGTTTATACAGGGGCTTTTAAGCGCTCAAAAAGGGCTTTTTGTTTTAAGGGGGACAATTCCTTAAAC GCACCCCCTTGAAAAAGAATCATTGAGCCTTTGAAGGCCTTTTGGGGCAAAATTTTAGGGAGAGAGA	2847 ACÁTTAAAACTTCTGAAGGTGGCACGCATGAGGCGGGCTTTAAAATGGGCTTGTCTAAAGCAATTTGCAÁTATATTG GCAATAATATTAAAACCAAAGAGTCACGCCCATCTCTGAAGATATTAAAGAGGGGTTGATCGCTGTTGTGAGCTTG AAAATGAGCGAGCCTTGTTTGAAGGGCAGACTAAATCCAAAACTCGGCAGTTCGTATGCGCGCGC	2849 GAATGGGGTGGAGATTGTAGGGTTGGAGCATTTGGATAAAGTGATTATTTAGATCAAGCCCCCATAGGCAAAACCCCCCATAGGCAAAACCCCCCATAGGCAAAACCCCCCATAGGCAAAACCCCCCAAAACCCCCCAAAACCCCCCAAAACCCCC	2851 ATACCACCTTTTGGCTTTTACTGGCACCCATTTTTGCAGCTAATTGCGATAAAACCACCCTTTAGGCACGACAGA GCAAAAGTTTGGGAAATGCTCCACCAATACACCATTATTGATGCGATCAGGGATAAAAACCTTTAGGCACGACAGA GCAAAAGCTTTGGGAAATGCTCCACCAATACACCATTATTGATGCGATCAGGGGATAAAAACGTTTTGCATTAGAAAAAAAA	2853 ICCATGAMAGGGTAGCGACGGCAATCTCCGTGCACGCCATCTGGCACGGTTACTTCTAACACACTGGGGAGCCGG CTGCAAAAGGGTAGCGAAACCGTAACAAATCTCAAAAAACAGCGCTCGCT
HP0938	HP0938	88860 1008 1008 1008 1008 1008 1008 1008	HP0938	HP1414

v	`
٣	7
↸	r

	• •	••	•	PCT/EP01/15428
2876 APLYEEHHQVRYDESVFKACVDLTSD OYMHDKFLPDKAIELLD=VGSRKKISPKKS GKKIGVDDVKETLALKLKIPKMRLSSDK GKKIGVDDVKETLALKLKIPKMRLSSDK GKLIRULEKSLKNKIFAQAEAISLVSNA SKIGHCGLSAKNKPVGS:FLFVGPSGVGK TELAKELAINLUHFERFDMSEYKEAH SVAKLIGSPSGYVGFEQGGLIVNAKK HPHCLLLDEIEKAHSINVYDLLLQVMD NATLSDNLGNQSFKI+VILIMTSNVGS KDKDTLGFFSAKNTK*VDKAVKELLTPE LRSRIDAIVPFNALSLEDFERIVSVELDK LKALALEQDITLKFHKI:	2878 EKDYTQGGYGVLFEGLDSSDNALILQH LQQNQIPYKVSKDDTILPKDKVYEERIT LASQGIPKTSKVGFEIFOTKDFGATDFD QNIKLIRAIEGELSRTIESLNPILKANVHI AIPKDSVFVAKEVPPSASVMLKLKPDM KLSPTQILGIKNLIAAA/PK Z880 PYJARNYPLEKSVLKE?HEALFGGVKG DEILKEIVFLAAKLKIPFLVCEMGYDQLK SLKECLEFGGYDAEFYK	2882 SIALSVRCVIHSLEKTLNDEEVNSAVQK ALEILEKEFNARLKG	2884 LVFVSGQLGIDVSTGEFKGADIHSQTT QSMENIKAILKEAGLG VIDSVVKTTILLK SLDDFAVVNGIYGSYFTEPYPARATFQ VAKLPKDALVEIEAIA	2886 FTNRKKRFRENACKNAEYSNHEASSH HKKEHRPNKKPNNHHIKOKHAKTRNYA OEELDSNKVEGVTEILHVNERGTLGFH KELKKGVEANNKIOVE:HLNPHYKMNLN SKASVKITPLGGLGENGGNMMVIETPKS ANVIDAGMSFPKEGLFGVDILIPDFSYLH QIKDKIAGIIITHAHEDHIGATPYLFKELD FPLYGTPLSLGLIGSKFDEHGLKKYRS YFKIVEKRCPISVGFFIEWIHITHSIIDS
2875 TCGCTCCCCTTTATGAAGAACACCAGGGTGCGTTATGATGAGAGCGTGTTTAAGGCGTGGGTTTAACGGGTGGATTTAACGGGTGGGT	2877 AAGAAAAGACTACACGCAAGGGGTTATGGGGGTTTATTTGAAGGTTTAGACTCTAGCGGTTAACCTTTACTTAC		2883 TCTTGTTTTTGTCTCTGGGCAATTAGGCATTGTAAGCACCGGCGGGGGTTTAAAGGCCGCAGCATTCATCTCAAAC CACGCAATCCATGGAAAATATCAAAGCGATTTTAAAAAGAAGCAGGGTTAGGGATGGGATAGCGTGAAAACGACTA TTTTATTGAAAAGTTTAGACGATTTTGCGGTGGTGGAATGGAATCTATGGGAGTTATTTACAGAGCCTTATCCGGCCA GAGCGACCTTTCAAGTGGCTAAACTGCCTAAAGACGCTTTAGTAGAAATTGAAGCGATAGCC	2885 CTTCACCAACCGCAAAAAGCGTTTCAGAGAAAACGCGCAAAAAAACGCTGGGTTTTCAACCAAC
HP1533	HP1533	НР1533	HP1533	HP1533

•	٥	>
r		

WO 02/066501 SAN SAN SAN SAN SAN SAN SAN SAN SAN SAN	N S S H N S S H	F 8528844	PCT/EP01/15428
2888 LYGGIACANLLHKNSGITIDIGGGSTEC ALIEKGKIKDLISLDVGTIRIKEMFLDKD EVKLAKAFIQKEVSKLPFKHKNAFGVG GTIRALSKVLMKRFCYPIDSLHGYUNG GTIRALSKVLMKRFCYPIDSLHGYUNGERIG DSIRSGALILSVVLEHLKTSLMITSGVG VREGYFLSDLLRHHYHKFPPNINPSLIS LKDRFLPHEKHSQKVKKECVKLFEALS PLHKIAGELASMGKILSVY I AHKHS	2890 NTLLAYLNTRNNDFNIQVFDSDEESPE KLEGTYKEIEKEFPFVIALLTKEGVEN LLONTTISTPTYVPTVNRAQLENGTER SLSERLYFGGIDYKEQLSMLTAFINPNS PVIEYDDGLIGERLRQITESLSIEVKH GENISYKOATSFSKNIFRKNDAFFKNSIL ILNTPTTKSGLILSQIGLLEYKPLKILSTQ INFNPSLLLTQPKDRKDLFIVNALQNS DETLIEYASLLESDLRHDWVNYSSAIGL	EVELNI LDPHFKKSFGENLEDNQVRYH NGIY. 2892 LSGRLCGLTHMDKCFYADNGSSCVEIA LKMSYHAHFLKNGTRRKKLFLSLSNSY HGETLGALSVGDVKLYKOTYTPLLLKN LTTPVPKNDHEIENSLNALKRLLDKHSE EICAFIAEPLLGCAGNIMHIYSARYLKQA VLLCKGKNIHIIFDEIATGFGRTGSMFA YEQCEIKPDFLCLSKGISGGYLPLSALL THNEIYNĞFYAPYE	2894 KKDACGFIYEISEFMKAYTALLKKÖDRY VYLLRYLPSRYWASILTTALYVKYPDFD ALKKLLVSYYYOTWIAGGTITRIKOTSIN IIKNVKSNKSVETIKELILNSIDSYNTFDO YLYNLWDSSSVYHSKWYRPVLALANY FMADEEKPHFIAMDAETQVEHILPÖTP KRGSQWNADFDKEKREEWVNNIANLT ILLKRKNAHALNGDFDERRKIYGGKDT SKVISCYDITKELYSNYRKWNIEKSLÖE RYKSLYNTITPVLHIEGGEDDFEDDFD
			18
2887 CGCTCTATGGCGGGATTGCGTGCGCGAATTTGTTGCATAAAATTCAGGGGATCACGATAGATA	2889 TGAACACCCTTTTAGCGTATTTGAACACCAGAAACGATTTCAATATCCAAGTCTTTGACAGCGATGAAGAAGCCCCTGAAAAAGAAAACCTATTAGACAAACCTATAAAGAAAATTGAAAAAAGAAAATTGAAAAAAAA	2891 GCTCTCTCAAAGGCTTTGCCAGGTCATATGGATAAGGTCGGTTACCACAATGAATTTATAAAGGTCGGTTACCACAATGAATTTATAAAGAATCAAATGCATTTATAAAGAATCAAATGCATTTATAAAGAATCAAATGCTTTTATAAAGAATCAAAATGCAAAAAGGCTTTTTTAAAGAATCAAATGCAAAAAGGCCCAAAAAGGCTTTTTTAAAGGCTTCTAAATGCCCAAAAAGCCACACACA	2883 GCAAÁAÁGÁCGÉTTGCGGGTTCATCTATGAGÁTCAGCGAGTTCATGAAÁAÁGCCTATÁCCGCATTGCTAAAÁAACAA GACCGATACGTCTATTTATGAGGTACTCCCCTCTAGGTATTGGGCCAGCATTTTAACGACTGCCCTTTATGTCAAA GACCGATACGTCTTATAAAAAGCTTTTGGTGTCTTATTACCAAACTTGGATTGCAGGAGCTTCAAA CGCATCAAGCAAACCAGTATCAACATTATCAAAAAGCAATAAGAGCGTTGAAACCATCAAAGGAGCTTATA AATGGCATCGACTCTTATAACACCTTTGATCAATAACTTATAGGAATGGGATAGCTCTTCTATTAACAGCATGAATGGATG AATGGGTGCCTGTCTTATAACACCTTTGATCAATAACTTATAGGAAAACCCCATTTTATCGCTATGGATG AATGGGTGCTCCTGTCTTTTTGCCCTAGCTAATTATTCAGGAAGGA
HP1224	HP1224	224	24
효	皇	HP1224	HP1224

Į		•
	~	•
i	_	ï

w	02/066501	•			PCT/EP01/15428
	IKKNGMM IKKONLV ETSERYH LSFTHHN NILNFSKI CANSLISI CKEYLTC LENIAILYF IGALSFYE FIKRYLN EGLNLEEA FIKMIGRL LKSYEKE KYSCMSV	2898 PTPYMKEPKODGARTAVVHKDGVHLE WVALGYKVPAFKHKDQVALDALSRLL GEGKSSWLQSELVDKKRLASQAFSHN MOLQDESVFLFIAGGNFNVKAEALQKE IVALLEKLKKGETTQAELJKLKINDKADF ISNLESSSDVAGLFADYLVQNDIQGLTD YQRQFLDLKVSDLVRVANEYFKDTQST	2800 DIHFKTLDSNQSVETIEV EIILPR	2902 IYEIEVKLGSGVVGVFKITWVAE	2904 SALIQWENNPSAKIATYAVYRFEANSK TPLRFGNITKNQFVDKDIAKVGVAYRY QVVSVDKDGLESHPSKEVRLFLER
	2895 CGATGAAGCGCTGTGCAAACAGCTCAAAATTTCAAACTITTAGAGCCAGTATTTCTCAAATCAAA	2897 TCCCCACCCCTTACATGAAAGAGCCTAAGCAAGATGGAACGGCAGTCGTGCATAAAGGATGGGGTCCATTT AGAATGGGTGGCCTTAGGGTATAAAGTGCCTTTCAAGCATAAAGATCGAGTCGCCTTAGACGCTAAGTAGGC TTTTAGGCGAAGAAAAGCTCGTGGTTGCCTTTCAAGCAATTAGGAAAAAAAA	2899 CAGACATCCATTTCAAAACCCTTGACAGCAGCGGGGGGGAACGGTTGAAGTGGGTTGAGGTTATATTACCTAGATAGT GAATCAACGAATGAAAAGCCACTTCCAATACAGCGCGTGGAAACGGTTGAAGCCTTTGACATTCTCAAAGACCC CCCTAAAAAACTCTATTGTGTGGGCGATACCAAGCCTTTTGGACACGCCTTTAAAAGCCGTTGACGCACAAGAA GACCCACCCCTTACAGCAACAACACACGATCACTCTAGGCTAGGCCTTGCTAAAAATGGCCGGTTATTGTGAGT GACCCACCCCTTACAGCAACACACGATCACTCTAGCTAGAGAGCCTTGCTAAAAATGGCCGGTTATTGTGAGT	2901 GGATITATGAGATTGAAGTCAAGCTTGGATCGGGGGTTGTGGGCGTGTTTAAAATTGATGTGGTGGCTGAGTAGAAA ATGTTTGAAGCGACGACGATTTAGGCTATAGAGGGGGAATTGAATCATAAAAAGTTCGCGCTCATTGGAGGCGATGG GCAGGTAACTTTGGGTAATTGCGTGGTCAAAGCCAATGCGAC	2903 CTTCAGCCCTCATTCAATGGGAAAATAACCCAAGCGCTAAAATAGCCACTTATGCGGTGTATCGCTTTGAAGCCAAC TCTAAAACCCCTTTGCGCTTTGGGAAAATACCCAAAAACCAATTCGTGGATAAGGACATGGAGTGGGGTTA TCTAAAAGGGTTTTGGGATAAGGATATCACCAAAATCGTGGATAAGGACATGAAGTGGGGTTGTTTTTAGAGGCTTA TCGCTATCAAGGGTTTTAATGCCCCATTTTTTAGCCAAGCTGGATTTTAAAACCTTTAGAATACCCCTTAATTGAAGGGGATT TTTGTTTCATAGGGAATTTTTAAGCTTAAAAAACCCCACTAAAAGCGGAAAAGCGAAGGGGTTTT AAAACAAAAATCAGGGCAATGATTTTTAAAAAAACCCCACTAAAATTGCAAAAAGCGCCTTTAAAAAAGGGGGTTTT AAAACAAGCTTTAAGGGATTATTGGCAATCTTTTGAGGTCATTTCCAAAAAATTGCAAGAAATTCTAAACATGGGGC GGAAAAAAACCCTTGATTTAGGAACTTTTGAAGAAAATTCAAAAAATTCAAAAAATTCAAAAAATCAAAACCCCTTGATTTAGGAACTTTTGAAAAAAAA
	HP1224	HP0134	HP1223	HP1223	HP1223

Ξ	
•	

VO 02/066501	3	
2906 VLAGLLTFLNRNECNIVGVSYLGYKÖK YSSHCEVSFEIATDKADWIRALINRKYQ DRIVELSSLDDAYES	2908 VFKDSKKDACGFIYEISEFMKAYTALLK KQDRYVYLLRYLPSRYWASILTALY KYPDFDALKKLLVSYYYQTWIAGGTITR IKQTSINIIKNVKSNKSVETIKELILNSIDS YNTFDQYLYNLWDSSSYYHSKWNRPV LALANYFMADEEKPHFIAMDAETQVEH ILPQTPKRGSQWNADFDKEKREEWWN NIANLTLLKRKKNAHALNGDFDEKRKIY GGKDTSKVISCYDITKELYSNYRKWNE KSLQERYKSLYN	2910 ASVLSALLLVGLGAAPKHSVSANDKRM GDNLVSVIEKOTNKKVRILEIKPLKSSO DLKMVIEDPDTKYNIPLVVSKDGNLIIG LSNIFFSNKSDDVQLVAETNQKVQALN ATQQNSAKLNAIFNEIPADYAIELPSTN AANKDKILYIVSDPMCPHCOKELTKLR DHLKENTYRMVVVGWLGVNSAKKAAL IQEEMAKARARGASVEDKISILEKIYST ÖYDINAGKEPEDLRTKVENTTKKIFES GVIKGVPFLYHYKA
28	8	782
2905 GGTTITAGCGGGTTTATTAAACATTGAATGAATGCAACATTGTGGGCGTGTCTTATTTGGGCTTAAAGGA CAAGTATTTAGCGGGTTTATTAAACTTATTGAAATGCCACAGATTGTGGGCGTTGGATCAGAGCCTTAAAGGAAT CAAGTATTCTAGCAATTGTGAATTATCCAGTCTGGATGACGCCTTATGAATCATAATAAGCCCTAATGAATCATTAGGAAT GAACATGGAACAAAAAATTTAGGAATTGCCTTAAAGAAGCCGGGGTTTGGATTAGAATCAT TGAAAGTTGGTGAGGAAATATTATGAAACCAATGAACGCTTAATGAAGCCGGGTTTGATTTAGGCCTCAGA TTTGCATTTAGGGCATACGGTATTGATCCAAAAACTGGCTTTATTGCAAAATGGGGCTTAGGGTTAAGTTTTTGAT TGGGGATTTTACCGCTATGATGGCGATCCTACAGGGAAAAATGTATTAGAACCGGGAAGTCTTAAGTTTTGAT TGGGGATTTTACCGCTATGATAGGCGATCCTAAAAAACTGGGGAAAACGCCGAAGTTTTAACCCTTAAGGGCAAGGCTTAAAAACGCGGAAGTCTTAAAAACGCGAAAATGTAAAAAACGGGAAAATGTAAAAAAACGCGAAAATGTAAAAAAACGCGAAAATGTAAAAAAAA	2907 AGGTGTTCAAAGACAGCAAAAAGACGCTTGCGGGTTCATGAGATCAGCGAGTTCATGAAAAGCCTATACCGCA TIGCTAAAAAAAACAAGACCGATACGTCTATTTATTGAGGTACCCCTCTAGGTTCATGAAATACCGATTTTAACCAACTTTTAAACGACT TIGCTAAAAAAACAATACCCTGATTTTGACGCTTTGAAAAGCCTTTATTATTACCAAACTTGGATTGCAG GCCCTTTATGTCAAAATACCTCAAACCGCTTTGAAAAGCTTTAAAAAGCAATAAGAGCGTTGAAACCCTT GAGGCACGATCAAGCAACCAGTTATAAAACCTTTTTTCATGGCAGATAACTTATGGAAACCCTTT CTGTTTATCATAGCAAATGGCTCCTGTCTTATAACACCTTTTGATCAAAAAGAGAAGAAACCCTTT TTATCGCTATGGAAATGGGTGCGTCCTGTCTTAGCCCTAATTTTCATGGCAGATGAAGAAACCCCATT TTATCGCTATGGAAAAGAAAA	2909 GAGCGAGTGTGTTCAGCCGCTTACTTCTTGAGAGACCCAATAAAACATTCAGTTTCAGCTAATGACAAACAA
HP1223	HP1223	HP1102

Q	١
~	٦
V	۲

WO 02/066501

HP1102	2911	2911/IGCÁTTGGGGGGGAATGTTAAAATGATCGTGGAAAAAAAATAAAAATTAACAAAAATTAACAAAATTAACAAAATTAACAAAATTAAAAAA	2040	AI COM MAN MAN TO MAN TO THE COLUMN TO THE C
		CGCGCTCCAAAAAATTAACGAATTAACCAAATGAACAAAAACGCTCTCTAGAACGCTCTCTTCTGAAAAAATGCTTTGAACCAAAACGCTCCAAAAAAATGCTTTGAACAAAAATGCTTTCTGAACAAAAATGCTTTGAACCGTTAGAACGCTCTAGAACACGCTCAAAAAAATGCTTTCTGAACAAAAAATGCTTTCTAGAACACGCTCAAAAAAATGCTTAGAACCGTTAGAACCGTTAGAACCGTTAGAACACGCTCAAAAAAGCGTTAGAAAAAGCGTTAGAAAAAGCGTTAGAAAAAGCGTTAGAAAAAGCGTTAGAAAAAGCGTTAAAAAGCGTTAAAAAGCGTTAAAAAGCGTTAAAAAGCGTTAAAAAGCGTTAAAAAGCGTTAAAAAATTTCAAAAAATTTCAAAAAATTTCAAAAAATTTCAAAAAA	N	ALGENVKMINEKUKINI QI ELQIMMQIAL QKNNEIIKLKMNQQNALLIFALKNSFEP SYTLKTOMEMLSOALGSSSDNAQYIAY NTIGIKAFEETLKGFETWLKVAMQKATL IDYNSLTGOALFQSAIYAFALSFSSMG APFGIIETFTLAPTKCPYLIJGLKISACLM EQVIONYRMIVALIQNKLSDADFQNIAY LNGINGEIKTLKGSVDLNALIEVAILNAE NHLNYIENLEKKADLWEE JLKLERETT ARNIASSKVIVK
HP1102	2913	2913 TGACAGCGATTTGAAAAACGACCCTAAGGAATTTTACGAACTCGCTAAGAACGATTTGTATCGTGAAGATATTGTCGT TTTTTCGCCTCATGGGGACACTTACACTTTACCGGTGGGTG	2914	2914 DSDLKNDPKEFYELAKNCLYREDIVVF SPHGDTYTLPVGAIALDFAYMVHSDLG DKATDAYINSKKALLNDELRSGDVVKII KGDKIIPRFIWMDQLKTSKAKNHLRIQRI RNRL
HP0495	2915	12915 GTAAAATCATTICTICAGCGATTIGAAAAAATCCACTCTCTTAATGGGTTTGACACTGATGAGCGATGAAACAAGGCCA TTATCAATTACATTAC	2916	2916 KIISSAFEKIHSLNGFDTDE AMKOAIINH YOSHLPLMPEGILLNACSIETLKELGE FISHQYSKKALSIPKKGDK.TALIELGE FISHQYSKRALSIPKKGDK.TALIELAMK NAQEIFSQEKTSNEDLILEEARSLFKLE CMPYRVEIFDTSHHSSSQCVGGMVY ENNAFOKNSYRRYHLKGSIDEYTQMSE LLTRRALDFAKEPPPNLWVIDGGRAQL NIALEILKSSGSFVEVIAISKEKRDSKAY RSKGGAKDIIHTPSDTFKLLPSDKRLQ WVQKLRDESHRYAINFHRSTKLKNMK QIALLKEKGIGEASVKKLLDYFGSFEAIE KASEQEKNAVLKKRI
HP0495	2917	2917 GCGTGCCTCACATCGTTGTTTCTTAAACAAACAAGACATGGTAGATGACCAAGAATTGTTAGAACTTGTAGAAATGG AAGTGCGCGAATTGTTGAGCGCGTATGAATTTCCTGGCG	2918	2918 VPHIVVFLNKODMVDDOELLELVEMEV RELLSAYEFPG
HP0132	2919	2919 CATGTGCGTTTGCGTTCAAGCTTACGCCGAGGATTACTTTTTTAGGGATTTTAAATCTTAGAGATTTGCCCCAAAA ACTCCATCTTGATAAAAAGCTCTCCCAAACAATACAGCCATGCAACTTAACGCATCAAAAACCTTCTAC ACTCCATCTTGATAAAAAGCTCTCCCAAACAATACAGCCATGCAACTTAACGCATCAAAACCTTAGCGCTTAGCGTTAGCGCTTAGCGCTTAGCGTTAGCGCTTAGCGCTTAGCGCTTAGCGCTTAGCGCTTAGAAAGCG TTTGGTGAGTAAGAATAAGCAATACGGCTTAAAAGGCTTATAAAAGCCTTGGGCTAAAAGAGCGTGGAACTATTACAGAGCGAAAAAAAA	2920	2920 MCVCVQAYAEQDYFFRDFKSRDLPOK LHLDKKLSQTIQPCMQLNASKHYTSTG VREPDKCTKSFKKSALMSYDLALGYLV SKNKQYGLKAIEILNAWAKELQSVDTY QSEDNINFYMPYMNMAYWFVKKAFPS PEYEDFIKRMRQYSQSALNTNHGAWG ILFDVSSALALDDNALLHNSAN

PCT/EP01/15428

440

				PC1/EP01/15428
2922 RDTGHFLDCSFDIHDSVGVLDEYFAQS EFFTNIEDFEKHLEQSKDMGKEINYLSV CTPTHTHFDHIRFGLRNGMHVICEKPL VLDPGEIQELKDLEVKHQKRVFSLLPL RLHCDTLALKEKIKSELDKNPSKVFDIT LTYISVQ	2924 K	2926 KVFDASREVYRYYHTQDFTNRPYNAN ASLYDIKEFFQGRNKQGKLNLPAKAKD EYYKQLYANLQDALKDLAKEIQPKVYE YGFLRE	2928 SSSGSNNGYTPČNSTNGSNKTSGNNC YEPNKQQNATTATATTDSNLQKVYND AQKIANIIASSGNNKGVENGLKQFFEAL KNNSSSLSNLCGNGSSGSSGTTCSG WLINLLGAIPTNGVSDTNNLINLLTEFIK TAGFIQNNDSSVSTSLTSAFQAITSAIS QGFQA	2930 SLLLALFIALYAISAVNKSKVEALKTEFIK iFNYAPKPEAMQPVVVIPPDSGKEEE MASESSKPASÖNTETKATIARKGEGSV LEGIDGGSILKLPSNLLFENATSDANQ DMMLYIERIAKIIQKLPKRVHINVRGFTD OTPLVKTRFKSHYELAANRAYRVMKVL IQYGVNPNQLSFSSYGSTNPIAPNDSL ENRMKNNRVEIFFSTDANDLSKIHSILD NEFNPHKQQE
	20	38 28 28	262	293
ASATI AGAGATITITI GGATT GGATT GGATT GGATT CATGATAGCGT GGGGGTT TTAGATGAGTATT GGGCGCAA TCAGAGTTTTT ACGAATATT GAAGAGTTT TGAAAAGCATTT AGAGCATCT AGGGGTAT GGGTAAAGAAAT CAACTATT TCAGAGTTT GGGCT ACGCCACGCCATTT GATCACATCCGTTT CGGGTT AAGAAACGGCATGCATTT GT GAAAAACCCTTAGTTTT AGACCCT GGCGAAAT ACAAGAATT GAAAGATTT GAAAAACCCTTAGTTTT AGACCCT GGCGAAATACAAGAATT GAAAGATTT GAAAAACCCTT GCGCTT GCGAAATACCAGGCCTT GAAAAGGGT GAAAAAAAAAA	2923 AAAGAC	2925 AAAGGTGTTTGACGCTAGCAGAGGTTTATCGCTATTACCACACAAGATTTCACAAACCGCCCCTATAACGCTA ACGCAAGCCTTATGACATCAAAGAATTTTTCAAGGCCGTAACAAGCAAG	2927 GTAGTAGTAGTGGCAGTAATAACGGCTATACGCCATGCAATAGGCACTGGGAGCAATAAAAACGAGTGGGAACAAT TGTTATGAACCCAACAAAACGCCACCACCACCACCACCCAC	2929 TGTCGTTGTTGCTCGCGCTTTTTATCGCTCTTTATGCCGTTTCAGCGGTCAAAATCCCAAAGTGGAAGCCTTAAAAA CCGAATTTATTAAGAATTTAATTAGCTCCCAAGCCCAGGCGGTTCGCCAAAATCCCAAAGTCCCGCCTTTCA CCGAAGAAGAACAAATGGCGAAGCGCCAAACCGGCTTCGCCAAAATCCCGAACCAAAGCTCC GGGAAAGAAGAACAATGGCGAAGCGCCAATTGATCAACCGCTTTTAGAAAACCCCTTTTGCTGCAAAATCCTTAAAAACTCC CTGCCAAGGCGAAGGCAATTGATCAATAAGGCAATTGTTTTTGAAAACCTCCTTTAAAAACTCC CTAAAAGGGTGCTATTAATGTGAAGACATGATGCTTTATTGAAAACCCCTTTAAAAACTCCTAAAAACTCC CTAAAAGGGTGCAATTAATGTGAAGAAGCATTACGGATGCTTAAAAACACCCTTTTTTTT
HP0132	HP1464	HP1464	HP1464	HP1464

•	_
•	•
4	ď

HP1464	293	146GCGTGAGCGCATTCAAAAACGCGATCATGGAAATTTTAAATTCTAAAACGGTGGCCGATGTTTTTGGTGAAAAC 12931 IAGGCGTGAGCCGATTCAAAAACGCGATCATTTAAATTCATCAAAACGGTTTTAGGCCAATTCT 1CAGGGTTTGAAAAATTCATCGTGAAAACTTTAGGGATTGATCAATAAATA	2932 GVSAFKNAIMEILNSKTVGDVFGENGL LNALDPTERKKIDOMLLEQIQAHSSGF EKFIVKTLGIENVENFINNWYGKQSLSS FANNFVPGGLNQALDKIGSS:SDAKDLQ NFLDKTTFGDILNQMIEQAPL NKLISWL GPQDLSVLVNIALNSITNPSKIELTSTISS IGEKALNDLLGDGVVNKIMSN QVLGQM INKIIADKGFGGVYQQGLGSILPQSLQD ELKKLGMGSLLGSRGLHNLWQRGNFN FVAKDYLFTNNSSFSNATGGIELNFVAG KSIIFNGKNTINFT
HP1464	2933	11111AGAGGTGCTTTTAAGTTTGGATTTTTCAAAACGCTAATGAGATCGATAGCAGTTTGAGAAACTCCATTGAATG GCTTAACAACGCCGGCGAGAGCTTAAAAACGAAATGAAGAATACGAGGCTTTTTTAGCGATTTCAATACGAGCA GCACCAACGACGAGCAGAGCTTTAAAAGCCTAACACCCGAAAACTCAAAAGCGAGGATTAAAAAGCTA GAAATCAATTGATAGAAACCACTACAAGGCTTTAAACGAAGCCTACAAACCAAGGGATAACAAATAACAAATCAATTGAACAAACA	2934 LEVLLSLDFFKNANEIDSSLRNSIEWLN NAGESLKTKMKEYEGFFSDFNTSMRT NEGEVSATLNANTENIKSEIKKLENGLI ETTRLLTSYGIFLNNARDSANNGITAN KTESLEALNGAKTSANNEITANGTGAL TNINEAKENNOGTENIKTGANTGAL RESATTGITTNKGEVLNSITGEKNGATS EITEAKKSAFNELLETLKPKFSGLFAGA YYIRNVIIFKADGRRKSRI
HP1464	2935	2935 CGGTGGCTAATGTGTTGCAAGAAAACTTTTAGGGAAAGATTATAAACAAAGATTGGACGCTATAAACCAAGAAGATTT CTAAAACTTATGGGAGTTTGTTAAACCAACACGGAAAAATTTGTGAGTGA	2936 VANVLQEKLLGKDYKGRLDAITKKLSK TYGSLLNQHEKFVSETALKGVDTDLSQ NAKILDTLGDEVARKLKANFTSAIGATA GVSGLAIAAKLTPKLMAKIGAY.LGAKVG GKFLAKIGTALSGSWTCGPFVPACTIG LWFGSDAAFNYIDEWLHRDDFKKEILN NINEVKENLKNSYKQGFNDSFVKISQE FQKSFKNAPVVEKKTIKEHIGDLNQ

ŧ		۰	١
٠	ď	٠	١
	_	3	
8	ς		

	ATTITICTTACATTGATGAG	
HP1464 2939 C	2939 CAAAGCAGAAGACACAAGAAAATAAAGAAAACTAAAGAAAACCAATAAAGAAAG	2940 KAEATGENKTKENNKAKESKIKESKIKE AKAKEPIPVKKLSFNEALEELFANSLSD CVSYESIIGISAKVPTLAQIKKIKELCGK YQKKLVSSSEYAKKLNAIDKIKKTEEKQ KVLDEELEDGYDFLKEKDFLEWSRSD SPVRMYLREMGDIKLLSKDEEIELSKQI RLGEDIILDAICSVPYLIDFIY
HP0011 2941000000000000000000000000000000000000	2941 CGČTAAATTTCTÄTTTTATTTATCAAAACTTAGGAGAACTAATATGAAGTTTCAGCCATTÄGGAGAAAGGETCTTAGTA GAAAGACTTGAAGAAGAAGAAAAACAGTTCAGGCATCATCATCATCATAACGCCATTAAGGAGAAAGCCTTTAATGGG GAAAGACTTGAAGGAGAACAAAAACCGTTCAGGCATCATCATCATAAGGAAGG	2942 AKFLFYLSKLRRTNMKFOPLGERVLVE RLEEENKTSSGIIIPDNAKEKPLMGVVK AVSHKISEGCKCVKEGDVIAFGKYKGA EIVLDGTEYMVLELEDILGIVG
HP0011 2943 GC CT TA TA CT CT CT TA CT CT CT CT CT CT CT CT CT CT CT CT CT	2943 GCACTICTAAAAAGAGAGCCGATAAGGGATTAAAAAAGGGTGTTCAAAGACAGCAGCAAAAAGAGGCGTTGCGGGTTCATC TATGAGAAACAGCGGGTTCATGAAAAAGGGTGTTCAAAAAAAA	2944 TSKKRADKGLKKVFKDSKKDACGFIYEI SEFMKAYTALLKKODRYVYLLRYLPSR YWASILTTALYVKYPDFDALKKLLVSYY YQTWIAGGTITRIKQTSINIIKNVKSNKS VETIKELILNSIDSYNTFDOYLYNLWDS SSVYHSKWYRPVLALANYFMADEEKP HFIAMDAETQVEHILPQTPKRGSQWNA DFDKEKREEWVNNIANLTLLKRKKNAH ALNGDFDEKRK

	_	<u> </u>	
2946 ALSQEERNKVDFMEFLÄQNNTKLDNL SEKEKEFGNEIEDFGKDSKAYLDALG NDRIAFVSKKDTKHSALITEFNNGDLSY TLKDYGKKADKALDREKNYTLGGSLKH DGVMFVDYSNFKYTNASKNPNKGVGA TNGVSHLEAGFNKVAVFNLPDLNNLAI TSFVRRNLENKLTAKGLSLQEANKLIKD FLSSNKELAGKALNFNKAVEAKSTGN YDEVKRAGNENELEKEVEK KLESKSGNKNKMEAKAJANSGNCDEI ALINKEANRDARAIAYTCINLKGIKRELS DKLEKISKDLKDFSKSFUEFKNGKNKD FSKAEETLKALKGSVK	2948 KELSSAMETEINLPFITAIDATGPKHLVK KLTRAKFESLTEDLMKETISKIESVIKDA GLTKNEISEVVMVGGSTRIPKVGERVK AFINKDLNKSVNPDEVVAVGASIQGGV LKGDVKDVLLLDVTPLSI.GIETLGGVMT KVIDRGTTIPAKKSQVFSTAEDNQPAV SIMVLQGERELARDNKSLGKFDLQGIA PAPRGVPQIEVTFDIDANGILTVSA	2950 EIHVDLPTSARILKQITLTYQDIDGSIHS KVVGIDKGIDWHYPLKLSQHTLDPAAF EKRYQIQDFDFLMASNTMILRSPYKILR SFVLVNPYRIVLDTQKGPLDIYQNMDL NQKFFSHIKVGTHKDYYRITLILDGKYR YLLEEKNGAYELKL	2952 FKPKESEDLLENFSNKKJMOELLGLLN OFILQSYKVEKEFKDYKALYEWVIEILP QAIWVVNENGSFFYKNS!LANQSHEVF NKAKLENFNTEIEHENKSYLVQQNSIQ GKQIITATDISAQKRQERLASMGKISAH LAHEIRNPVGSISLLASV.LKHANEKTK PIVVELQKALWRVERIIKATLLFSKGIQA NRTKQSLKTLESDLKEALNCYTYSKDI DFLFNFSDEEGFFDFDLMGIVLQ
2945 GAGCATTGAGTCAAGAAGAACAAAGTAGATTTCATGGAATTTCTTGCACAAATAATACTAAATTAGACAAATTAGACAAATTGAGCAAATTGAGTCTAAATTAGACAAATTGAGCGAAAGGAAAGGAAAGGAAAGGAATTGAAATTGAAATTGAGGAAAGGAAAGGAAAGGAAAAGGATTTCAAAAAGAGAAAGAA	2947 AAAGAACTGAGCTCTGCGATGGAGACTGAAATCAATTTGCCCTTTATCACCGGGCGGACGCTACCGGGCCTAAACATTGAAACATTAAAAAAACTTAAAAAAACTTGGAAAGAATTGAAAAGAAGAAGAAGAAAGA	2949 AGAAATCCATGTGGATTTGCCCACGAGGGCTAGGATCTTAAAACCAATCACGCTCACTTACCAAGATATTGATGGCT CTATCCATTCTAAAGTCGTGGGCCATTGATAAAGGCATTGATTTTAACGCTTTAAAACTCTCCCAACACCACCCTTG ATCCAGCCGCCTTTGAAAAACGCTACCAGATCCAAGAGATTTTTTAATGGCAAGCACACGACACACCACCGTTG CCCCTTATAAAAATTTACGCTCCTTTGTGCTAGTCAATCCTTATAGAATCGTGTTAGACACGCAAAAAGGCCTTTGG ATATTTATCAAAACATGGATTTAAACCAGAAGTTTTTTTCTCACATTAAAGTCGGCACGCAAAAAGATTAACGCCTTTGG ATATTTATCAAAACGGGAAATACCGCTATCTTTTGGAAGAAAAAAAA	2951 TTTAAACCCAAAGAGGGGGGTTTTTTTTTTTTTTTTTTT
HP0496	HP0136	HP0136	HP0136

HP0136	AAGGCCATTCCGCTGATTTGCAAGGCCGAGATGCCTTTGCAAGCGCCGAACAGGCCCAACAGGGAAAACCGCCGCTTCCGCCAACAGGCCCTAGTGCTTTTGCAAGGCCCGAGTGCCTTTGCCAACACACAC	AIPAVLQGRDVIAQAQTGTGKTAAFAL PIINNLKNNHTIEALVITPTRELAMQISD EIFKLGKHTRTKTVCVYGGQSVKKQCE FIKKNPQVMIATPGRLLDHLKNERIHKF VPKVVVLDESDEMLDMGFLDDIEEIFD YLPSEAQILFSATMPEPIKRLADKILEN PIKIHIAPSNITNTDITQRFYVINEHERAE AIMRLLDTQAPKKSIVFTRTKKEADELH QFLASKNYKSTALHGDMDQRDRRSSI MAFKKNDADVLVATDVASRGLDISGVS HVFNYHLPLNTESYIHRIGRTGRAGK
HP0136	CCACTIGCCCCIAAACACIGAGAGCIAIAICCAITCACATCGGAAAAATTCTACGATTAAAGATTCTGAAAGACGCCGA 2855 CCAAACCTCCCTGTTTATTGGACATTCCCATTCTTTAGACGTGAAAAATTCTACGATTAAAGATTCTTCTA TCAAAAACGCTTCAATAATGAAGTGGATGTGGAAATTGAAAACAAAC	2956 PNLPÝYLDPILLDVKNSTIKDLKDAľKK RFNNEVDVEIETNGRLRIIDNSSKESPI SLALSALDAKGLEVAGIPTNNASEYČK TYFNKEGAKLESNVAČIPAČNGAANGS TKLSEAAKGSLENSVFNMKLNDVNGLF LEACMNLĎNNGAFLSLPNG
НР 0136	2957 TTTTGAAGTGGATAACAATACCGACACTCTAGCGAGTTTTAGAGGCACCCAAACCATAAGGCTAAAATGGGGCTC CAGGAGGTACACGAAATTGCGGCGGCAAAAGGGCGAAGATCATTGTGGTGCCACCAGGAACGCAGGTTTT CAGGAGGTACACGAAATTGCGCGGGCAAAAGGGCGAAGGGTGTTAGCGTGCCACCAGGGAACGCAGGGGGGG TGTAGGGAATGCACATTTTAAAAGCGGCGACTAAACAACACCACTTACGCGCAAAAGGCTTAGAGGGGTTGAAAA ATGCGTGCGTTTGGAATTAAAACTCATCGCTGATATAGGGTTAGTGGGCTTCCTAATGCGGGTTAAAAAAAA	2958 FEVDNINTD LASTRG I KHRKAKNGAP GGTRNCAGKKGEDKIIVVPPGTQVFVG DELWLDLVEPKERVLALKGGKGGLGN AHFKSATKQQPTYAQKGLEGVEKCVR LELKLIADIGLVGFPNAGKSTLISTISNA KPKIANYEFTTLVPNLGVVSVDEKSGFL MADIPGIIEGASEGKGLGISFLKHIERTK VLAFVLDASRLDLGIKEQY
HP0136	2959 GCCCCCAAGACTCACTTATAACGGGCTAGAAGAAAGAAAG	SABOL PFRLI TNSLDERNANGERE TEDENANTY NFTKSSNNTNFKGGGSOKKSEDLEIVL SARIIKVLENGNYFIYGNKEVLVDGEKO ILKVSGVIRPYDIERNNTIQSKFLADAKI EYTNLGHLSDSNKKKFAADAMETQMP Y
HP0136	2961 AAGGCCATTTCCCAACAAAAGATTCAAGCTAAAATTGAAGATTTAGCCGAAAACTATGAAAACCATTATTGAAGGC 2961 AAGGCCATTTCCCCAACAAAAAAGGCTAAAATTGAGGCCTCAAGGCCGTCGCGCTCCCGCTCGCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCTTTTAAAGAATGACCAAACCATTCTTCAAACAACATTCTCGCAAACCATTCTTCAAAGAATGATTTTCTCGCAAACCATTCTTTGAAACAACACTTGAGGTTTTTTTT	2962 KAISOOKIQAKIEELGENYENAIIEGKIV GKNKGGYIVESOGVEYFLSRSHSSLKN GANHIGKRVKACIIRVDKENHSINSRK RFFEVNDKRQLEVSKELLEATEPVLGV VROITPFGIFVEAKGIEGLVHYSEISHK GPVNPEKYYYKEGDEVYVKAIAYDAEKR RLSLSIKATIEDPWEEIQDKLKPGYAIKV VVSNIEHYGVFVDIGNDIEGFLHVSEIS WDKNVSHPNNYLSVGQEID

v	٦
Ч	۲
₹	r

. 1	are a second or the second or		
HP0136	2963 ATTGAAAATTCC ATATTTGAAAAA	2963 ATTGAAAATTCCAGCGCGCTAGAAAGGGAATTGAAACAAAAGAATGAACATTTAGAGAACGCTTTAAAAGAAGA ATATTTGAAAAACGCATGGCTTTTAGAAATGGAAAAACAAAAGAAAATCTTTCACAATAAAAAATTGGAAATTGGAAAAA	2964 IIENSSALERELKOKNEHLENALKEOEY IKNAWLLEMEKOKEIFHNKKLELEKSY
•	TCCTACCAACA	TCCTACCAACAAGCCCTAAATATCTTAAAAAGCGAAGTCGCTTCAAAAGGATACTAGCTGCATGCA	QQALNILKSEVASKDTSSMHKEIHKAS FIL SKHKTNOFIDOITTNEOANEKARKA
	AAAGCGCGCTA	AAAGCGCCTACAAGATGAAGCGTGCTGGTTGTACAAATTTTAGACAAGGGCTATTATTGGATAGAAAGCGAGGTT	NESYLIVOH DROYWIETEL CAMPLINATION
	TGGCATGCGTT	TGGCATGCGTTTAAAAAGCGCATGGGAGTTTGTTGAAAAAATCCAAAAACCCCCTAAAAACAAATTCAAACCCCCTAA	GSLLKKIQKPPKNKFKPPKTTIPKPKEA
	AACAACCATTC	AACAACCATTCCTAAACCTAAAGAAGCGAGCTTGCGCCCTTGATTTAAGGGGGCAACGCGGGGAAGAAGCCCTGGAT	SLRLDLRGQRSEEALDLLDAFLNDALL
	TTACTAGAGGCTTTTTTA GATTTTAGAAAGTTTGT	TTACTAGACGCTTTTTTAAACGACGCGCTTTTAGGGGGGCTTTGAAGAAGTGCTGATTTGCCACGGCAAAGGGAGGG	GGFEEVLICHGKGSGILEKF
HP0136	2965 CAACTCCAAAC	2965 CAACTCCAAACCCATTTTGATAAAAAAGAAGCGCATTTGAAGCATTTAGAAGCACAACACAAAGAATTTGTAAGAGT	2966 QLQTHFDKKEAHLKHLEAQHKEFVRD
	GAAAAAGGCTA	GAAAAACGCTATTTAGAAAAAGGAAAAAAAAGGGCTTGAAAAAGAACGCCCAAATTTTAGAACAAGAAAAAGAAATTTT	EKRYLEKEKKELEKERQILEGEKENFK
	AAAAAACAGCG	AAAAAACAGCGCGCTGTTTGTAAAGAATCTCAAGCCAAAGCGCTAGACGCGATGCTCAATTACATGGCTTATACTAA	KORAVCKESOAKALDAMLNYMAYTKD
	AGATTA	AGATGAAATTAAAAGCCATGATTTAGAGCAATTAGAAGAATTAGAAGCCCCAAAAAAGCGCCCTTAATCAGGCGTTA	EIKSMILEOLEEELEAOKSALIRRYEKE
	I GAAAAAGAAG	1644AAAAGAAGCCAAAGAAGAGGGCCAAAAAAAAAAAAAA	AKEEGKKKSYAILAEAIAKFAGNYAAE
	AALIAIGCGGC	AATTATEGECAGAGAATTTAACAACTCGTTTTGCTTTGCT	NLTTRIALPCSDYIGRVIGKDG:KNIEAFK
	GGGAAAATAT	GGGAAAATATTGAAGCGTTAAAAAGGTCAGCGGGGTTGGATATAGCGAAGGTTGCGAAGTTGTGTTT	KVSGVDIEFSEDSSELCLSSFNLYRRE
	GICCAGIIICA	GICCAGIIICAAICIIIAICGGCGGIGAGCGAGCGGGGGCGAGACGCCIIAAIAGAAGACGGCCGIAICCAGC	VASETLKILIEUGKIQPNKIEEVYHKVAK
	GGTGTTAGAATI	CTAACAGGATTGAAGAGGTTTGGAGCTATGGAAGAT GGTGTTAGAATTAGAAGCTTGGAAGCTATGGAAGAT	NLEKELLSEGESVVLELELGAMED
HP0136	2967 TTTGAATAAAGA	TTTGAATAAAGAGCCTTTGAATGAATGCATTGAAGCGTGCGT	2968 LNKEPLNECIEACVFKIDGETIVTDDLSP
)) :	AAGCCCAGCGA	AAGCCCAGCGAGCGACGCTTTCACACGAAGCGATATTCCTTTACACGCCAAAAGCCATGCTAAAAAACCGGATTGAAA	ASDAFTRSDIPLHAKAMLKNEIENYEO
	ATTACGAACAAC	attacgaacaacgcatcaaagccattaaaactaaaggcgttcctgtagcgtatgtgggcgatgtggtfggcacagga	RIKAIKTKGVPVAYVGDVVGTGSSRKS
	AGCTCCAGAAA	AGCTCCAGAAAAAGCGCGACGAACTCTATCATGTGGCATTTTGGTAAGGACATTCCTTTTGTGCCTAATAAAAGGAC	ATNSIMWHFGKDIPFVPNKRSGGIVIG
	TGGGGGCATTG	16GGGGCATTGTGATTGGGGGGTGATCGCTCCGATTTTCTTTGCGACTTGTGAAGATAGCGGGGCGTTACCCATT	GVIAPIFFATCEDSGALPIVADVKDLKE
	GTGGCTGATGT	GTGGCTGATGTTAAGGATCTAAAAGAGGGCGATTTGATTAAAATCTATCCTTATAAAGGCGAAATCACGCTGAACGAT	GDLIKIYPYKGEITLNDKVVSTFKLEPET
	AAAGTGGTTAG	AAAGTGGTTAGCACTTTTAAGTTAGAGCCTGAAACTTTGTTAGATGAAGTTAGGGCCTTCTGGGCGTATCCCTTTAATC	LLDEVRASGRIPLIIGRGLTNKARKFLG
	ATCGGTAGGG	ATCGGTAGGGGTTTGACGAATAAAGCGCGTAAATTCTTGGGGCTAGGCGAATCTGAAGCGTTTAAAAAGCCATCCG	LGESEAFKKPSAPKSDAKGYTLAQKIV
	CTCCTAAAAGC	CTCCTAAAAGCGACGCCAAAGGCTACACTTTAGCCCAAAAAAT1GTAGGGCATGCTTGTGGGGTAAAAGGGGATCTTA	GHACGVKGILPGTYCEPKVT7VGSQD
	CCTGGGACTTA	CCTGGGACTTATTGTGAGCCAAAGGTTACCACCGTGGGCAGTCAAGACACCACACGGGGGGGG	TTGAMTRDEVKELASLKFDAI'FVLOSF
	GTTAAAGAGTT	GTTAAAGAGTTAGCGAGTTTGAAGTTTGATGCGCCTTTTGTGTTGCAGAGTTTTTGCCATACCGCTTACCCAAAG	CHTAAYPKPSDVSLHATLPGI:ITQRGG
	CCTAGCGATGT	CCTAGCGATGTGAGTTTGCATGCAACCTTGCCTTATCACTCAAAGAGGCGGTGTGGCGTTGCATCCGGGCG	VALHPGDGVIHTWLNRMGLPDTLGTG
	ATGGCGTGATC	ATGGCGTGATCCATACATGGCTGAATCGCATGGGATTGCCTGATACTTTAGGCACAGGGGGGGATAGCCACACGC	GDSHTRFPLGISFPAGSGLVAFAAVTG
	99111222111	T CCCT T GGGCAT AGT T CCCG	MPLNMPESVLVKFKGEMNFGILKDL
			VIVAIPTTAIRNGELIVERNGRIVVENGRI
	•		CANON PROPRIES ROURS TO ENTRY OF THE PARTY O
			VEDKETI KKRRDAMOAWVONIPVI JED
			DSNAOYAAVIEIDVAEITEPILACPNDPD
			DVATLSEVLADTTGKRPHAIDEVFIGSC
			MTNIGHFRAFGEIVKNAPPSQARLWVV
			PPSKMDEQELINEGYYAIFGAAGARTE
			VPGCSLCMGNQARVRDNAV/FSTSTR
			NFDNRMGRGAKVYLGSAELGAACALL
			GR

v	
_	
J	
4	
-	

066501		PCT/EP01/15428
2970 GFRRGKVPLSLVKTRYQAQIEQDAQE EMIQEVLKNAFKELGIENKDLIGSPNLT KFEKKDTHFEIEADIGLKPTIVLDKIKEC VPSVGVEVPNEEKIDERLKOLAKDYAK FVDTNTQRKAQNDDKLTIDFEGFIDNA PFEGGKAENFNLLGSKQMLEDFEKAL LGMQAGEEKEFPLTFPSKYHAEHLAG KEAFFKVKLHQIQAREMLEINDELAKIV LANEELKEKLIENLDEKIVFDLPKTIIEÒE MDLLFRNALYSMQAEEVKSLQESGEK AKEKRESFRNDATKSVKITFII	2972 IELVHKTIKÖVIDAMEKIDKNMPTFIGITD FGQSSLNFTIRVWAKIEDGIFNVRSELI ERIKNALDANHIEIPFNKLDIAIKNQDSP K	2974 IERVHDEFVFARYTKANYENTYYDTEF SWILKEASAYFPOIDEASLFTDLODYFN SWKELSKNAKDSAQKQALAQKTEALT HNIKDTRERLTTLQHKASEELKSVIKEV NSLGSQAEINKRIKEVENNKSLKHANE LRDKRDELEFHLRELLGGNVFKSSIKT HSLTDKDSADFDESYNLNIGHGFNIIDG SIFHPLVVKESENKGCLNQVYFQSDDF KVTNITDKLNQGRVGALLNVYNDGSN GTLKGKLQDYIDLLDSFAKGLIESTNAIY AQSASHYIEGEPVEFNSDEAFKDTNYN IKNGSFDLIAYNTDGKEIARKTIATPITT MNDIIQAINANTDDNQDNNTENDFDDY FTAGFNNETKKFVIQPKNASQGLFVSM KDNGTNFMGALKLNPFFQGDDASNISL NKEYKKEPTTIRPWLAP
	297	297
2969 GGCTTTAGAAGGTAAAGTCCCCCTTAGCTTAGTGAAAACCCCGTTATCAAGCCCCAAATTGAACAAGACCGCTCAAGA AGAAATGATTCAAGAGGTTTTGAAAAACGCTTTTAAGGAATTAGGGATTGAAAATAGAGTCCCTCCGCCCAA TCTCACTAAATTTGAAAAAAAAGACGCTTTTGAAATAGAAGCGGACATCGGCTTAAAACCCACCATTGTTTAGA TCTCACTAAAGATTTTGAAAAAAAGCGCGTGGGAGTTCCAAATGAAAAAATGACGATTGATT	2971 TATTGAACTGGTGCATAAGACTATAAAAGATGTTATTGATGCAATGGAAAAATTTGATAAAAAATTTTATT GGGATCACGGATTTTGGACGAAGTTTCACCATTAGGGTTTGGGCAAAGATTGAAGACGGAATCTTTAA GGGATCACGGATTTTGGACGAACTCAAAAACGCTGAAAACGCTAAGACCAAACCAAAGATTGAAGATTCAACAACAAGCTAA TGTGCTATTAAAAAATCAAGAGACTCCTAAATGATTGGTGTGTGAGTTGATTGA	2973 ATTGAAAGGGTGCATGATGAGTTTGCTCGTTACACGAAAGCTAATTACGAAAACACTTATTACGAATTTACGAATTACGAAAATTACGAATTACGAATTACGAATTACGAATTACGCATTTACGCATTTACGCATTTACGCATTTACGCATTTACGCATTTACGCATTTACGCATTTACAAAAAACGCTTACAGCGAGCCTTTTAATTCATTAAAAAAACACGCATTAAAAAACGCTTACAGCCTTACAACGCCTTTTAAACAAAAACAACAAAAAAAA
HP0136	HP0136	HP0136

2/060	6501			PCT/EP01/15428
<u> </u>	FPEPVIHIAVEPKTKAUGEKMIGVALUN LAEEDPSFRVMTQEETGOTLIGGMGE LHEIIVDRLKREFKVEAEIGOPOVAFR ETIRSSVSKEHKYAKOSGGRGOYGHV FIKLEPKEPGSGYEFVNEISGGVIPKEYI PAVDKGIOEAMONGVLAGYPVVDFKV TLYDGSYHDVDSSEMAFKIAGSMAFKE ASRAANPVILEPMMKVEVIEVPEEYMG DVIGDLINFRRGOINSMDDFLGLKIVNA FVPLVEMFGYSTDLRSATCIGRGTY	DCPGRADY VANNING SAADGPMPGTREHILLSRCINGVPHIVY SAADGPMPGTREHILLSRCINGVPHIVY FEPGDOTPIVAGSALRALEEAKAGNV GEWGEKVLKLMAEVDAYIITPERDTEK TFLMPVEDVFSIAGRGTVVTGRIERGV VRVGDEVENGIRPTOKTTVTGVEMFR KELEKGEAGDNVGVLLRGTKKEEVER GMV OREEIAKHHSATHLLQSALREVLGSHVS ORFEIAKHHSATHLLQSALREVLGSHVS		LOLKEDEYERLLEGKKLL SSKEKLNDK ALALEVLENTHKITHALESVGHSAEFLK SALLEASALLEKEQAKLEECERLDIEKV LERLGMLSGIIKDYGSIMHAKERLGHVK NELHNLKEIDSHCETYHKEIERLKTECL KLCEEISGFRKEYLAGFNALLSAKAKOL LLKSPSLVLEDAPMSEKGAQKLVLNLQ NSQLETLSSGEYSRLRLAFMLLEMEFL KD
2976		2980	2982	
A SANTECEGIGGITITAGAGAAA	2975 GCGTTTGTGGGCTTAAAAGACACGCCTAACCGGGGACACGCTTTGCGATGAAACGAAAGAAA	GGATTTACGATCAGCCAAGGGCG IGGGAAAAACATGATCACCGGTGCGGCGCAAATGGACGGGGGGATTTTGGTTG 2977 GATTGCCCAGGACACCCAAGGGCG IGGGAAATGATCACCGGTGCGGCGCCAAATGGACGCGTGCACTCACACTAGGACTCATGTAAAAAACATGTAAAAATGGACTCATGTAAAAAATGTAAGAAATGGCCGAATTG TTCTGCCAGCTGATGGCCCTATGCTCAAACAAGAAGAAATGTTAAGAACTTTAAGAAATGGCGAATTG TTGAGCGCGTATGAACAAAGAAGACAGGATGACCTCTATCGTAGCGGGTTCAAGTGCTTTAAGAGCTTTAGAAGCAAAA TTGAGCGCGTATGAATTTCCTGGCGAAAAAGTGCTCTATCGTAGCTGAAGTGCTCATTCCTATCCCTACTCCAG GGCTGGTAATGTGGGTGAAAAACTTTCTTGAAAAGTGAAAAATGTTTTTTTT	2979 CGCTTTGAAATCGCCAAACCATAGA CGCTTTGATTCCGCATGCTTAAATAGCGCTTTGAAATAGCGCTTTAAATAGCGGAGTTTAGTCGAATTCCAAGCGCTTTGATTCCCGCAGTGGAGCCTTTAAAAAAATTTCCAGCACCTAAATAGCCGGGGGGTTTAGTGGATTTGTCAAAAATTTTCAAGCACCTGAAAATGTGCGGGTGGTGGAGCTTTAAAAAGCTTTAAAAAGCGTTTAAAAAAATACTGGAAAATACTGGGGGTTTAGGGTTTGTAAAAGAGGTTTGAAAAGAGGAATTGTAAAAGAAATTGTGGGGGG	2981 CAAAACGAAAA I AAGAGATAAAA GAAAGGGTTTCCAAAAGGATTTAGAAGAACGATTGTAGTAAGGAAAAACT AGAAAGGCGATTGTTAGAGGATAAAAGCGTTTCCAAAAGGCGTTTTAGAAAAATTTTAGAAAAACTTAGAGAAAAACT AGAAGGCGATTATAAAAGAGGTGATAGAAAATACCATAAAAATTGGAAAAAATTAGAGAGCGTGGCTGCTTTAGAAAAACGGCTTAGAAAAAAAA
	HP0136	HP0136	HP0136	HP0136

		2		L
ī	2	t		2
_			Ξ	1
1	•			
		3	Ŀ	
7		1	Г	

LETKAIASSHSKGAQIM	ATTCAAAAGGCGCGCAGATCATG	
FELYGEPAQSCLELAVGCEDADGFLEK	TTTGGAATTAGGGTTGGGTTGGGAAGGTGGGAAGGTGGGAAGGTGAAGGTGGAAGGGGGG	
DDAIALAGFNPKKESVAGFVWKVMEQ	CITITIES CANADACA CANADAC CONTINUE CANADACA CONTINUE CANADACA CAN	
ALEYALAEEPYKPFYKHSVLKLAGYLH	CAAAATTGTCTCAATTTGTAGAGTCTAAAATCATTAAGAACGCTTTAGAATACGCTCTAGCGGAAGAACCTTACAAGC	
OFRI SAIRPSTESCAKI SOEVECKIIKM	AM ISAUGACECT I AGAAAT CAAAAATTATT GCAAGAGCGTTTGAGTGCGATTCGCCCAAGCGGAATCTAGCG	
INLLEHRIEPKDITILCATNODALFIKNYI	ACA I CACA CACACA ACCTITIA GAACA CATCG TATTGA GACTAAA AGATATTA CCATTTA TGCGCCAC	
VTDGYVKVSI VADEREI I DOVI DEAD	CIAMARCI I CICAAAA I AAAACA I GI TACAGACGGCTATGTTAAAAGTCTCTTTTAGTGGTGATGAAAGAGAAATTGTTATT	
TIFKKAYONSPTAYI FOKYPKTSONKH	CT CAN CALL TO THE STANCAR THE LAWARANCE HAVE CAN CAN CAN CAN CAN CAN CAN CAN CAN CAN	
FESVSKDFYHDNLEFNHRSAPLIINYVN	THE ACTUAL TANK THE CANADAC THE TANK THE CANADAC THE CONTRACT OF THE CONTRACT	
AKWHRSVFFVGDVKQSIYAFRGSFSSL	GARTITION CONTINUE CO	>
2988 ILIDEFODTSLNDYKILAPFIDEIKAGIGO	GGATAGGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA) :
	2987 ATTITICATION CANCAGA CAGGA CAGGA CATT CAACATTT A ACCOCCTTT A TO TO CAGA T	HP0136
	ACCCT IN THE CONTROL OF THE CONTROL	
	CAACAATAAAATGTATTGACAGAAAAGAGCTCCAACAACGCCAAAGTAACCAAATCCGTGATATTTTAGGACTAG	
	GCTAGCAATTTGCAAGCTCAAGAAACCACACACTTTGGGTAAGGTAACCACACAGAGGACTTTTGAATA	
•	TTTTAGAAAAAGTAAAAAGGCTAAAAGAAATGCTTAGAAATCAATTTCGTATCGTGTTTGTCTTGTATTGTC	
	TTICTTAATCCTAAAACAAATTTAAGGTATTAATAAATAGAATAATGTAATAACCTTAGGTTTAAAAACTTGACTAAAAT	
	ACGCTTCTTCACGAACAGTGCTTGATTCAGCCGCTCAGTAAAATGCTAAAAAATGTTTTTTTAAAAAAATAATAAAAAAAA	
	GCAACCAGCCAAGCGATATTTCCGCCAAAACGCTGAAATCAATC	
	AAAAAAAGCGCGCTTATAGACCCTTTCAATGGGGGAATACCATTATCATAGACAAGTTAGACTTGTGACTTGTGACTTGTGACTTGTGACTTGTGACTTGTGACTTGTGACTTGTGACTTGTGACTTATAGACGTGACTTATAGAAAAAAAA	
KIRYESNL	COCATA A A COCATA TA CA CA CA CA CA CA CA CA CA CA CA CA CA	
KTRYKEITELYLKISKLEISPNSOVGASV	A MET CONSTRUCTION OF THE STATE	
OELIOKMMOENOYLLIFDALKDI SHAL	GAAATTCAAGAGCTTATTCAAAAGATGATGCAAGAAAACCAATACCTTCTCATTGAAGACGCCCTGAAAGATTTGAGC	
2086 KDOWISYAH DI EXTOL DAILY SYSTEM	2985 CTTAAAACCCCAAAAATAAGCGTGAATTTGGATCTTTTCTACACGCAATTACCCAATAAGGTTTATTTA	HP0136
DEHGLKKYRSYFKIVEKRCPISVGEF	AATCGTAGAAAAGCGCTGTCCCATTAGCGTGGGCGAATTTA	-
GATPYLFKELQFPLYGTPLSLGLIGSKF	GGCACGCCCTTGAGTTTGGGGCTGATTGGCACCAACGCTTCAACATTGAAAAAAAA	
VDILIPDFSYLHQIKDKIAGIIITHAHEDHI	ATTATCATCACCCATGCCCATGACCCATGACCATGACCCATGACCATGACCATGACCATGACCATGACCATGACCATGACCATGACCATGACCATGACCATGACCATGACCATGACCATGACCATGACATACAT	
NMMVIETPKSAIVIDAGMSFPKEGLFG	AAGAGGGGCTTTTGGCGTGGTTTTAATCCCCAAAAGCGCGGTGTGTGT	
NPHYKMNLNSKASVKITPLGGLGEIGG	GAGATTGGGGGGAATGATGATGATGATGATGATGATGATG	·
NERGTLGFHKELKKGVEANNKIOVEHI	STATE AND CONTROL OF THE STATE OF THE STAT	
VI HELVOEVANTALIEN BOOKER TO THE TOTAL THE TOT	AAACATGCCAAAACTTACGCCCAAGAATTGGATTGCAACAACAAAGTAGGGGGGTTACGGAAATTTTGCA	
29RA I VSNH FA SCHHKK EHDDNIKKDNINLULK	Z S S S S S S S S S S S S S S S S S S S	051071

нР0379	2989 CAGCGGCAAACTATTGGAAAGAGCAAATCATTGAAGGCTCCTGATGTTTGTACCCCTACTTATTGTAACCCTA ACGCTCCTTATAGCAACCTTCAACCGTCGCTTTTCAGGTATGGTTGAATTTTGGGGTGAGAGCCAATATTTACA ACGCTCCTTATAGCACCAAAACTTCAACCGTCGCTTTTCAGGTAGCAGTTTTTGGGGTGCGGGTCCTAACGCTACT AGCATAATGGCGTAGAGGTTTTTTTTTT	2990/AANYWKEQIIEAKGPDVCTI ^J TYCNPNA PYSTKTSTVAFQVWLNFGVRANIYKHN GVEFGVRVPLLINKFLSAGFNATNLYY HLKRDYSLYLGYNYTF
HP0137	2991 GCTCCAAGCATCACTAAAGATGGCGTGAGCGTGGCTAAAGAGATTGAATTAAGTTGCCCGGTAGCTAACATGGGCCG CTCAACTCGTTAAAGAAGGTTGGCGAAAACCGCTGATGCTGCCGGCGATGGCCACGACGACGCGCCGTGCTGG CTTATAGCATTTTTAAAGAAGGTTTGAGGAACATCACGCTGCGGCCGAAAAAAGCGACCGAC	2992 APSITKDGVSVAKEIELSCP/VANMGAO LVKEVASKTADAAGDGTTTATVLAYSIF KEGLRNITAGANPIEVKRGM DKAAEAII NELKKASKKVGGKEEITQVATISANSD HNIGKLIADAMEKVGKDGVI: VEEAKGI EDELDVVEGMQFDRGYLSPYFVTNAE KMTAQLDNAYILLTDKKISSNIKDILPLLE KTMKEGKPLLIAEDIEGEALTLVVNKL RGVLNIAAVKAPGFGDRRK
HP0137	2993 GGGTGACGATGCGGCTTGTGAGGCCAGAAGGCATTTTCAACAACAACAACAACAAAAAAACCCCACACAACA	2994 GDDAACELVRPEGIFNINNGGHOKHHT KMSIPKAPDDFKPFIKKIHRDFNORNLV PVEHKIYNGEKPLEMPNTLKANEMRLH LGKEADYEQKDLMVGFENSESHILVV SQDLSARIALMKLFAQNFKTANKELLFY NAEKRLARELDELKKHHITPWOGPLGS VLDTAMNPNSVLVIDNINNEAKELHDKIG VEKLRSFLEKATDNEQYCIIFAHDLKQI QANYDLSKLKELLNNHFKQRILAFRCN GENLSAIKKDLPLLTNELNALFVELSKD SHTEFRPFSL

_	۰,
`	:
v	7
~	۲

_			
	YSKKPKRR		
	IFELSKIGLNQQEIDAIQNPKEKTPKPSN KKTPQHERARSFKKGQHRDRHPKTNH		
	VSEGIISLYEQLTEIFEPSQLVLKLLSLQ	GCATGCAAAAAAATTGAT	
~-	RIGRTGRAGKKGMAITLYTPLEYKELLR	GGGAGAACCGGGCGAGCGAAAAAAGGCATGGCGATTAGTAACACTTTAGTAACACTTTAGAATACAAAAGACTTTTAC	
_	VASRGLDISGVSHVFNYHLPLNTESYIH	GGGGCTAGATATTAGCGGTGTTTAAACAAAAAATGACGCTGATGTAAAAAAATGAGAGTGGTGGCTACAGATGTGGCGGAGTCGT	
	DMDQRDRRSSIMAFKKNDADVLVATD	AAGAAGCCGATGAATTGCACCAATTCCTTGCTTCTAAAAATTACAAAAGCACCGCCTTGCATGGGGATATGGATCAAA	
	FTRTKKEADELHÖFLASKNYKSTALHG	TGAGAGGGCCGAAGCGATCATGCGCCTTTTAGACACCCCAAGCACCCAAAAGGGCATTGTTTCACGCGCACTAAAA	
	(EPIKKLAUKILENPIKIHIAPSNITNTUTO	ACCCTATTAAAATCCATATCGCTCCTTCTAATATCACTAACACGCGACATCACCCAACGCTTTTATGTGATCAATGACCA	
	MGFLDDIEEIFDYLPSEAQILLFSATMP	TAGCGAAGCCAGATTTTGCTTTTTTCAGCCACGATGCCAGAAGCCATTAAAAAGAAGAATAAAAAAAA	
	LDHLKNERIHKFVPKVVVLDESDEMLD	CASCILLA AND AND AND AND AND AND AND AND AND AN	
_	YGGQSVKKQCEFIKKNPQVMIATPGRL	CACACACACACACACACACACACACACACACACACACA	
<u>-</u>	TPTRELAMQISDEIFKLGKHTRTKTVCV	LANAGARGUCCIAGIGAICACGCCCAGAGAGATTAGCCATTAGCGATTAGCGATGAGATTTCAAATTGGGCAAAC	
<u> </u>	OTGTGKTAAFALPIINNI KNNHTIFAI VI	GCACAAGCCCAAACAGGCACAGGAAAAACCGCCGCTTTCGCTCTGCCCATTATCAACAACCTTAAAAACCAACC	
1	seded	30011 GAAGCCGGCTICACTTCCCCATTCAAGAAAGGCCCATTCCGCTTTTCCAAGAAGAAAAAAAA	HP0137
T.:.	3000 GFFDFDLMGIVLQNFLYNAIDAIEALEE	2899 556 111116AU111GA111GA111GGGATTGTGTTGCAAAATTTCTTGTATAACGCTATTGATGCGATTGAAGCCTTAG	12/213/
	KEYLHONIKFFVNPT	ACAG ACAG ACAG ACAG ACAG ACAG ACAG ACAG	
_	ISTOMSPEVSOKHLKEAVIEEIVYKVLS	CARCAGACIO CARCAGACIO CALICACIO CALOCACATICO CACATICO CAGAGATITA CACATITA	
· >	LPFLRPDGKSQVSVRYENNKPVSIDTIV	GUI CAAAAAAGAAAAGACAACACTCTGCCTTTTTTAAGGCCTGATGGCAAGTCTCAAGTGAGCGTGTATGAAAA	·
. E	ETETLMPLPIHLAHOLTFALAOKRKONT	TTGGTTATGCAAAGAGACTGAAACGCTCATGCCCTTACCCATTCATT	
<u></u>	NOGYÓBEDGEGAGDOG MEGYACK	GAGCAAAGCCCTGATATTAATCAAGGCGTGGATAGAGAAGATGGCGAGTTGGGGGGGATCAAGGGGTTTATGT	
=	GFCMITGELKTSVYAPMQEIAREVVKKI	TGGTTAAAAAGATTGGTTATACGGCTCTTTATGCTTTACAGGAGCTTTACAGGAGCGCGCGC	
7	2998 DOISDAVLDYIIERDOKAKVACETLVSN	TITICIAACGGGTTTTGCATGATCACTGATCACTGATCACTTAAAAAACTTTAATTATTATATATA	2010
	DKNTGKSOEIKISGSSGLSDSEIEKM	ICI CCAAGAGGGGI GCCGCAAATTG	1007137
	IAPAPRGVPOIEVTFDIDANGII TVSAO	GGITTTACAAGGCGAGAGAGTTGGCAAGGGATAATAAATTTGGTAAATTTGATTTGCAAGGCATCGCTCCAG	
	AVSIMVLOGERELARDNKSI GKEDI OG	AGAGGCACGACTATTCCGGCGAAAAATCTCAAGTGTTCTCAACCGCTGAAGACAACCAGCCGCTGTGTCCATTAT	
<u>, , , , , , , , , , , , , , , , , , , </u>	GOVERGUNEDVELLEDV PLSLGIETLGGV	GATGTGCTTTTATTAGACGTTACGCCTTTAAGCCTTGGGATTGAAGCTTTAGGGGGGCGTGATGAAGCTTAAAGCTTTAAGAGTGATGAATTGAATTGATTAAAGCTTTAAGAGTGAATTGAAGTTTAAGAAGTTTAAGAGGGGGG	
(1)	VKAFINKDLNKSVNPDEVVAVGASIQG	CONTROL AAAAGCGTCATCATCATCATCATCATCATCATCATCATCATCATCAT	
œ	DAGLTKNEISEVVMVGGSTRIPKVQER	TGGTGATGGTGATGGTGATGGTTAATATTAATAATTAAT	
¥	VKKLTRAKFESLTEDLMKETISKIESVIK	INTERCOGNET TO A SOCIT OF THE SOCIET OF TH	
	AKKELSSAMETEINLPFITADATGPKHL	CAACGCCI AAAAGAAGCGGGCTGAAAAAGCGCTAAAAAAGAACTGAGCTCTGCGATGGAGACTGAAATTGCCCTT	
	SEFKSETGIFIKNDVMAI ORI KEAAEN	ATCGTGATTGATTTCTTAGCGAGTGAGTTTAAAAGCGAAACGGGCATTGAAATTAAAAACGATGTGATGGCGTTG	
z «	INNESENIMATOLGGGI FDVI VLETGDN	TTTAGAAACAGGCGATAATGTCGTGGAAGTTTTAGCCACAGGGGGCGATGCGTTTTTAGGGGGGGG	-
9	TKEAGTIAGLNVLRIINEPTSAALAYGLD	CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE CANTINU	
A	2996 AESYLGESVTEAVITVPAYFNDSQRKA	2995 GCTGAAAGTATTTGGGCGAGGGGTTAGGGAAGCGGTGATCACGGTTCCAGGTTATTTTAACGACAGCCAAAGGA	HP0137

_	•
v	5
<	۲

066501		PCT/EP01/15
3004 GHCGPWPYYQCTGTTNGTYSAYHVYI ANLESGNRIGTGGAANLIFNGVDSINI ANATITCHNAGIYSSSMITFSTGSMDNS GNLNGLNSNGKLSVYGTTFTNEAKDG KFIFNAGQAVFENTNFNGGSYQFSGD KFIFNAGQAVFENTNFNGGSYQFSGD SLNFSNNNQFNSGSFEISAKNASFNNA NSNLQIAGNAVFGNSTNGSONTANFN NTGSVNISGNATFDNVVFNGPTNTSVK GOVTLNNITLKNLNAPI.SFGDGTITFNA HSVINIAESITNGNPTILVSSKEIEYNN AFSKNLWQLINYQGHGASSEKLVSSA GNGVYDVYSFNNQTYNFQEVFSQNS ISIRRLGVNMVFDYVDIMEKSDHLYYQN ALGFMTYMPNSYNNNLGNANNTIYYY DKSIDFYASGKTLFTKAEFSQTF	KSELIMMS TINFLATION OF TOTAL MENTER AND LEGIAKSMOHEITTIEGLNELKTIIAVAK ONEFLACPKIGIRIELHSTGTGWAKAKS GGINSKFGLSSTEVLE AMRLLEENDLL EHFHMIHFHIGSQISDI SPLKKALREAG INLYRHQDKNYTLEE FSADVYFLLREI VKNKOEIEPDIFIESGRYISANHAVLVAP VLELFSHEYNEKSLKIKENNNPPLIDEM LDLLANINEKNAIEYLHDSFDHTESLFTLFDLGYIDLIORSNTEVLADSFDHTESLFTLFDLGYIDLIORSNTEVLAUKKAVQLLYKKDHNDILRIQEQVGIERYLLNCSFFQ SLPDYWGLRQNFVMPLNKLDEKFTR SASLWDITCDSDGEIAFDSTKPLFLDI	3008 KENAEGKYNTLSVKNKGLEAELDMLN EKFEKLKNMYAGVECFEKRGKNIKEGI VKTNPKVLGAPSNEVEELAFLERIEKG MQEFNVFYPKRLTVNFHTALKSTSLSP LSVLSGVSGTGKSELPKLYVHFGGLNF LSIAVQPTWDSPE
3003 TGGGCATTGCGGACCTTGGCCGTATACCAATGCACGGCGCACTAACGGCACTTATAGCGCCTATCATGTTTAATGGCGTATAATTTCAATGGCGTAGATAGTTTCAATGGCGTAGATAGTTTCAATGGCGTAGATAGTTTCAATGGCGTAGATAGTTTCAATGGCGTAGATAGTTTCAATGGCGTAGATAGTTTCAATGGCGTAATGGTAGTAGTTTTCCCCGCAAAGGAATTCAATGGCGCAAAGGCAAATTCGCAAAATTCGCAAAATTCAATGGCCAAAATTCAATGGCCAAAATTCAATAGGCGCAACTTTTCACTAAGGGAATTTCAATAGCGGTTTTAATGGCGCAACTTTAATGGCGAAAAAAGCAATTCAATAGCGGTTTTAACAACACACAC	3005 AGTCAATCAAATGCCTCGTHGTHICCLINAGISCAGGGGGATCACCGTGAATGCCTTTAAAGACAAA GCAAGTCTGAACTCATCGCAATGAGTTAACCAAAGCCTGAAGCCCCCTATCACCGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTTAACGATTGAGTTGAGTTTGAGTTTGAGTTTTAACGATTGAGTTTGAGTTTTAGCGTTTGAGTTTTAGAGGGTTTTAGCGTTTGAGTTTTAGGGGTTTTAGGGGTTTTAGGGGGTTTTAGGGGGG	3007 AAAAGAGAACGCAGAACAAAATATAACACTCTTTCAGTCAAAAATAAGCAATTAGAAGCTGAGTTAGATATGCTTAA CGAAAAATTGAAAAACGCCAAAAAATTGAAAAACGCCAAAAAATTGAAAAAACGCCAAAAAATTGAAAAAACGCCAAAAAATTGAAAAAAACAAAAAAAA
4P0137	HP0137	HP0137

Г	٧	ı
v	٦	ı
·	٠	
	•	

HP0137	3009 TAAAC	CGAATITICAAA GGOTTITA CAAAA AA CAACAA AA CAACAA AA CAACAA AA	2/
	AGAATA CGCTCA AAAAAC ACATTI ATTGCG TACCTI TATTGG TCGTTG	AGAATATTTGAAAAGAAAAGAAAAAGGAAAAAGGAAAAGCGTCCATCAAGGCTATTTGAAAAGCGATAGCGCTATAAAGCGCAAGCTATAAAGCGCAAGCTATAAAGCGCAAAGCTAGCGCAAGCTAGCGCAAAAGAAAAGAAAAAAAA	3010 KTEFERLYKLKRASILARENLSPSYKEY DILKRDFDESGNLRVHOGYFSGDSVALN SKEKESKKEDIEANDIKMILSEKEKLLS TO STAPPERSYKEY GEWENLYKLLS TO STAPPERSYMALOGGWONPNIFTLIK LANSTSETSRHQQVGRGLRIAINOGGK RVTHGFLKGNDNAFYKINYLDMLVSGE EVGFIEGLOKEIEASSFIGGGNALDRED LAKLGLNEREINKLFVELENSNALEFDE TNNAYKIIAPICETMQNNEER
	3011 GGCAAAA AATTTGAT AATTTGAT GCCCAGG GCTTTAGG ATAATTTG TAAATAT TTTTGGAA ACCACAC	3011 GGCAAAGACCTTTTTATCACAGGGGCTGTTGGATCGGGCAATGAGTGGGAAAACCGGTGGGGGGGCGATACTGGTT TTTGAAAGCCCTAATGGGGCTTATTTTCAAAATAACAGAGCCGGGCGGCGCAACTGTTTTGGTT AATTTGAATTTCCAATAACGCGTGAATTTGACAACACAGATTTTGGCAACCCGAACCCCTAATGGGGGCTTTAATGCT ATGGGGCCAAAGATTACCAATATGAATTGAAT	3012 AKDIFITGAVGSGNEWKTGGGAILVFE SSNELSANGAYFÖNNRAGTQTSWINLI SNNSVNLTNTDFGNQTPNGGFNAMG RKITYNGGIVNGGNFGFDNVDSNGATT ISGVTFNNNGALTYKGGNGIGGSITFTN SNINHYKLNLNANSVTFNNLTFNGG WFVFNIPDAHVNFQGTTTINNPTSPFV NMTGKVTINPNAIFNIQNYTPSIGSAYT LFSMKNGSITYNDVNNLWNIIRLKNTQA TKDADKNHTSSNNNTHTYYVTYNLGG TLYNFRQIFSPDSIVLQSVYYGANNLYY TNSVNIHDNVFNLKNINDDKADTIFYLN
			ATTPWANGSIPKSNSTVREGGYEGVN WGKTGYITGTFTADRVYITGNMMTGN

/066501		PCT/EP01/15428
3014 HSSSATAPTNETLEANAMINFAFLGAIK ANGLVDESKYLONTTIGTLDLGPNATF KANHLIVNNAFNNNSNYRADISGNLNV VKGAALSTNENGLNVGGDFKSEGSLIF NLNNKTNQTIINVAGNSTIMSYNNQALI HFNTQLKGGAYTLINAKFMLYGYDNQII RGGSLSDYLKLYTLIDFN3KRMQLNGD SLSYDNQPVNIKDGGLVVSFKDNQGQ MVYSSILYDKVQVSVSDR;PMDIHAPSL EYVIKYIQGSAGLDAIKSAGNNSILWLN ELFVAKGGNPLFAPYYLGDNPTEHIVT LMKDITSALGMLSKPNLKNNSTDALQL NTYTQAMSRLAKLSNFASFDSTDFSE RLSSLKNORFAKSNLKSNR OKLKNNLWATGVGGVSAYGYSGFY GVNVGYDFIKGVIVGGYAAYGYSGFY ERITNSKSDNVDVGLYAFAFIKKSELTF SVNETWGANKNNYGYDFMKNKSIILK POIGLRYYYIGMTGLEGVMHNALYNOF KANADPSKKSVLTIELALEINRHYFNTN SYFYAIGGFGRDLLVNSMGDKLVRFIG NNTLSYRKGELYN	3016 SSALERELKGKNEHLENALKEGEYLKN AWLLEMEKOKEIFHNKKLELEKSYQQA LNILKSEVASKDTSSMHKIEIHKASEILS KHKTNQEIPQIITNFQANEKARYKNESV LIVQILDKGYYWIETELGMRLKAHGSLL KKIQKPPKNKFKPPKTTIPKPKEASLRL DLRGQRSEEALDLLDAFLNDALLGGFE EVLICHGKGSGILEKFVKEFLK	3018 PLGFGIAKUDAPISKELCA I YPVLNWK DENLGSYAVFCNSLSKEKILKESASER VIEIDESFVLKALDFTYPFI.NEAYSNKM AHKNIGVVELLKALEENKLKNSDGES LYRLVILYEDKPCESVESAYMKLLALSL GKAPLRSLNLEGIFNQLSINAAWSGNKP YELEWLRMNEVALKMRDHFPSIDFIDK FPRYLMQLIPEFDNIRLLDSSKTRFGAY LGTGGYTQMPGASYVNFNAGAMGVC MNEGRISSSVVNGAGTDIGGGASVLG VLSGGNNNPISIGKNCLLCANSYTGISL GDGCVDAGVAILAGSVIEIEENEFKKLL EVNSALEKHANNLYKGKELSGKNGVH FRSNSQNGKLIAFRSVKKIELNONLH
100	301	
3013 TCATTCTTCAAGCCCCAACCCAACCAATGAAACACTAGAAGCGAATGACGAATTTTCAAAGCCCAACCCTTTAAAGCCCAATGGATTTTCAAAAGTTTTTCAAAAGTTTTTCAAAAGTTTTTCAAAAGTTTTTACAAATGGTTTTAAACGCAATTAAACGCAATTAAACGCAATTAAACGCAATTAAACGCAATTAAACGCAATTAAACGCAATTAAACGCAATTAAACGCAATTAAACGCAATTAAAACCAATTAAACGCAATTAAACGCAATTAAACGAATGAAT	3015 TCCAGCGCGCTAGAAAGGGAATTGAAACAAAAGAATGAACATTTAGAGAACGCTTTAAAAGGGCAAGAATATTTGAAA AACGCATGGCTTTAGAAATGGAAAAACAAAAGAAATCTTTCACAATAAAAAATTGGAATTGGAAAAATCCTACCAAC AAGCCCTAAATATCTTAAAAAGCGAAGTCGCTTCAAAAGATACTAGCTCCATGCATAAAGAAATCCTACCAAC AAATTTTAAGCAAACAAAACA	3017 GCCTTTAGGTTTTGGCATTGCCAGAGTGGATATTGCCAGAAAGAA
SE CONTRACTOR OF THE PROPERTY	.ee	.0 .
HP0137	HP0137	HP0137

ė		۰	
•			
	-	۰	
۰		ı	ŀ

1 - 1 - 1 - 1		PC1/EP01/154	128
3020 SVLSCTKLPLEDAKYLASLEKPSIKAPL KSVFKDTFKNDEIIAQLPYDPILNILCHI LQDEGIEFYFMHESRSGEALLYYEALF KTPKRLITPTKKFVLENNFSTFPFKDEI EFLSATPNSIV. YLSFKRPTRLLHANG SLKTLLSVSFDFNKMFNALKQDEKASR MLQNYATKFPDFYARVELSKYDLGGA NLLDFFCILGFVLGYSEDFCTQSVIPLA KECLRPKGPRIDYKILKDNSLKMALNFS KIMHSAMSFRLAGVENEILSLGILDSLA EFLGNFIWDNAQNFSVQEVTIAGDFFG EKVFLDLFVRYFPKTLALKTHAFLDYE	3022 GĎLSDĎKVNARLGELETICVEEĎPMYE CEVAIEKILEĎLGIPSSKHNDLMKTLPS SDKFKILLAOVLFPKPDILLLDEPTNNLĎ LNAIEWLENNLKRHEGTMVVISHĎRHF LNAVCTHILDLDFHSVREFSGNYDĎWY IASTLIAKQČEAERNKKLKEKEELEKFIA RFSANAŠKAKOATSROKOLĎKLĎIQSL AVSSRŘĎPSIIFKPKŘTIGNEALECENI	3024 SEGRGESLONNPNLSKKDVKIVEKILS KNDIKAAEMKERYLKEGLYVLNFMSSP GSGKTTMLENLADFKDFKFCVVEGDL GTNRDADRLRKKGVSAHGITTGEACH LEASMIEGAFDLLKDEGALEKSDFLIEN VGNLVCPSSYNLGAAMNIVLLSVPEGD DKVLKYPTMFMCADAVIISKADMVEVF NFRVSQVKEDMQKLKPEAPIFLMSSKD PKSLEDFKNFLLEKKRENYGSTHSF	3026 EDIEKLHGNTLSPLQIPQDLTYQPVLST KVNISVNLNPKDHLKGVQDFFLNDKGE IIKERFLNQDINALANNDNEPIDATNRK LNISIOKEDGKKEDFVFTYGDAEKGEN QFKTLGDLOKLLKEKTGLDLNLIKSEKD AKSPPLLLEIANPSQTPITFSLSGGIADK
TAGAGACGCTAAATATTTGGCCAGTTTGGAAAAACCCTCCATCAAAGC TTGAAAAACGATGAAATCATCGCCCAGCTATGGAAAAACCCTCCATCAAAGC TTCAAAAACGATGAAATCATCGCCCAGCTATGAACCCATATTGAA SGGATAGAATTTGTTTTTATGCATGAAAAATAATTTTTCTA ACGCTTGATCACCCCCAATTCTATCGTTTTGTATCTCAGCGCCCCCCCC		<u> </u>	3025 TGAAGACATTGAAAAATTGCATGGCAACACCCTTTGCCCCTAGAATCCCCCAAGATTTGACTTACCAGCCCGTGCT 303 TAGCACGAAGTTATTATTAAACGTGAATTTAAACCCTAAAGACCCTTTAAAAGGCGTGCAAGATTTTTCTTAAACGAT TAGCACGAATAACGATTATTAAGGACGTTTTTAAACCCTAAACGCTTTAAAAGGCGTGCAATAACGATAACGATTAGA AAGGGCGAGATTATTCACTAATTAAACATTAAACCATTAAACGCTTTAGCGAATAACGATTAGAATTTCACTTATGA TGCCATCACTAATCGCAAAATTAAACATTCAAAAAAAAAA
HP013/	нР0137	HP0137	HP0137

/066501		PC1/EP01/1542
3028 DTSDDEKEQLDIDRIDKRPVSEHLKN TNKHELYELLGFYQKEI.DKKQNHSAFK NFAILNGLDRDFERETNIGYSVLKKKEM LLNKLEHLDKRLLDKNÉHLLAQLRNE VKTKQNIQYNTLTNPILLAQLRNE VKTKQNIQYNTLTNPILLAQLRNE ANDPTYKLNONTYELVSKQLGDYQNT MILLAKERLLFLEQDLKOKEEEFERAK EHYVKSSKHYRETSLS PKEKQGFLKQI KQFSKISKDILYTCNEIIGANRFLTHYDN LNLEKVLEHAKDTKLE(XEIQAITKEPN NDEPWIEFGKKEQARAKAHYQAMLEK EKAKELAKQQANTLHSNELDDDPKAH AGLKQNDNTNFKGRNR	3030 KQRTEHDLEMISATGVCKGIENYARHF TGKAPNETPECLFOYLGIFEREFLVIVD ESHVSLPQFGGMYAGDMSRKSVLVEY GFRLPSALDNRPLKFDIETHKNCQFLF VSATPNKLELELSKKNVAEQIIRPTGLL DPKFEVRDSDKQVQDLFDEIKLVARG ERVLITTLTKKMAEELCKYYAEWGLKA RYMHSEIDAIERNHIIRSLRLKEFDILIGI NLLREGLDLPEVSLVAIMDADKEGFLR SETSLIQTMGRAARNAINGKVLLYAKKIT QSMQKAFEITSYRRAKJEEFNKIHNITP KTVTRALEEELKLRDDEIRIAKALKKDK MPKSEREKIKELDKKN RECTKNLDFE EAMRIRDEIAQLRTI	3032 QTRPFICPKCIEPIDVN EALYKUIEUEN GNKFLAGOKEFEKEVNEKRAGYLSYF KNLEGKEETLKEREKEJDAKFDEAVK GASALALQDERAKIIEEARKNAFLEGO KGLELLOKELDEKSKOVGELHOKKEGI ERLKRENNEAESRLKAENEKKLNEKLD LEREKIEKALHEKNELKFKOGEGLEM LRNELKNAGRKAELSSJOFGGEVGEL AIEEFLRÖKFPLDCIEEIKKGGRGGDCI GOVVHTREFONCGKIYYESKRTKEFOKA WVEKLKSDMREIGADVGVIVSEALPKE MERMGLFEGVWVCSFIEFFK
		3031
HP0137	HP0137	HP0137

•		
1	•	1
•	e	٠
		Į

	AIGAAAAGA		KKRALYDRYGKKGLNGAGASOGDFSD	
		ATGRANDERGEGEGECUTIATION AND AND AND AND AND AND AND AND AND AN		
_	AAGCTCTAT	AAGCTCTATCGCACCGGATTATTTGCAAAACCCTTGAATTGAGTTTCAAAGGAGGCGGTTTTTGGCTGTAAAAAAACCCAT	FFEDLGSFFEDAFGFGARGSKROKSSI APDYLOTI FLSFKFAVFGCKKTIKVÓV	⋖ 117
	TAAAGTCCA	TAAAGTCCAAATACCAGAGCGTTTGTGAAAGTTGCGATGGCACGGGCGCTAAAGACAAAGCCCTAGAGACTTGCAAG	OSVCESCDGTGAKDKALETCKOCNG	
	CANTECAN	CAM I GCAN GCAN GATOTT AND SOCIET OF SOCIETING SOCIETING SOCIETING SOCIETION OF SOC	QGQVFMRQGFMSFAQTCGACQGKGK	
	CTANTANTO CTANTANTO	GCGATAATCCTTCAGGGCAATTCATCATCATCATCATCATCATCATCATCATAAAACCTTATAAAGGTTAAAGAATTGAT	IVKTPCOACKGKTYILKDEEIDAIIPEGID	
	AAGAGGGG	OCCENTATION OF SAGGER 11941 GATERARA COCCATOR 1961 GCT 1 AAAAA 1 AAAGGCAAT 16ATACGAGAAGGGAAA AAGAGGGGATTTGTATTTAGAAGCGCGAAGTCAAAGAAGAAGAAGAATTCAAAGCGCGAAGCGCAAATGCAATTAATT	DONRMVLKNKGNEYEKGKRGDLYLEA	
	AAGCGCCG	AAGCGCCGGTGTTTTCACCACTATCGCTTTAGGGCATACGATTAAAAGTGCCGTCTTTAAAAGGGGACGAACTGGAA	GHTIKVPSLKGDELELKIPRNARDKOTE	
	TTATAGAGG	I I AAAAA I CCCT AGAAACGCCAGAGACAAGCAGACTTTTGCGTTT AGAAACGAGGGGGGTGAAACACCCTGAAAGCTC TTATAGAGGGAGTTTGAT	AFRNEGVKHPESSYRGSL	
HP0137	3035 TTCAGCCAG	3035 TTCAGCCAGAATGAACTCAACGATATTTTAATGCTCTTACTGGATGGCTATATCCAAAACGAAAATAAGGCGTTT	3036 FSONELNDILMI SLI DGYIONENKAESP	177
	AGCCCCTT	AGCCCCCTTTTAGGCGCGCGCTTGAAGAAAATTCACCCCGATTAGAGAAGCTAGAAAAAGAAAG	LLGALEEKFTRLEKLEKERRLLEDKKRF	: *
	I AAAAAGCG	AAAAAGCGIII CCAAAAGGAII I AGAAGAACGAII GAAATII I GAAAAATGAAATTAGAGAGGCTGGATTTAAAAGA	AKDLEERLNFEKMKLERLDLKEDEYER	2
	AGAI GAAIA	ATACACTOCA CONTROL OF THE ANALYSIS OF THE ANAL	LLEOKKLLSSKEKLNDKIALALEVLENT	7
	199898119	OF INVENTOR INCOME AND INVENTOR INCOME AND INVENTOR IN THE ANGERGE OF THE AND INVENTOR IN THE AND INVENTOR IN THE ANGERT OF THE ANGERT OF THE ANGENT OF THE	HKITHALESVGHSAEFLKSALLEASAL	
	AAGTTAAA	AND TOTAL CONTINUES OF THE CONTINUES OF	EKEQAKLEECERLDIEKVLERLGMLSG	□
	10100000	ANNO TO THE WAY WELL I LEGATION OF THE SECRET AND THE SECRETARY OF THE SEC	IKDYGSIMHAKERLGHVKNELHNLKEID	<u></u>
	ACCIONAL OF TAXABLE IN COMPANY OF TAXABLE IN	ASSECTION OF A WAY CAREED FOR THE STANDARD FOR THE STANDA	SHCETYHKEIERLKTECLKLCEEISGFR	×
	TTTAAGCGC	ATTAAGGGGTAAAGGGAAAGATTTGCTCGTAAAAAAGCGGCTTTGGAAAGAGGGTATTTAGCGGTTTTAAGGCTCT TTTAAGGGGCTAAAGGGAAAGATTTGCTCGTAAAAAGGCCCAAAAAGCGGTTTTGGTT	KEYLAGFNALLSAKAKDLLLKSPSLV	¥
HP0137	3037 TGTGCGCAG	TGTGCGCAGTGGGGATTGCAAGGAAGATTGCGCTTATTGCACGCAAAGCTCACCATCAAGGAGCGATCAAGGCC	3038 VRSGOCKEDCAYČTÁSSHHOGAIKBY	45
	TATAAATTTA	TATAAATTTAAAGATGAAAAAGTGGTTTTACAAGAGGCTAGAGCGTTAAGACAATTAGGGGCTTTAGGGTTTTGTCTG	KFKDEKVVI OFARAI ROL GALGEOVY	, ¥
	GTTACTTCA	GTTACTTCAGGGCGCGAATTAGACGATGAAAATGCGAATACATCGCTAAATTTAGCTAAAGCCATCAATCA	SGRELDDEKCEYJAKI AKAINOFFI GI H	돌
-	ATTGGGCTT	ATTGGGCTTGCATCTAATCGCATGCTGCGGGGGGGGGTTTGGAGCAATTAGAATTTTAAGAGATGCGGGCATC	LIACCGRADLEOLEFLRDAGIHSYNHN	E
	CATAGCTATA	CATAGCTATAACCACAATTTAGAGACTTCGCAAAATTTCTTCCCTAAGATTTGTTCCACGCACACATGGGAAGAAAGG	LETSONFFPKICSTHTWEERFITCENAL	Ξ
	TTATCACAT	TITATCACATGCGAAAACGCTTTAAGGGCGGGGTTAGGCTTGTGCAGTGGGGGGGATTTTTGGGCTTAATGAGGT	RAGLGLCSGGIFGLNESWEDRIEMLRA	돐
	GGGAAGAIC		LASLSPHTTPINFFIKNPVLPIDAETLSA	춫
-		THE CONTRACT AND CONTRACT OF THE CONTRACT OF T	DEALECYLLAKEFLPNARLMVAGGREV	<u>-</u>
	TTTTGAATA	TITTGAATA	VFKDNDKKEAKLFE	щ
HP0137	3039 TTTGAAAGC	3039 TTTGAAAGCGTTTCTAAGGATTTTTACCACGATAATTTGGAATTTAACCACCGCAGTGCGCCTTTAATCATTATTG	3040 FESVSKDFYHDNI EFNHRSAPI IINYVN	16
	TGAACACCA	TGAACACCATTTTTAAAAAGCTTATCAAAATTCCCCCACCGCTTATTTGGAGCAAAAATACCCTAAAACTTCTCAAAA	TIFKKAYONSPTAYLEQKYPKTSQNKH	7
		PARACTICAL MARKET CONTRACTOR OF THE MARKET CONTRACTOR OF THE MARKET CAN CONTRACT OF THE MARKET CAN CON	VTDGYVKVSLVADERELLLDQVLQEAQ	딾.
	AGAAATCAAA	AGAAGUTCAAAAUCTTTTGCAAGGGGTTTTGAGGCTTTTGAGGTATTTACCATTTTATGCGCCCACTAATGACGCGCTTTT AGAAATCAAAAATTATTTGCAAGGGGGTTTGAGTGCGATTGGCCCCAAGGATATAAGGAATAAAAAATTAAAAAAAA	NLLEHRIEPKÖITILCATNÖDALEIKNYL	ૅ ટ્
	TGTAGAGTCT	TGTAGAGTCTAAAAATCATTAAGAACGCTTTAAGAATACGCTCTAACCGCAACAACAACATAACAACAACAACAACAACAACAACAACA	CENTUALIST DESCRIPTION OF THE SERVICE OF THE SERVIC	òί
	CGTTTAAAA	CGTTTAAAAGTCGCTGGATACTTGCATGCCATTGCCTTTAACCTGCTTTAACCTTAAAAAAAA	ALETALAEEPYRPFYRHSVLKLAGYLH	Lì
	CAGGCTTTG	CAGGCTTTGTGTGGAAGGTGATGGAGCAATTTGAGCTTTATGGAGAGCCTGCACAAAGCTGTTTGGAATTAGCGGTT	DDAIALAGFINFKRESVAGFVWKVMEQ FFI YGFPAÓSCI FI AVGÓFÍANGFI FK	ج ن
	GGGTGCGAA	GGGTGCGAAGATGCCGATGGATTTTAGAAAAATTAGAGACTAAAGCGATCGCTTCCCCATTCAAAAGGCGCGCA	LETKAIASSHSKGAQIMTIHKSKGMQFP	ğ
	וסאוראוופארו	CALICACAAAICIAAAGGGCAIGCAAIICCCIIAIGIGAICGIGIGCGAAC	IYVIVCE	1

	3044 SSYGYDIRVGSEFMLFÜNKNALIDPKN FDPNNATKIDASKEGYFILPANAFALAH TIEYFKMPKDTLAICLGKSTYARCGIVN VTPFEPEFEGYITIEISNITNLPAKYYAN EGIAQVYFLOGDEMCEJSYKDRGGKY EGIAQVYFLOGDEMCEJSYKDRGGKY SO46 KETATTINQEIAKYHEKSIDKAALGLYEL	() c () . () -
3041	3043	3045
HP0372	HP0372	HP0010

_	_
u	-
•	٦
_	e.

	INN			
	YYKESALLNKKASYMPVLLWHTAWSF	OOC ATGCCTGTGCTTTTGTGGCATACGGCATGGTCGTTTAAAAAATCAA ACATGCCTGTGCTTTTGTGGCATACGGCATGGTCGTTTAAAAAAATCAA		
	NSYRLYYVRYVLGEVAYGEKRYREAIK	AGAAGCCAAAGGGGGTTTGTTGTTGTGTTAGAAGCCAATAGTTACAGACTTTATTATGTGCGTTATGTTCTTGGAGAAGT		
28	EIFQEALSFFKNKSYAEAKERLLWLEA	TTGAGTTTGATAAAGACTTGTCTAAGCAAAAAGAGATCTTTCAAGAAGCTCTGTCTTTTTTAAAAATAAAT		
54:	NALNEGEEKAEKPLKSNAPANK I PSLK AESPKNOEGKTÖEKAKIEFDKDI SKOK	TCCGGCTAATAAAACCCCCTCTTTGAAAGCCGAATCCCCAAAAAATCAAGAGGGAAAAACTCAAGAAAAGGCGAAAA		
17.	OLDKONKEMSELLTKLSODLVSQIALIO	ACCAGCAAGE IAICCAGCAGIIAGACAAGAAAAIAAAGAGAGAGGAGGATGAGTGAATTATTGACCAAGTTAAGCCAGGATTTG		
PU —	QANTLKQQSQTLEDLRNEIHANQQAIQ	I I C'ECKAGEANG I ECHAGEC I NACHCECT I NAGCAGCATT CECANACTIT TAGAGGATT CAGGATT CAGGATT CAGGCTA ACCAGGANGA A CANACTA A CANA		
/L	GANKIKDLNNAILSGEESLRALKASGEV	TGAGGGGCAGGCTAATAAGATTAAAGATCTCAATAACGCTATCCTTTCCCAAGAAGAATCCTTACGAGCCTTAAAAGC		
	3052 GEPSAFDLOSGATKKELKÖLGINSKNF SNILTKIHSÖVFANTOAOFGI RSIVYFG	3031 GEGEGAGCC FICAGCG FITGCAAAGTGGGGCTACCAAAAAGAACTCAAGCAGTTGCAAATCAATAGTAAGAA TTTTTCTAATATTTTGAGAAGCGTTTGAAATTCAAAGTTTA TTTTTTTTTT	1506	HF0010
		IACATIAA	1200	0,000
	LENPLDLYSSUGIGFERILLEWLUKIKN	TTGGTTTCTCCAAGGCATAGGATTTGAAAAACCCTTTTAGAATGGCTTGATAAGAAATTGATCTTATAAGT		
	FIFKHLLPNAKUYLYPHUYNGYVKODY	CCTAACGCTAAAGATTACCTTTATAAACGCCTAAACGCTAAAATAAAAAAAA		
	LACSPKSNTAYRAINOALDCVQKGSLY	CGGCTTATAGAGCGATCAGAGCTTTGGATTGCGTTCAAAAAAAA		•
	LNLAASCLFAVKOIGYPEARIILSQCVIY	GALLILI GUGAGUGAGGA ALI I GGI AACGCI AACCCGAACGCCCTTAATTTAGCCGCTTCTTGTTTGCTTTGCAGTCAA		
	AGGENPEFIARRLVIFASEDIGNANPNA	AAAACGCTTCCATCTATATCTGGCGCGCGTTGCTGCCGGGGAAAACCCCGGAATTTATCGCCAGAAGGCTGGT		
_	THYNLTSALIKSLRGSDENASIYYLARLI	NAME GATGATCTTATAGE GATGATGATGATGATGATGATGATGATGATGATGATGATG		
	AKIEDPITLKTLOSLRPHSLNDGSYSDD	TTAAACCTTTTAGATTTGAGCGCTAAAATAGAAGATCCTATCACTTTAAAAACGCTACAATCCTTACGGCCTCATAGCC		
	CELTENASCEDARE CONTROL	CATTECTCAAAAACAAATAGAGCCTGGCGCTAAAACCTATCTTTTAAACAACAGGCGCTGGCGACGCTAGAGCGTTA		
	3050 PIMEKDHALILGASTODPNYSLSHAIRS	TCCGATCAAGAAGTTTTATTTTTGAATTAACCCCCCTAAACAAGAGGATTTAAGACAGGATTTAAACAAAGAAAAAAAA	.	
	ROCSTPASV	3040 CCC CATTA TOO A A A A CATO A CONTINUE A STATE OF CONTINUE A S	30,00	00000
	LNVTKLLGFSSPLYNRYYSSVNEVVSP		_	
	QQGGGFGVNVGRMLGNRTHVSLGYN			
	LTNPRIFDSWYSSTINLYADYRISYQYI			
	NIATGGGRSYPGMPKGAGRMFAGNLS			
	YGGLMLNGSVSERNLFGTGOSMSI YA			
	TKLRNSENSLRRIGFFSKVKIEEKRVN SELMDLIVEVEEDBIDGLOTOLOTOL			
- -	DVIISGNORTSDRIIRRELLLGPKDKYNI			
=	KPDLDKDEKNGLVKVIYRIEVGDMVYIN	AATTITAAAACCGAAATCGCCGATAAGGGTTATGCGTTTGCGGTGGTGAAGCCAGACTTGGATAAAGATGAAAAAA		÷
	VENICHTER AVER TERMENTER IN TERMENTER IN THE INTERPRETATION INTERPRETATION IN	CTTAAAAACCTTAGAAAAAGCGCTTAAAGTGAAAAGGAAAGATGTCTTTAATATTGAGCATTTAAGAGCGGATGCGCA		
$\overline{}$	HISSPELKTOFSTHDAKLHYKVKEGIQY	GCTTCATTATAAAGTCAAAQAGGGGATCCAATACAGGATTTCAGACATTTTAATAGAGATTGACAACGGGTAGTGACCCGTAGTAGA		
	KLRLDQLEYDSMRIQDVYMRRGYLDA	GTATATECETAGEGETTACTTACATACACCATATATATATACACTAGAATACGATTCTATGCGTATCCAAGATGC		
7	RRMIESLSANKORDFMGWMWGI NDG	CCATTTATGAGGGGAAGCGCGAAATTAAAACGCCGCATGATTGAATCTTTGAGTGCGAACAAGCAACGAGATTTCATG	.	
$\overline{}$	GALLIVFDVNRGDSIYIKOSIYEGSAKI.K	CACAGAAAAGGCCATTATTGATCGTGTTTGATGGGGGGGG		
_	TALKTALEGOGYYGSVVEVRTEKVSF	AATTAGAGCATGCTAAAAACGGCTTTAAAAACCGCTTTAGAGGGGCAGGGCTATTATGGGGAGCGTGGTGGAGGTGCG		
$\overline{}$	EKDGLKSOMGIKKGDTFDEOKI FHAK	TTATGGGACTGAAAAGGAAAAAGACGGCTTAAAATCCCAAATGGGGATCAAAAGGGCGACACCTTTGATGAGCAAA		
*	FEGGII FEHEDEKARIAGVEIKOVALI	TATGCCACTTTTGAAGGCGGCATATTAGAGTTTCATTTTGATGAAAAGCCAGGATTGCCGGGGTAGAAATCAAGGG		
$\overline{}$	MKVKSISYVGLSYMSDMLANEIVKIRV	CTGGGCGATATTGTGGATTGTAAAAAATAGACACCGCTGTTTTGGCTTTGTTCAATCAA		
fire.	3048 NEAPKNEVORNEACKETPOSNOTPKE	3947 AAA I GAAGELI CCAAAAAA I GAAGI I CAAAGAAA TGAAGCTCAAAAAAGAAACCCCCCAATCCAAACGCCTAAAAGA AAATGAAAGTCAAGTC		01.00.10
				2

HP0010	3053	3053 GACGCT AAAGAAATCGCTATGCAACGATTTGACAAACCATAAGATTTTTTGAAATCCTTGCGGATAAAGTGAGC GCTAAAGACAATGTGATAACCGCATCAGGGAATGCGATCTTATTGAATTATGATGTGATATTCTAGCGGACAAGGTG CGTTATGACACTAAAACCAAAGAGGGTTATTAGAGGGGAATATCAAGGTTTATAGGGGGCGAGGGTTTGCTGATAA AACCGATTACGTGAAATTGAGTTTGAATGAAAAATATGAAATCATTTTCCCCTTTTATGTCCAAGACAGCGTGAGCGG	3054	3054 DAKEIAMQRFDKQNHKIFIELADKVSAK DNVITASGNAILLNYDVYILADKVRYOT KTKEALLEGNIKVYRGEGI.LVKTDYVKL SLNEKYEIIPPFYVQDSVSGIWVSADIA
		GATTTGGGTGAGCGCGGATATTGCCAGCGGAAAGGATCAAAATATAAGGTTAAAAACATGAGCACTTCAGGGTGCA GCATTGATAACCCCATTTGGCATGTCAATGCGACTTCAGGCTCATTCAACATGCAAAAAATCGCATTTGTCTATGTGGA		SGKDQKYKVKNMSTSGCISIDNPIWHV NATSGSFNMQKSHLSMWNPKIYVGDI
		ATCCTAAGATCTATGTCGGTGATATTCCTGTATTGTATT		PVLYLPYIFMSTSNKRTTGFLYPEFGTS
		1GGGTTTTTATACCCTGAGTTTGGCACTTCCAACTTAGACGGCTTTATTTGCAACCCTTTATTTA		NLDGFIYLOPFYLAPKNSV/DMTFTPQI RYKRGFGLNFEA
HP0371	3055	3055 CCCTCAAGTITGTCTAGCGTAAAGGGGCTATAAGCTTTGTGAGTGCTTTTGGGATGCGGGCGTGCCTAGAGATGCGC I ICATTTACTTGCCCTCTAAAGGGAGCGATATTAGCGAACATCTTTAAGAGATGAAAGCATCCAGTTTGCCATTTAA	3056	3056 PSSLSSVTGYKLCECFWDAGVPRDAL Y1 PSKGSDISFHI LRDESIOFAII TGGF
		CCGGGGGGGGAAGACACCGCTTATAAAATGTTAAAAGCTAACCCCACTTTAGCCTTGAGCGCTGAAACAGGCGGTAA		DTAYKMLKANPTLALSAETGGKNATIV
		AAACGCCACCATTGTGAGCAAATGGCAGACAGAGAGCCAGGCGATTAAGAATGTTATCCATTCAGCTTTTAGCAATT		SKMADRDQAIKNVIHSAFSNSGQKCSA TSLLVLEKEVYEDENEKKTLIDATI SLS
	· • • • • • • • • • • • • • • • • • • •	TAATAGATGCGACTCTAAGCCTTAGCGTGGGCGATCCTTTTGATTTCAAAAACAAAATCGGCGCTCTAGCGGACAAG		VGDPFDFKNKIGALADKPNEKVIKAIDE
		CCTAATGAAAAGGTCATCAAAAGCCATAGATGAATTAAAAAGCTATGAAAATTACGAAATCCCGGTAAGCTTTGTCAAT		LKSYENYEIPVSFVNDNPYLMKPSIKYG
		GATAACCCCTATTTGATGAAGCCAAGCATCAAATACGGCACTAAAAAGGCGATTTCACGCACCAAACTGAGCTTTT		TKKGDFTHQTELFTPILSVIMEAKDLDE
		ACGCCCATTTATCCG1GATGGAAGGTTTTAAAAGATTTAAAGAATATTAAAAAAAA		AIEIANS I GTGL I SALESLUEREWETTL FRIFAGNIYINKPTTGAIVI 130PFGGVK
		TCAACAAGCCCACCACCACGAGGAGCGATTGTCTTGCGCCCAGCCTTTTGGGGGGGG		KSAVGFGRKVGIFNYITQFVNICQEEED
		GAGGAAAGTAGGCATTTTCAACTATATCACGCAATTTGTGAATATCTGCCAAGAAGAAGAAGAAGAAAGCGCCTTAAA		ENALKNPLSEALENLTQKGYDEHTHEL
		AAACCCCTTAAGCGAAGCCTTAGAAAACTTAACTCAAAAAGGCTATGATGAGCATACGCATGAGTTGAAGCGCGCGC		KRAIFMAKSYAYHYKHEFSQTKDYVKI
		TTTTATGGCAAAAAGCTACG		RGEDNLFSYTKVKSVGYRITEKDTLSD MLG
HP0371	3057	3057 CGCAATCTGTTTTAAATTCAATGCCAAGAATGCGATCAGTTTCACCAACAGCACGAATTTAAGCTCTGGTTTGTATC	3058	3058 OSVFKFNAKNAISFTNSTNLSSGLYOM
		AAATGCAAGCTAAAAAGCGTGTTGTTTGACAATTCCAATTTAAGCGTTTCAGTGGGGACAAGCAGTATTAAAGCCAATG		QAKSVLFDNSNLSVSVGT:SSIKANAINL
	-	CGATCAATCTTTCTCAAAATGCCTCTATTAATGCGAGCAACCATTCAACCTTAGAACTTCAAGGCGATTTGAATGTGA		SONASINASNHSTLELQGDLNVNDTSS
		ACGACACCAGCTCGCTCAACCTCAACCAAAGCACGATTAATGTTTCCAATAACGCCACGATATAACGAATTAACAACGAATATAACAAATTAAAAAATAAAAAAAA		LINENOSTINVSNNATINDYASLIASNGS HI NENGAVNENSANITTSI ANSSIVEKG
		I I GALLI GEGAGI AALI GGELICI EACHT AALI I LAACGGGGGGGGGGGGGGTT AATTTAATTTAAGGAATAACTCTTCTTTAGATT) AATAATTCCTCTATCGTGTTTAAGGGGGGGGGGGGGGTCTTTAGGGGGGGG		AVSLGGOFNLSNNSSLDFJGSSAITSN
		TCCAAGGCTCTAGCGCTATCACCTCTAACACGGCGTTTAATTTCTATGATAACGCTTTTTCTCAAAGCCCCATCACTT		TAFNFYDNAFSQSPITFHQALDIKAPLS
		TCCATCAAGCCCTTGACATTAAAGCGCCCTTAAGTTTGGGAGGCAACCTTTTAAACCCTAACAACAGCAGCGTGCTG		LGGNLLNPNNSSVLDLKNSQLVFGDQ GSI NIANIDI I SDI NDNKNEVXNIIDAD
<u> </u>		GATTTRACAGACAGACAGATTTTTTAAAAAAAAAAAAAAA	-	MNSNWYERISFFGMHINDGIYDAKNOT
		GCATGCACATCAATGACGGGATTTATGATGCTAAAAACCAAACTTATAGTTTCACTAACCCCCTTAATAACGCCCTAA		YSFTNPLNNALK
		АА		

159

c		u
ū	7	Ξ
7	٠.	•
	₹	٢

GTMIL	CAGGTATAGTGAGTGGGGTTGTAGCCAAAGATGTATGGAACATGAACGGCACTATGATCTTA
QDETSPVKQAFIGKSDPTFVLAQYTPIE	I GETAATUUUNI IGAI GAUAAAAGGAAAGGAGAAAAGAAGATGAAACAAGACCCTGTCAAACAGGCCTTTATAGGCA AGAGTGATCCCACATTTGTTTAGCGCAATACACCCCCATTGAAATCACTGTGAACTTGTAAAGTAAAAAACAATTGAAATTAAAAGTAAAAGAATAAAAGAATAAAAAA
LKNKKEKSGEFVDENGNPIDDKKKAEK	GCAGAAACTGCCAAGAATATCAGTGAAATCGCTCTTAAGAACAAAAAAAA
IKDKNLEAKLAKALGGNKKDDDKEKSK	ASSENTINGGESTAAASSAAAAAAGTAAAAAATCCACAGAGGAATTIAGAAGCTAAATTAGGCTAAAGGCTTTAGGTGGCAATAAAA AAGATGACGATAAASAAAAAAAGTAAAAAATCCACAGGCAGAAGCTAAAACAAATAAAAAAAA
VDADKIASONPIYASIEPDIAKQYETEKT	I MANUELLA LI IGALI GA I GUGGATA A A I GUGGATA A I GUGATA I GUATA GA GA TATA GA GA GA TATA GA GA TATA GA GA TATA GA GA TATA GA GA TATA GA GA TATA GA GA TATA GA GA TATA GA GA TATA GA GA GA TATA GA GA GA TATA GA GA GA TATA GA GA TATA GA GA GA TATA GA GA GA TATA GA GA GA TATA GA GA GA TATA GA GA GA TATA GA GA GA TATA GA GA GA TATA GA GA GA TATA GA GA GA TATA GA GA GA TATA GA GA GA TATA GA GA GA GA TATA GA GA GA GA TATA GA GA GA GA TATA GA GA GA GA GA GA GA GA GA GA GA GA GA
NMAAKGYPLLPMDFKNGGDIATINATN	AAACCTTTGATAACATGGCGGCTAAAGGTTATCCATTGTTACCAATGGATTTCAAAAATGGCGGCGATATTGCCACTA
3064 SECLDNLDDPTDQEAIEOCLEGLSDSE	3063/AGCGAGTGCTTGGATAACTTAGGATTAAAACGACCTACTGATGAGGGCCATAGAGGCAATGTTTAGAGGGCTTGAGCGATAG
	GGGCAGTGATGGGTTGCTTAAAAGCTATCAAGAAGCTGAAGAATCGCTGATAAAATCGGCTACCTGTCATTA
	CGAAGGTCATGGCTTTAATGAGCGATAAATCCAAGGCCAAAAGCGTGATGAAGGAAG
	GGTATGGGTTTTTGAGCGAGAATCAGAATTTGTAGAGATTTGCTCGCACCATTCTTAGAATTTATAGAATTTCAAAACA
-	CCA111A11C1ATCGCTGACAAGGACGCCCACTACCTCAATACGGCTAGCGCAAAAGTGTGTGT
	CONTROLLORARAGO LLIAMAN LOCALGAN LARAGAGA GANTAAAA GAAAA GGAAAAAAAAAAAAAAAAA
	GAAGTGGAATACCCTTGCAAGGTGGTTTCTGTTGAAGTGGGAGACGCTCAACCGGTAGAATACGGCACAAAACTCA
	GGA I AAAAAAGAAGATTI CGTGCTTT CGCCTATGGTAGGCACTTTTAT CATGCACCCTCCCCTGGGGCTGAGCCCTT ATGTCAAAGCGGGCGATACGCTTAAAAAAGGGCAAAT CGTGGGCATTGTAGAAAGCGATGAAAATCATGAAATT
	CTCCAGCCCCCATTATGGTAGAAAGCGAGCATGCCAAGCGTCCAAACCCCTGTGCCTATGGTATGCACCCTATTGT
3062 IDRYEPF	3061 GAATAGATCGTTATGAACCTTTCTGAAATTGAAGAGTTGATCAAAGAATTTAAAGCTTCTGATTTGGGGCATTTGAAAT
YYYDKSIDFYASGKTLFTKAE	
ONSISIRRI GVINNVFDYVDMEKSDHLY	HILVACAMACAGCAHLICIAICCGGCGTTIGGGCGTTAACATGGTGT
SSAGNGVYDVVYSFNNOTYNFQEVFS	CAAGGGGGTATATGGTGAAGGGTGGAAAGGTTGTTCAAGAGGGGGGTAATGGCGGTTTATGATGTGTGTATTCTTTCA ATAACGAAAGCTAGAATTTGCAAGAGGTTTTTTCACAAAAAAGAGGATTTTTATATGGGGGTTATGAAGAGAGGATTATATATGGGGGTTAAGAAAAAA
FNAHSVINIAESITNGNPITLVSSSKEIE VNNAESKNI WOLINYOGHGASSEKI V	TATCACTCTTGTAAGCTCTTCTAAAGAAATTGAATACAACAACGCTTTCAGTAAAAAATCTATGGCAGCTCATCAACTAC
SVKGQVTLNNITLKNLNAPLSFGDGTIT	GTCTTTGGGGGATGGGATGGGATTACTTTTAAAGGCGCCCTTTAAATAACATCACTTTAAAAAAACCTGAAGGCCCCTTT
I NANSNLQIAGNAVFGNSTNGSQNTA NFNNTGSVNISGNATFONVVFNGPTNT	CTCTCAAAATACCGCTAATTTTAATAATACCGGCTCTGTTAATATTTCAGGGAATGCAACCTTTGATGTGGTGTTT
NNANFNNSASFNFNNSNATTSFVGDF	GTTGTGGGGGGATTTCACTAACGCTAATTCAAATTTCAAATTCCCCACCCA
SGDSLNFSNNNOFNSGSFEISAKNASF	GGAGTTACCAATTCAGCGGCGATAGCTTGAATTTTCAAACAACAACAGTTCAATAGCGGTTCGTTTGAAATTAGCG
DNSONLNGLNSNGKLSVYGTTFTNEA	TCACTAACGAAGCTAAAGATGGGAAATTCATTTTCAATGCAGGGCAAGCGTTTTTGAAACACCCAACTTTAATGGCACCACTT
SINIANATITOHNAGIYSSSMTFSTQSM	ACCATCACCCAACATAACGCCGGAATCTATTCAAGCTCTATGACTTTTT
TOTO TOTO TOTO TOTO TOTO TOTO TOTO TOT	3059 TCATGTGTATATCACAGCGAATCTGCGTTCTGGCAATCGTATAGGCACCGGTGGGCAGCTAATCTAATCTTTAATG

_
•
-
ч

HP0371	3073	3073 TACGAATTITAATCAAGCCACGCTCAATTTAAGGGCTAAAAATATCCATATCAATTTCCAAGGCGTTTCTACTTTTAAA	3074 TINFNO	3074 TWENDATI'NI RAKNIHINEOGVSTEKO
	_	CAATCTCAATAACTCAAGGTTGTTGAATTTCAATGGCAAGCTTTTCAACGCTCTTAAAGTGGAAGGGGAAACGAATTT CAATCTCAATAACTCAAGGTTGTTGAATTTCAATGGCAATAGCGTTTTCAACGCTCCTGTGAGTTTTTATGCTAATGAT	NSTMIN	NSTMNLAESSOASFNALKVEGETNFNL
		TCTCAAATTTCTTTCACTAAATGGGGGCTTTTAATTCTGACGCTTCTTTTGATTTAAGCAACAACAGCACCTGAATTT	SFTKLA	NNSSLLNFNGNSVFNAPVSFYANHSQI SFTKLATFNSDASFDLSNNSTLNFOSV I
-		TITTAGETITTEGETOTAAAAGGGATTTEGAATTGAATGTGTGTTAGCAATGAGGGAA	LLNGALI	LLNGALNLLGNGSNNLAINAKGNFSFG
		GATGTGTTGCAAGCCCAAAATATTGATGCTTAATGGGGAATAAACGCTATCAAAAAAAA	SKGILN	SKGILNLSYMNLFGGDKKTSVYDVLQA
		GATTGACAAGGCTGATTACTCGTTTGATAACGCCGTTC	ONIDGEN	QNIDGLMGNNGYEKIRFYGIQIDKADY
HP0371	3075	3075 GATCAATITCACGCAGTATCAGGGTAAGCTTTCGTTTATTTCTAAAGATTTTTCTAACATTTCATTAGATACCTTAAACG	3076 INFTOYO	3076 INETOVOCKI SEISKÕESNISI DTI KIÄT
		CIACIAACGEAIIAACGETIAATGETCETAAAAATGACATTAGCGTTCAAAAAGGTCAGATTTGCGTGAATGTTTTAAA	NGLTLN	NGLTLNAPKNDISVOKGOICVKW NCM
		THE CRATEGORITH TARGET CONTRANCE TO A TOTAL OF THE CONTRANCE OF THE CONTRA	GEKKAH	GEKKAHSSSATAPTNETLEANANNFAF
		THAGATTAGGGCGAAACGCTACTTTAAAACCCAATAATAGTAGTAAAAATACTAGGGGAC	LGAIKAN	LGAIKANGLVDFSKVLQNTTIGTLDLGP
		AGGGCTGATATTAGCGGTAATCTCCAATGTGGTTAAAGGAAGCGCTTTTAAGAATAACGCTTATAAGAATAACTGTAATTAC	NATFKA	NATFKANHLIVNNAFNNNSNYRADISG
		GGGCGATTTCAAGAGCGAAGGGTCATTAATCTTTAATCTTAACAATAAAACCAATCAAACGATTATTAATGCAAGAATGTGCAAA	N N N	NLNVVKGAALSTNENGLNVGGDFKSE
•		CAATTCTACGATCATGTCTTATAACAATCAAGCTTTAATCCATTTTAATACCCAACTCAAGCAAG	NOALIHE	SOCIETIVE INCLUINVAGINATION OF THE NOTE OF THE NAME OF
<u>-</u> -		A I I AA I GCGAAACGCATGCTTTATGCTTATGACAATCAATCATTCGTGGAGGGAG	YDNOIR	YONOIIRGEST SDYLKI YT! IDENEKRM
		ATTABACATOCOCOTATTOTOCTATACOCOCATOCATOCOCATOCOCOCOC	GUNGDS	QLNGDSLSYDNOPVNIKDGGLVVSFK
		GITCAAGTIAGCGTCTCTGATAAGCCCATCGATTATTAAAATCAGGGGGGGAAATGGTGATCTATCATTATGATAAA	DNGGON	DNGGOMVYSSILYDKVQVSVSDKPMD
		AGTGCTGGTTTGGATCAAATCTGCAAGGCAATAATTTCAATTCAATTCAATGCAAGGC	IHAPSLE	HAPSLEYYIKYIQGSAGLDAIKSAGNN
		GGGTAAT	SILWLNE	SILWLNELFVAKGGNPLFAPYYLDDNP
			TEHIVTU	TEHIVTLMKDITSALGMLSKPNLKNNST
			DALOLNI	DALOLNTYTOOMSRLAKLSNFASFDST
			DFSERLS	DFSERLSSLKNORFADAIPNAMDVILKY
			SORDKLY	SORDKLKNNLWATGVGGVSFVENGT
			GILYGVA	G1LYGVNVGYDRFIKGVIVGGYAAYGY
HP0371	3077	CTI GGCAGTA A GG TT T GA A TT A CCAT CT CA A TO CA A CO CT CA A CO CT CA A CO CT CA CA CA CA CA CA CA CA CA CA CA CA CA	SGF YEK	
· }		TAGACAAGAAATGGAGCAAAATGTTGAAAAACAAAAGCCCTTGTAAAAAACGAAATTAAAAAAACAAAATTAAAAAAAA	3078 LGSKVLN	3078 LGSKVLNYDVIDKLKDADEKALIAPLDK
		GCCCGGTTAAAACGCTTTCAGATTATTCCACTTATCAGCCGAAAAAGCAATGTTACAGGGATTGTTACAGGGTTCAGGGGTTCAGGGGTTCAGGGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGGAATGTTAACAGGAATGAAT	TI COLON	NMECINVERCIRAL VEIK I LLSALKGPVK
•		AGCGTGGGGGTTGGCGTGCCTATTCAAGATATTAAAGTGGATGTGCAAAATTTAAGGGGAAGAGAAATTATAAAAAAATT	I CSDYSI Velochio	LSDYSTYISKKSNVTGDALSASVGVG
		GGGGCGAAATTTCTTCAAGAGGATATTTTTAGCCAAGTGGATACCACGCTCAAGTTTTACACAAAAAAAA	A COLLA	OPICION OVICE CONTROL OF THE CONTROL
		CTACGCCGTTAATATTAAAGCAGGAATGACTTTAGGCGATGTGGCTCAAAGCATCACGGACGCTACCAATGGCGAAG	MTI GOVA	MI GOVACII CATTI CIIVADI AVIIKAGI
-		SALESE I AL I EL GAL GAAAACA GEGEGAT GACCCCTACCAATTAAT GGTGAATACCAAAAACACCGGCGAAGAC	GNDPYOL	GNDPYOLMVNTKNTGFDNRVYFGSHI
		ANCUSATOLIA I I I I I I I I I I I I I I I I I I	OSTLTNK	OSTLTNKNALSLGVDGSGKSEVSLNLK
		CUCHAMANULUMAULUMAULUMAULUMAULUMAULUMAULUMAU	GADGNM	GADGNMHEVPIMLELPESASIKOKNTAI
		TTTAAAATTTGATCGCTAATGGGGGATTATTTCATAAAAGGGGGGCTTTAGAAATGAAAATTTTCATAAAATTAAAAATTAAAAATTAAAAAATGAAAAATGAAAAATTAAAAAA	OKAMEO	OKAMEOALENDPNFKNLIANGDISIDTL
		CGTGGGGGAAACATTGAAAGTTAAAAGGGAAGTAAAAGGTAAAAGAAATT	HGGESLII	HGGESLIINDRRGGNIEVKGSKAKELG
		ATTTATTAAAAAGCTCTCGCACGATAAAAGAGGGTAAATTAGAAGGGGTGATAGAATTAGAATTAGAAAGGTGAATAGAATTAGAAAAGAAATAAAAAA	FLOTTTOE	FLOTTTOESDLLKSSRTIKEGKLEGVVS
		TGAGTGCTTTAACCAAAGAG	LNGUKED	LNGGKLULSALIKESNISEENTDAIIQ 1
HP0371	3079	CITTCGCCCTTACAAATCCCCCAAGATTTGACTTACCAGCCCGTGCTTAGCACGAAAGTGAATATTAGCGTGAATTT	308011 SPI OIPO	308011 SPI OIPODI TYOPVI STKVNISVNI NP
		AAACCTAAAGACCATTTAAAAGGCGTGCAAGATTTTTCTTAAACGATAAGGGCGAGATTATTAAGGAGCGTTTTT	KDHLKGV	KDHLKGVQDFFLNDKGEIIKERFLNQDI
		TAT CANCALCACATOR AND CONTRACTOR AND	NALANND	NALANNDNEPIDAITNRKLNIS
				_

06 <u>6501</u>			T/EP01/15428
MINYKILDLFCGAGGFSAGLECLEEFDA LIGLDCDKQALITFENNHKNAIGVCGDI TQTEIKEKVIKLAKKLEIHAINIGGPPCGG FSNKGKNLGLKDPRNF_FLAINIGGPCGG FSNKGKNLGLKDPRNF_FLAINIGGPCGG FSNKGKNLGLKDPRNF_FLAINIGGPCGG ASRESPDFNLLEPSQSVNCNBRRFNN GASRFSFDFNLLEPSQSVNCNBRRFNN KDSPKLYNHQATNHSCAALEKLKINK EQGKECLPKNLHGKQCJFKSTWGRLN WNKISPTIDTRFDTPSNGTNSHPELHR SITPREAARIQSFSDNY;FYGNKTSVCK QIGNAVPPLL		ACHNEDLNYTLQNIFNEIEKSSLGTPSE ENVKGLFADLDVNSNI:LGSSHQNRVE KLTKILEAIGGMQLGDYLKSGIDVFGDA YEYLMAMYASNAGKSGGEFFTPQEVS ELLAKITLHGOESVNK/YDPCCGSGSL LLQFSKVLGDKNVSKG:YFGQEINLTTY NLCRINMFLHDIN S088 KALNQMSEREQILIQL'YFEELNLSEIK	3090 KRLSNDRFSGNELNDILMLSLLDGYIQ NENKAFSPLLGALEEKFTRLEKLEKER RLLEDKKRFGKDLEEFILNFEKMKLERL DLKEDEYERLLEOKKILSSKEKLNDKIA LALEVLENTHKITHALESVGHSAEFLKS ALLEASALLEKEQAKL
3087	3084	306	300
ATTTTGATTTTGTG SCTAGATTGCGATAAAGA TCAAAGCCAAATTAAAGA GCCAAAGCCATAAAGCC GCCAAAGCCATAAAGCC AGGAATTAAAGAAGGG CTCAAAATTAAAGAAGGI GCGGAAGCCGTTTGAAGCI ACCCTATCCAATCAAGGG ACCCTATCCAATCAAGGCAAGCAAGCAAGCAAGCAAGCAA	TCCTCTICTAG 1083 AACGAACAGAACCCAATAAAATCGCCTTAGAATTTTATGAAGTTTTGAGCCAAGTTTGAAGCGATGTGCGCGCACCCC 1083 CACTCTAGCGACCCCACCACCAGCCAGCTCAGCTCATATTGGCAGCACCGCCGGATATTTGAG CACTCTAGCGAACGCCCACCACCAGCAGCCGTCAGCTCATATTGGCAGCGCCGGATATTTTTTTT	3085 GCCGAGCGTGGAAGAAAACCCTTATTGAACAAAAAGGCTTTTTCATCCGCCCAAGCGCTTTGGCCAAAAATCTTGGCAAAAATCTTGGCAAAAATCTTGGCAAAAATCTTGGCAAAAATCTTGGCAAAAATCTTGGCAAAAATCTTGAAAAATCTTGAAAAATCTTGAAAAATCTTGAAAAATCAATAAAAAATCTTCAATCAA	
HP1122	HP1122	HP1122	HP1122 HP1122

2/066501	1	<u> </u>
3092 AWIPAWLLFIGHWV	3094 IDGQKEALYGGIACANLLHKNSGITIDIG GGSTECALIEKGKIKDLISLDVGTIRIKE MFLDKDLEVKLAKAFIQKEVSKLPFKHK NAFGVGGTIRALSKVLMKRFCYPIDSL HGYEIDAHKNLAFIEKIVMLKEDQLRLL GVNEERLDSIRSGALILSVVLEHLKTSL MITSGVGVREGVFLSDLRHHYHKFPP NINPSLISLKORFLPHEKHSQKVKKECV KLFEALSPLHKIDEKYLFHLKIAGELAS MGKILSVYLAHKHSAYFI	3096 LFTHSGKISIKNAPYKLDNTPIEENCAC YACKRYSKAYLHHLFRAKELTYARLAS LHNLHFYLELVKNARNAILEKRFLSFKK EFLEKYNSRSH
	3093 ICATTGATGGCGAAAAAGAAGCGCTCTATGGCGGGATTGCGTGCG	GCAGGTIGCAAACGCTATTCTAAAACGCGCCCTATAAATTGGATAATTGCATATTGAAAATTGCTTGC
	HP0634	

NEGCD NEGVG ADRGS ADRIND DLMLE SLPLT ILEDSK (KSDK	GVKG YDQLK ANPM LAGLE MKCEE	GGGAT GGGAT
3098 NKHLDTTMVSEFVGKTRAFIKIQEGCD FDCNYCIIPSVRGRARSFEERKILEQVG LLCSKGVQEVVLTGTNVGSYGKDRGS NIARLIKKLSQIAGLKRIRIGSLEPNOIND EFLELLEEDFLEKHLHIALQHSHDLMLE RMNRRNRTKSDRELLETIASKNFAIGT DFIVGHPGESGSVFEKAFKNLESLPLT HIHPFIYSKRKDTPSSLMTD SVSLEDSK KRLNAIKDLIFHKNKAFRQLQLKLNTPL KALVEVQKDGEFKALDQFFNPIKIKSDK PLRASFLEIKEYEIKERENHAVF	3100 PYIARNYPLEKSVLKEPHEALFGGVKG DEILKEIVFLAAKLKIPFLVCEMGYDQLK SLKECLEFCGYDAEFYK SLKECLEFCGYDAEFYK 3102 AGDIVAIAGFNAMDVGDSVVDPANPM PLDPMHLEEPTMSVYFAVNIJSPLAGLE GKHVTANKLKDRLLKEMQTNIAMKCEE MGEGKFKVSGRGELQITILAENLRREG FEFSISRP	3104 IQKTKLIESIAKAFNESHVSAIEVIKFESK RYDPQTNRIITEQSSTLKIRDYANALOK EINALLLDFAKDERLPLKFTLELYNALN KEHFTNSPKKAFKLLKGIIKCKLHE 3106 GVFKANQIDITGTIRSGNGAI(TGGGAT LVFNAQKRLNIANAHLNNDKAGLQNS WMNFIVNNGNLNVTNAKFSNOTPHGG FNI KANNITWDKGSVNGGGNFGVDNA DSNGATTISGVTFNNNGTLYKGGENS AGNSLTLENNTFNSYNINAKAQNLIFNN NSFNGGSYSFNDTKNTTFKJTNLINS DPFSRLKGSVSIENNSYFNIERDLTDKT TYTLLSGNSIKYNNQALAGGCFFKKFM EFNPLWWRTTDSIKSG
VSEFVGA SVRGRAF SVVLTGT GIAGLKF FLEKHL! KSDRELI KSDRELI KKDTPSS FHKNKAI GEFKAL	PYIARNYPLEKSVLKEPF DEILKEIVFLAAKLKIPFLN SLKECLEFGGYDAEFYK AGDIVAIAGFNAMDVGDI PLDPMHLEEPTMSVYFA GKHVTANKLKDRLLKEM MGEGKFKVSGRGELQIT FEFSISRP	IQKTKLIESIAKĀFNESH RYDPQTNRIITEQSSTL EINALLLDFAKDERLPLK KEHFTNSPKKAFKLLKG GVFKANQIDITGTIRSĜA LVFNAQKRLNIANAHLN WMNFIVNNGNLNYTNA FNLKANNITVDKGSVNK DSNGATTISGVTFNNNG AGNSLTLENNTFNSVNI NSFNGGSYSFNDTKNT NSFNGGSYSFNDTKNT DPFSRLKGSVSIENNSV TYTLLSGNSIKYNNOAL EFNPLWWRTRDSIKSG
HLDTTM CNYCIIP CSKGVQI SSKGVQI RELLEED INRRNRT IVGHPGE IPFIYSKF LNAIKDL LVEVQKE RASFLEIF	PYIARNYPL DEILKEIVFL SLKECLEFC AGDIVAIAGE PLDPMHLEE GKHVTANKI MGEGKFKVI	TKLIESIK DPQTNRI DPQTNRI ALLLDFA HFTNSPK FKANQID NAGATIS NGATIS NGATIS NGATIS NGCSY NSLTLEN SRLKGS STLKGS NPLWWR
3098 N SECTION OF SECT	3100 PY DE SU2 AG 3102 AG GK MG FEI	3104 IQK RYCK ENY WW WWN SI DP-I DP-I TTT
244804F0+0FF	A S S S T S	F098 @85@@885085@
3097 AAAACAAGCACCACCACGATGGTGAGCGAGTTTGTGGGAAAACTAGGGCGTTTATTAATGATCCAAGAAGGCGGCGCGCGC	3099 GCCCTATATCGCTAGAAATTATCCTTTGGAAAAATCCGTCCTCAAAGAACCGCATGAAGCCCTTTTTGGGGGGGTTA AAGGCGATGAGAATCTTAAAAGAAATCGTTTTTTTTTT	1103 ATATCCAAAAAACCAAGCTGATAGAATCTATCGCCAAAGCGTTTAATGAGAGCCATGAGGTGCTGAGGTAATCAAATTGAAATCAAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAA
4	4 4	4 4
HP0634	HP0634 HP0634	HP0634

١	4	>
١	Č	5
٩	Ē	٠

WO 02/	066501		PCT
	3114 VIAKKKALGVLDIKAYAGH IPFNTYKĞD GLIIATPLGSTAYNLSAHGIYUHALSQS YILTPLCDFSLTQRPLVLGAEFCLNFCA HEDALVVIDGQATYDLKANQPLYIQKS PTTTKLLQKNSRDYFKVLK'EKLLWGES PSKKR	3116 LSNPIKMDFASGKQPGVQKATNQIHQ GIQNIQQNIPSQVLTPQIQAGMQGVMQ GFGALSSTLEAPLLFSKQNVVIGALSIIY PLYMGGARFTWVRIADLMQKDANEVY RLKKLSTFQELVSVYYGMVLNAEVAET LEEVEKGHYKHFQNALKN QKVGGIAR VETLGAQVAYDKAHIASVYAKDVLEVS QLSFNSILSSKDDLVPSSKLEIRTEKNL PDLSFFVSSTLNSYPVLKTLENQIQISK ENTKLQIAKFLPQVSFFGS-YIMKQNNS VFEDMIPSWFVGVAGRMI*ILSPTGRIQ KYQASKLAELQVSSEQIQAKKNMELLV NKTYKETLSYLKEYKSLLSSVELAKENL KLQEQAFLQGLSTNAQVIIDARNILSSIV VEQXSVAYKYIVSLANLMALSDHIDLFY EFVY	
467	HP0634 3113 TGTGATCGCCAAAAAAAAAGCTTTÄGGGGTTTTAGACCTCAAAGCTTATGCAGGCCCATACGCCCTTTAACCACCTTTAAAAATTTGAATTTGAGTTTTAATTTGAGGCGCATTGTGCAGTGCATGTGTGAATTTTAAAATTTGAATTTGAGTGCTCATGGGCCGATTGTGCATGTGCATGTGTGAATTTTAAACGCAACCCCTTTAGTGTTAAAGGCCAATGTTTAAACGCAACCCCTTTAAAAAATTTGAAAAAAAA	HP0634 3115 TCTCTCTAACCCCATTAAAATGGATITTGCCAGGCCAAAACCGGGCGTGCAAAAGCCACCAACCAGGTCATC AAGGCATACAAAACATCCCACTTTAGAAGTTTTAGAGTTTTAGACCCCTCAAATCCAAGCGGCATGCAGGGGTT ATGCAAGGTTTTGGGGTTTGAGAAATTTTAGAGCACTTTTAGATTTAGTTTAGCAAAATGTGGTTTGGGGTTTGGGGTTTGGGGGTTTGAGCAAAATGTTGGGGTTTGAGGAAAATGTTGGGGTTTGAGGAAAATGTTGATGCAAAAAGAGCTTTTTAGAGAAATGTTTAGAGAAAATGTTAAAAAAAA	

c	2	ć	5	
i	i	ì	5	
	ì		F	

3124 KECKLMTHYCNAWKN	3123 AAAGAATGCAAATTGACGCATTATTGCAACGCTTGGAAAAATTGAGCATGCTAGAGATTAAAGATGAGCGTAAAAG AGAGCGTTAAAGGTCATTTAGCGGAGGTTTTAGGCTTTGTAGAAAACATTTCGCTTTAGAAACTAGCGCGCTAAAAA AGAGCGTTAAAGGCTATGCACCCCCTTAAGAGAAGACGAGCCTAAAAACCCTAAACCTTAAGAGCTATTGAGCTTTTGAGC CAAAACAACAACAACAGGATCATTACTTCGTTGTGCCCAAGATTGAATAGGTTTCATATCAAACAACAAAAAAAA	312	HP0830
STZZ KWI GLEEVILLSSSG GAMEASVISIC OKELLFVNAGKFGERFGKIAKAHSIKA HELVYEWDTPAGVDEILSVLKANPNID AFCIGACESSGGLRHPVEKIAGAIKETN PNVFVIVDAITALGVEPLEITHVDALIGG SGKAFMLPPAMSLVALSONAIERIEER NVGFYFULKSELKNÖRNNTTSYTAPIL HTLGLQRYFELVQNLGGFFALYR			
3120 LRSFLIMADIQRRDFLGMSLASVTAIGAI ASLVAMKKTWDPLPSVVSAGFTTIDVA INMQEGGFSTVEWRGKPVYILKRSKKE GFNEKRDFKVGESVFTTAIQICTHLGCI PTYQDEEKGFLCPCHGGRFTSDGVNI AGTPPPRPFDIPPFKIEGTKITFGEAGA EYKKMMAKA	ATTAAGGAGTITITITAATCATGCAGATATTCAAAGGCGTGATTITITAGGAATGAGCCTTGCTAGTTTACAGCTATA GGGGCTATAGCGAGTCTGGTAGCGATGAAAAAGGCTTGGGAATGGCGTTGTTTCAGCCGGTTTTACGA GGGGCTATAGCGAGTCTGGTAGCGATGAAAAAGGCTTCCCAAGCGTTGTTTCAGCCGGTTTTACGA CCATAGATGTGCGCAATATGCAAGAAGGGCATTTTCCACCGTGGAATGGCGTGGTTTTTACCACCGTTTAACAAAAAGGGCTTTAATGAAAAAGGGCGTTTTAAGAAAAAGGGCTTTTAGAAAAAAGGGCTTTTAGAAAAAAGGGCTTTTAGCGCATTTAGGGGGGGCGTTTTAAGAAAAAGGGCTTTTAGTGCCATGGGGGGCGTTTTAATGAAAAAAGGGCTTAAAAAAAA	<u></u>	HP0634
3118 NRVALEEILALKPSLLSFSADKFFNSAD AGIIMGQKERVEALKNHPLYRVLRVGKI TLTLLFCSLKAWINHQEDITIHALLNQTK TLTLLGSLKAWINHQEDITIHALLNQTK DALLQKALKLYALLKPLELNVSIASSFS KIGNLFGRELESFCVKIQPKNTRALNSE KLYLKLFQKGVIARISCEFVCFEVFSLN EKDFEKIALVLEEILNKA	3117 CAAACAGAGTGGCTTTGGAAGAATTTTAGCCCTAAAACCATCGCTTTTAGCGCGGGATAAATTCTTTAACA GTGCGCAAGCGGGCATTATTATGGGGCAAAAGAACGGGTTGAAAAAACCACCCCCTTTATAGAGTTTTA GGGGTGGGTAATTATGGGGCAAAAGGATTGCATGAAAACCACCCCCTTTATAGAGTTTTA AGGGTGGGTAATTGAACCATTATTGCAACAAAAGCATCGATCATTTAAAGCATTAGAAT TGAATGTGAGCATATTGCAAAAAACGGCATTTTGTATGCAAAAACGAAAAGCGTTTTAGAAAAAAA TCCAAATGTGAGCCTCTAGCTTTTCTAAATAGGGAATTTTTTAAAAAGGAAATTGCTGTATGCGTGAAAA TCCAAGCCCAAAAACGACAGAACTTTAAATAGTTGAAAAAAAA	. · · · · · · · · · · · · · · · · · · ·	HP0634

c	7
V	0
₹	t

066501		PCT/EP01/15
3126 SVILVTLGASMHAQSYLPKHESVTLKN GLQVVSVPLENKTGVIEVDVLYKVGSR NETMGKSGIAHMLEHLNFKSTKNLKAG EFDKIVKRFGGVSNASTSFDITRYFIKT SQANLDKSLELFAETMGSLNLKEDEFL PERQVVAEERRWRTDNSPIGMLYFRF FNTAYVYHPYHWTPIGFMDDIQNWTLK DIKKFHSLYYQPKNAIVLVGDVNSQK VFELSKKHFESLKNLDEKAIPPYMKEP KADGARTAVVHKDC VHLEWVALGYKV PAFKHKDQVALDALSRLLGEGKSSWL QSELVDKKRLASQAISHNMQLODESV FLFIAGGNPNVKAEALGKEVALLEKLK KGEITQAELDKLKINCKADFISNLESSS DVAGLFADYLVQNDIQGLTDYQRQFLD LKVSDLVRVANEYFKDTQSTTVFLKP	3128 SEKASKTKNSAIEVSNTKASAMKNETI GSGDLKKVCEKIKSALPFGIISAFKPFK DAFYRDFNHNEQKLI.IGAAKSGCIQSS ADKLAQLKTRLLYWQDKSVKVDWDKP ILIKDFFKGNNYLYRFFCFLLGKHFMDR FLKNNAKASVKDFMSSKEFVAKYRYTP KQNTERAKKLQSYLEINKRDFIGFVQAL NSLKDNPQDPFLPNEETS	3130 DEMRAGAFERTNRKKRFRENAGKNA EYSNHEASSHHKKEHRPNKKPNNHHK QKHAKTRNYAQEELIJSNKVEGVTEILH VNERGTLGFHKELKKGVEANNKIQVEIL LNPHYKMNLNSKASVKITPLGGLGGIG GNMMVIETPKSAVKITPLGGLGGIG GNMMVIETPKSAVKITPLGGLIGS KFDEHGLKKYRSYFKIVEKRCPISVGEF IIEWIHITHSIIDSSALAIQTKAGTIIHTGD FKIDHTPVDNLPTDLYRLAHYGEKGVM LLLSDSTNSHKSGTTPSESTIAPAFDTL FKEAGGRVIMSTFSENIHRVYQAIQYGI
3125 GTTCTGTCTTGTTAGTCACTTTAGGAGCGAGCATGCACGCAATCTTACTTA	3127 GGAGCGAGAAAGCCTCTAAAACTAAAAACAGCGCCATTGAAGTTTCCAACAGGAAAGGCTTCTGCTATGAAGAACGAA ACGATTGGAAGCGGCGATCTTAAAAAGGTGTGTGAGAAATCAAAAGGGCACTACCCTTTGGGATCATCTCAGCCTT TAAACCCTTTAAAGACGCTTTTTACAGAGATTTCAATCATAATGAGCAAAAGTTACTGATAGGGGCAGCTAAAAGCCT TTGCATTCAATCTAGCGCTGATAAACTGGCTCAGTTAAAAACGCGCTTACTCTACTGGCAAGACAAATCTGTTAAAGT GGGATTGGGATAAACCCATTTTAATCAAGGCTTCTTTAAAAGGCAATAATTACCTTTATAGGAGAAATTTTTTAAAGAATAACGCTAAAGGCGATAATTAAT	3129 TGATGAGATGCGAGCCGGAGCGTTTCACCAACCGCAAAAAGCGTTTCAGAGAAAACCGCAAAAAAACCGCCAAAAAAACCGCGAAAAAA
HP0830	HP0830	HP0830

HP0830	3131	3131 GAAGCAAAACAATTCGGTGTTTGAAGACATGATCCCTAGTTGGTTTGTGGCGTGGCGTGGCAGCGATCCATTATTTT	
		CTCCCACAGGGCGCATTCAAAAATACCAAGCGAGCAAATTAGCGGAGTTGCAAGTGAGGAGAAATCCAGGC TAAAAAAAACATGAAAAATACCAAGCGAGCCAAATTAGCGGAGTTGCAAGTGAGGAGAAATCCAGGC TAAAAAAAACATGAATTATTATAAAAAAAGAGTTGCAAGAGTTAAAAAAAA	SISTINGINGS TEDMICSWING REGENTLES PTGRICKYCASKLAELCVSSECICAKK INMELLVNKTYKETLSYLKEYKSLLSSV ELAKENLKLOECAFLCGLSTNACVIDA RNTLSSIVVECKSVAYKYIVSLANLMAL SDHIDLFYEFVY
HP0406	3133	3133 GGGATTGAAACTTTAGGGGGGGTGATGACTAAAGTGATTGAT	3134 GIETLGGVMTKVIDRGTTIPAKKSQVFS TAEDNQPA
HPÓ406	3135	3135 AGCAATACACAGAAAGATTTGGTTAAAGAACAGAAAGATTTGGTTAAAGAAAG	3136 SNTOKDLVKEGKDLVKEGKDLVKEGK DLVKEGKDLVKTGKDFIKYVEGNCGEN HNQFFIEKGGIKAGIGIEVEAECKTPKP AKTNOTPIOPKHLPNSKOPRSGRGSK AGELIAYLGKELEFLPYSGKAJAKGVDF YRPSSIAYLELDPRDFKVTEEWGKENL KIRSKAGAKMLEMRNPQAHLSNSGSLL KVGKIFADVNKEIEAVANTEKKAEKAGY GYSKRM
HP0406	3137	3137 CAAAAGACAAGAAAAACAAAAGACAAGAAAAAACAAAAGGACAGAACAAAAACAAAAAGAAAAACAAAAAGAAAAACAAAAGAAAAACAAAAGAAAAACAAAAGAAAACAAAAGAAAAACAAAAGAAATAC TATAGAGACTAACAATCAAATAAAAGAACAAAATTGCCAAGAAAACAAAAACAAAAAGAAATTAGGAATTA GCAAAAAGATTTGGTTAAATAGGCAGAACAAAATTGCCAAAAACCTGCAAAAACCAAAAAATTATTAAAAATTAGGAATTTGCAAAACCCTGCAAAAACCCTGCAAAAACCCTGCAAAACCCTGCAAAACCCTGCAAAACCCTGCAAAACCCTGCAAAACCCTGCAAAACCCTGCAAACCCTGCAAAACCCTGCAAAACCCTGCAAAACCCTGCAAAACCTGCTAATTGCTGCAAAAGCTTTTTTGCTGCAAAACCTTTAATTGCTGCAAAAGCTTTAATTGCTGCAAAAGCTTTAATTGCTTCAAAAGCTGCTTTAATTGCTGCTTTAAAAGCTGCTTTAATTGCTGCTTTAAAAGCTGCTTTAAAAGCTGCTTTTAGAACTTTAAAAGCTGCTTTTAGAACTTTAAAAGCTGCTTTTAGAAATTTTGCTGAAAAGCTTTTAGAAATTTTGCTGCAAAAGCTTTTAGAAATTTTGCTGAAAAGCTTTTAGAAATTTTGCTGCAAAAGCTTTAAAAGCAAAAATTGCTGAAAAAATTTTTTAAAAACCAAAAAATTTTTAAAAACCAAAAAA	3138 GKTEGEKÖKTEGEKGKTEGEKGKTSN IETNNQIKVEGEGGKTEGEKGKTNNTG KDLVKYAEGNCGENHNGFFIKKLGIKG GIAIEVEAECKTPKPAKTNOTPIOPKHL PNSKQPHSQRGSKAGEFIAYLGKELF LPYSQKAIAKQVNFYKPSSIAYLELDPR DFKVTEEWQKENLKIRSKAQAKMLEM RDLKPDPQAHLPTSQSLLFVQKIFADV NKEIEAVANTEKKAEKAGYGYSKRM

2/066 <u>501</u>			P	CT/EP01/15428
3140 KTNKSGIELANSQIKAEGER ZKTEGEK GKANKSAIELEGOKGKTINTJRDLIKEG KDFIKETEGNCGENHNGFFIKKLGIKG GIAIEVEAECKTPKPAKTNO: PIQPKHL PNSKQPHSQRGSKAGEFIAYLOKELEF	3142 ELNQAQKEVLNTLKKPIPQAĞKSVSIAA IEHEEVIKFSSTQSELDIVLGGGIAKGGL YLVGGSPGVGKSTLLLKVASGLAKNQ QKVLYVSGEESLSQIKMRAIRLDCIEKE LYLLNEINWPVIKANIESENY FACVIDSI QTLYSPEISSAPGSISQVREITFELMRL AKTRDIAIFIIGHITKEGSIAGFRVLEHM VDSVLYFEGDPSRELRILRSIFKNRFGP TSEIGLFEMKEQGLVSAKEASSLFFSK EEPMEGSAITITLEGSRALILEIQALVSE CSFGSPKRLANGFDTNRLNIALIALLE	3144 LDDKNNYNFTKSSNNTNFKGGGSQKK SEDLEIVLSARIIKVLENGNYFIYGNKEV LVDGEKQILKVSGVIRPYDIERNNTIQ	3146 MEEMRKEIIAVIQKYTKSSDIHIFKTLDS NQSVETIEVEIILPR	3148 EPLEKKAIENDLIDCLLKKTDELSSHLV KLOMGFEKAGEESKVLIENAKNDGYKI GFKEGEEKMRNELTHSVNEEKNDLLH AITTLDEKMKKSEDHLMALEKELSAIAI DIAKEVILKEVEDNSOKVALALEELLK NVLDATDIHLKVNPLDYPYLNERLONA SKIKLESNEAISKGGVMITSSNGSLDGN
3139 AAAACAAAAGAGAGTGGGATAGAACTCGCTAATAGTCAAATAAAAGCAGAAGAAGAAGAAGACAAGAAGACAAGAAGAAGA	3141 AGAATTGAACCAAGCCCAAAAGGAAGTTTTAAACACGCCTTAAAAACCGGATCCCACAAGGCGCAAAAAAGCGTTTCTAT CGCTGCAATTGACCATGAAGAAGTGATTAAGTTTTCTTCACTCAAAGCGAATTGGATTTTGGGTGGG	3143 TTTAGACGATAAGAATAACAATTTCACCAAATCCAGCAATAACACGGAATTTTAAAGGCGGTGGCTCGCAAAAAAA GAGCGAAGGTTTTAGAGATTGTGTTGGCGAATCCATTTAAGGTGCTAGGAAACGGGAATTACATCTATGGGA ATAAGGAAGAGAGTTTCATCTATGGGAATCCTTAAGGTGGTGGGGAAACGGGAATTATTTCATCTATGGGA ATAAGGAAGTGCTAAGGAAGTGGGAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGGAAAAGCAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAA	3145 CATGGAGGAATGCGTAAAGAATCATTGCGGTCATTCAAAATACCTAAAATCTTCAGACATCCATTTCAAAACCCTTTGGGAGGATTCAAAACCCTTTGGAGATGGAGGCATTCAAAACCCTTTGGAGTAGTGGAATGAAAAGGCCACGGGGATTCTCAAAGAGATGGAATGAAAAGCCACGACGAGCCACGAGCCACGAGCCACGAGCCACGAGCCACGAGCCACGAGCCACGAGCCAAGAGCCACGAGCCAAGAGCCACGAGCCAAGAGCCACGAGCCAAGAGCCTTTTGGACACGCCTTTAAAAGGCGATCTTGGCGTTGCTAAAAAAGGCTTTGAGCGGGGGGGG	3147 AGAGCCTTTGGAAAAAAGCGATAGAAAACGATTTGATTGA
HP0406	HP0406	HP0406	HP0406	HP0406

ľ	•	
ľ	•	
٠	*	
	-	

HDOVIDE	TIADITO		
0.000 P. C. C.	2 2 2 2 2 4 4 5 5 6 6 6 6 7 7 7 7 7 7 7 7 7 7 7 8 7 8 7 8	TAGGCGAAAAAGGIGAACCCCTAGCGTTTCCTACAAAAGGCCCATTTCCCAACAAAAGGTTCAAGCTAAAATTGAAGAA TTAGGCGAAAACTATGAAAACCATTATTGAAGGCCAAGAATAAAGGATAAAGGGGGGTTATATCGTGGAGTC TCAAGGCGTGCATCATTCCTCCTCCCCGCTCCTCTTTTAAAGAATGACCCAAACCATATCGGCAAACGCGTTA ACGGTGCATCATTCGTGTGGAAAAGCAATCTTAGAAATTTCTCGCAAACGATTCTTGAAGTCAATGACA AACGACAACTTGAGGTTTCTAAGGAAATGTTAGAAGCCACAGAGCCGTGTTAGCGGTTTTTGAAGTCACCACTCATCAAGGCGATCATGATCACAAAAAGCGATCACAAAAAGCGATAGTGAAAAAATAGTAAAAAAAA	3150 SEKGEHPSVSYKKAISOOKIOAKIEELG S ENYENAIIEGKIVGKNKGGYIVESOGVE SYFLSRSHSSLKNDANHIGKRVKACIIRV O YFLSRSHSSLKNDANHIGKRVKACIIRV O DKENHSINISRKRFFEVNDKRQLEVSK ELLEATEPVLGVVRQITPFGIFVEAKGIE GLVHYSEISHKGPVNPEKYYKEGDEVY VKAIAYDAEKRRLSLSIKATIEDPWEEIQ DKLKPGYAIKVVVSNIEHYGVFVDIGND IEGFLHVSEISWDKNVSNIEHYGVFVDIGND
HP0406	3151CG 177 177 177 177		3152 VDFKIAČNEGEEQDLWFSRRNASČSIS VYGKKKLNEDVTVPRASLPSLLQEVAK ISOKYGFKIPCFGHTGDGNVHVNIMLE OPKRDLEKGHEAMEEIFÖAAISLEGTL SGEHGIGI SKAKFMPLAFNHSFMFI FR
	248E98E48	AAGATTTAAAGCATTTTAAAATGGGTTGTTGATCCTAATAATATTTTAAACCCTTTTAAAATGGGGTTGT AAGATTTAAAGCAAGCAAGGGTTGTTTTAGAA AAGATTTAAAGGGGAAGCGCATGAAATCGGTGTTTATGGAGCGGCGGTCGTATAGGGAAACTGCTTTTAGAA GAATTAAAAGGGGTTAAAGGGATTAGCGCTATCTAGCGTGTTTGTT	NIKKALDPNNILNPFKMGL
HP0406	3153 AG CG GT(3154 EEITERLKECHASLNLDKKDIELKHPIKS TGIYEIEVKLGSGVVGVFKIDVVAE
HP0406	3155 AV GAI ATT A AAT TGA GAA	3155 AAAGGTTATCCATTGTTACCAATGGATTTCAAAAATGGCGGCGATATTGCCACTATTAACGCCACTAATGTTGATGCG 31GCAAAAATAGCTAGCGATAATCCTATTTATGCTTCCATAGAGCCTGATATTGCCAAGCAATAGGAAAAAACC ATTAAGGATAAGAATTTAGAAATTAGCTTAGGTTTAGGTGGCCAATAAAAAAAGGTGACGATAAAAAAAA	3156 KGYPLLPMDFKNGGDIATINATNVDAD KIASDNPIYASIEPDIAKGYETEKTIKDK NLEAKLAKALGGNKKDDDKEKSKKSTA EAKAENNKIDKDVAETAKNISEIALKNK KEKSGEFVDENGNPIDDKKKAEKQDE TSPVKG

wo	02/066
	1 - ~

HP0406	3157	3157 AATGCAAAGCTCTTCAGGCGAGAATGTTTTTCATACGATCTTAAAACGGAATATGTTTTAGACCCTAAGATTTTTCT GAGACGATGAAAAGGCATGGTTTTGATTTTGTGGATATTAGACGGGGTGTCTTTAAAAGAGTGGGAATACGATTTTTCT	MKRHGEDFVORDEN EN TOTAL STORE OF THE STORE O
		TTACAAGAAGTCAAGCCCCTAACGCGAGAGTCTTAG1TTTGAGTAGCGAACCTGTGGAG111AAGGAAGCGAAGC	LSVNQNAYLKISSNNPL/NQPKIIFYDEN
		TTTTTTATGATGAAAACTTAAAGATGATTCAATGCTTGCT	LKIIQIIAKENRQQEIALNILNGVRFIHIT
		CAATGGCGTGCGTTTTATCCATATCACTGACGCAAAAAACCCTATCGTTTTAAAAAATGGGATTTCAGGCTTGAAAAAAA	
		IGCGATGCCTTAATAATAATAATAGCGATCCACCCAATATTTACCAAAAAAAA	
		CTCCCGCTTCTATAAAAAGGACAGCCCACCAATTAATAAAACCAAACCATACAAAAAAAA	
		CCAAGCAATAGTGAAACGCCGCTCACAATAGAAATTCCAAAGCGGGTTTTAAAGATCTTAAATAATCAAAAAACAAAAAAAA	
		ATGICTECTACAAATTCCCCACTAAAAGAAATCAAAAACAACCACCAATTCAAATGAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAAAA	
		GCACIAC	3160 TKSTTNDAKIGLNYOHEFLLCYAKDKN
HP0406	3159	3159/AACAAAA I CCACAAAA BA BA BAAAAAAAAA I COGATTA GAAAAATTA CAAAAAA GOOGGATAACGACCCTAATGGAGCATGG	YTNLLGGEKNLENYKNIDDNDPNGAWI
		ATTATTATATATCTAGCGCAAAAGTGGGAATATGAAAACGGGGTATTTGGAGTTACTAATCCTTACACAAAA	NDNPSAKSGNMK GYFGVINPT INKV
		<u> FEGRATTATCCGCCTGTGGGTATGTTTTGGCGTTTTTCACAAAATACGATACAAAAACACATTGATGATGATGAGGGGCGGAT</u>	UYPPVGMPWRPGUNICALINGTON
		TECTTTANA A A A A A A A A A A A A A A A A A	KKEHKUNEKGFIYKKYI.KULKI ICKIF
		AAAACTITIGATAGTITIGATATTTAGCGATAATTGTTATATGAACCAAGCGGCGACTAAAGAACTITTAAATTTGGGAA	DSLIFSDNCYMNQAAI KELLNLGMGET
		Tressacaatattitacttatccaaaaggggggagaatttatgaaaaaaatcattctgcattcaaccacgggaagggg	FTYPKGVEFMKKIILHSI I PNEGDIILDF
		ISCENCATOTT THE SATTEMENT OF THE STREET OF T	FAGSGTIVHAVMELNAEUKGNKETILV
		CCTAATAGGGGAATHTATHAGHTGAATHGATGAAGAGAGATAAAAGAAGATGAAAGCGCTTATGATTTTTGTAAGAAG	QIDEEIKEDESAYDTCK/\ELKSAKPVIS
		CALTA A A A STATE CALAR CONTROL THE CONTROL OF THE	DITIERVKRAAOKISOLSKDSGLDLGFK
		ATTATO A A A A A A A A A A A A A A A A A	VYTLODKVOIINDKEEITLFNRSDLTPF
		CAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	DKALNLALQCGKTLNQALEIIIKDKLYKC
		ACCETTANT CANGGET AGGRET AGGRET AT THE TOTAL CANAGE CON A CONTROL OF THE TOTAL CONTROL OF THE	EDAYFCIVCDEEAGEYLAKSKNEMIFL
		CATGAAGAA	DGYEEIDLEAFLNLNASFRERLSVVI
000	2464	SAGGAAGAATATTGAAAAAG	3162 ALKEQEYLKNAWLLEMEKOKEIFHNKK
HF0406	2	AATTGGAATTGGAAAATCCTACCAACAAGGCCCTAAATATCTTAAAAAGCGAAGTCGCTTCAAAAGATACTAGCTCCA	LELEKSYQQALNILKSEVASKD1SSMH
	_	TGCATAAAGAAATCCATAAAGCGAGCGAAATTTTAAGCAAAACACAAAAACAAAAGAAAG	
		ACTITICAAGGCAAGAAAAGCGCGCTACAAGAATGAAAGCGTGCTGATTGTACAAATTITAGACAAGGGCTATTATT	EKAKYKINESVLIVOILUKIST TVVIETELIS
		GGATAGAAACCGAGCTTGGCATGCGTTTAAAAGCGCATGGGAGTTTGTTGAAAAAAATCCAAAAAACCCCCTAAAAAG	MRLKAHGSLLKKIUKPFKINFFFFI II I I I I I I I I I I I I I I I
		AAATTCAAACCCCTAAAACAACCATTCCTAAACCTAAAGAAGCGAGCTTGCGCCTTGA I I AAGAGGGCAAACGCAG	LNDALLGGF
		CGAAGAAGCCCTGGATTTACTAGACGCTTTTTAAACGACGCCTTTTTAGGGGGGCTTTG	

₹	۲
•	۰
4	۲

HP0406	3163 TC	3163 TGCCACTTTGAAGGGGGCATATTAGAGTTTCATTTGATGAAAAAGCCACCATTGCCCTACAAAATCAAGAATTCAAGAAAATCAAGAAATCAAGAAGAATTCAAGAAAATCAAGAAAATCAAGAATTCAAGAAAAATCAAGAAAATCAAGAAAATCAAGAAAATCAAGAAAAATCAAGAAAAATCAAGAAAAATCAAGAAAAATCAAGAAAAATCAAGAAAAATCAAGAAAAAAAA		//
	LA	ATGGGACTGAAAAGGAAAAAGACGGCTTAAAATCCCAAATCCCAAATCAAAAGGGGTTAAAAATCCAAAGGGGTTAAAAATCAAGGGGTTTAAAAATCCAAAATCAAAATCAAAATCAAAAATCAAGGGGTTTAAAAATCCAAAATCAAAATCAAAAATCAAAAATCAAAAATCAAAAAA	3164 ATFEGGILEFHFDEKARIAGVEIKGYGT	GYGT
-	<u>F</u>	TTAGAGCATGCTAAAACGGCTTTAAAAAACCGCTTTAAGAGGGGGGAAATAATAATAAAAAAAA	EKEKDGLKSQMGIKKGDTFDEQKLEH	KLEH CO
	<u>8</u>	CAGAAAAGGTCAGTGAGGGTGCATTATTGATCGTGTTTTCATCTCAATACCCCCAATACCAATACAATACAATACAATAAAAAA	AKTALKTALEGGGYYGSVVEVRTEKVS	TEKVS
:	TA	ATTTATGAGGGAAGGCGCGAATTAAAACGCCGCATGATTCAATTTAAACAAAAAAAA	EGALLIVFDVNRGDSIYIKQSIYEGSAKL	GSAKL
	5	CTGGATGTGGGGGTTGAATGACGGGAAATTGCGTTTAAATTAAAAATAAAAAAAA	KRRMIESLSANKORDFMGWMWGLND	GLND
	TA	ATATGCGTAGGGGTTACTTACATATTTTTTTCCCTTTTTCAAGATCTACTTTTCAAGATCTTTTCAAGATCTTTTCAAGATCTTTTTCAAGATCTTTTTCAAGATTTTTTCAAGATTTTTTTT	GKLRLDQLEYDSMRIQDVYMRRGYLD	GYLD
	Ē	TICATTATAAAGTCAAAAGGGGGGATCCAATACAAGAAGGGGGGATCCAAGAAGGGGGGAAGGAAAGAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAAGAAGAAGAAGAAGAAAGAAGAAGAAGAAGAAGAAGAAAGAAGAAGAAGAAGAAAGAAAGAAAA	AHISSPFLKTDFSTHDAKLHYKVKEGIQ	(EGIQ
	<u> </u>	AAAACCTTAGAAAAAGCGCTTAAAAACCTTAAAAACCTTAAAAAACCTTAGAAAAACCTTAGAAAAAACCGGTAGTCCCCT	YRISDILIEIDNPVVPLKTLEKALKVKRK	ZKK
	<u> </u>	TITTAAAAACCGAATCCCCGATAACCGTTTATAACAAACCGAAA	DVFNIEHLRADAQILKTEIADKGYAFAV	AFAV
	<u> </u>	SECTION AND THE ANALYSIS AND THE SECTION OF THE SEC	VKPDLDKDEKNGLVKVIYRIEVGDMVYI	MVYI
	<u> </u>	CGCACGACGATAGEATT AT TACA A CONTROL OF THE CONTROL OF THE CATEGAT CATE	NDVIISGNORTSDRIIRRELLLGPKDKY	OKY
	É	TICCGAAAATICTTTAAGGCGTTTAGGAATICTTAGGAAAATICTTAAGGAAAATICTTAAGGCGGAAAATICTTAAGGCGGAAAATICTTAAGGCGGAAAATICTTAAGGAAAATICTTAAGGAAAATICTAAGGAAAATICTTAAGGAAAATICTAAGGAAAATICTAAGGAAAATICTAAGGAAAAATICTAAGGAAAATICTAAGGAAAATICTAAGGAAAATICTAAGGAAAATICTAAGGAAAATICTAAGGAAAATICTAAGGAAAATICAAGAAAATICAAGAAAATICAAGAAAATICAAGAAAATICAAGAAAAATICAAGAAAAATICAAGAAAAATICAAGAAAAATICAAGAAAAAAAAAA	NLTKLRNSENSLRRLGFFSKVKIEEKR	EKR
	<u>₹</u>	GATTATATA CONTROCCONTROCCONTROCCONTROCCONTROCCONTROLOGICA AND CONTROLOGICA AND CONTROLOGICA AND CONTROLOGICA A	VNSSLMDLLVSVEEGRTGQLQFGLGY	3LGY
	<u>}</u>		GSYGGLMLNGSVSERNLFGTGQSMSL	SMSL
MDOADS	3185 44	AATCCTCAAAAATCCCCCAAAAAACTTAAAATCCCCCCAAAAAA	∀ X	
00+0	S S	ACCOSTANTOR OF A SACRETATION OF A SACRET SAC	3166 KIAQKIAQKVKIDGFRRGKVPLSLVKTR	KTR
	? E	TTAGGGATTG ANGUCAMON TO ANGUAGA CONTRACTOR OF THE ANGUAGA CONTRACTOR O	YÓAÓIEÓDAGEEMIÓEVLKNAFKELGI	<u> </u>
	- C	PARTITION OF THE PROPERTY OF THE PROPERTY OF THE PARTITION OF THE PARTITION OF THE PARTY OF THE	ENKDLIGSPNLTKFEKKDTHFEIEADIG	ADIG
	Ē	SCORPEGE I MANAGECTALE I I I I AGALAAGA I CAAGA GAGT GCGT GCGT GGGAGG GAAG	LKPTIVLOKIKECVPSVGVEVPNFFKID	Š
		ANGENTAL CONTROLL OF THE PROPERTY OF THE PROPE	ERLKOLAKDYAKFVDTNTORKAONDD	QQN
	ξ <u>ξ</u>	ACCESSION OF THE SAME AND AND AND AND AND AND AND AND AND AND	KLTIDFEGFIDNAPFEGGKAFNFNI II G	
	2 0	AGOCTORAN I I CAN I I L'ARI I I L'ARI I I L'ARGCAGTAGAATGCTAGAAGATTTTGAAAAGGCTCTTTTAGGCATGCAAG	SKOMI FDFFKALI GMOAGEEKEEDI T	1 0
	3	<u>CEGE I GAAGAAAAAGAATTCCCTTTGACTTTCCCTAGCAAATACC</u>	FDRX	-
HP0406	3167 AA	3167/AAAAAAGAAGGGTATTTGGCTGTTGCTATGAATGGCGAAATTGTTTTACGCCCCGATCCTAAAAGGACCATACAGAA	3168 KKECVI AVANNOEIVI DDDDVDTIOKV	
	₹_	AAAATCAGAACCCGGGTTGTTATTCTCCACTGGTTTGGATAAAATGGAAGGGGTTTTAATCCCAGCCGGGTTTTGTCA		<u>ا</u> ک
	AG.	AGGTTACCATACTAGAGCCTATGAGTGGGGAATCTTTGGATTCTTTACGATGGATTTGAGCGAGTTGAGCATTCAA	SELFO GLUNMEGVLIPAGFVKVI	
	GA.	GAAAAATTCTTAAAAACCACCCATTCAAGCCATAGCGGGGGGTTAGTTA	TEL MOGENTUSE I MULDELLUICEKFLK	ار ا
	₹	TAATGACGCGATCAAGAGCGCTTTGAATAAGATTTTGCAATACGATAGAAATAGAAAAAAAA	I I HSSHSGGLVS I MVKGTDNSNDAIKS	AIKS
	<u>8</u>	GAATTTAGAATCTTATCAAAAAGACGCCAAGGAATTAAAAGGCAAAAAAAA	ALNKIFANIMQEIDKKLI QKNLESYQKD	8
	<u> </u>	AAGAACGCTTGAACAAACTGCTTAAAAGGGGGTTTTTAGCGTTCTTTTTTAAACGCCTCAACTAAAAGGGGGGTTTTTAAAAGGGGGGTTTTTAAAAGGGGGG	ARELKGKKNK	
	崖	TACTTACACCATCATCAAAGAAAAGATCTAGGATACCAACGATTTTAAGCCAAAGAAAG		_
	¥	ACCCTCCGTGTTTTACTAAGCCTAAAAAGCCTTAAAAAAAA		
	AAC	AAGCGTGGTGCAAATGTCATGGCTACAGAGTAGGGAAAAATTTGAAAACCATTCAAAATACCGAGACATTCCTTTTGC		
	<u> </u>	A GIT CATITATE GETATA A CANTITITIC CTA A A A A GEGETA CONTINUATE CONTINUATION OF THE C		
	AS.	GATTACGCTTATGGGTTTTTCTTAAAAATAAGGCGTGTTGGGCCGATAGTTTGAGGGAGAGTTCGCAAATCCCTAAA		_ <u>I</u>
	N N	AGCTATAGAGAAAAATTGCAAAGAAAAAGAGACTTTTATTAACGCTATTTTTTATGGCGCGGGGGTGACTTTTTATACA		<u> </u>
	3	ימרפרווו	-	Γ/

2/066501		PCT
3170 FSLKIPIGVEEGEKIRVRINGKTGRTTR GDLLLEIHIEEDEMYRREKDDITGIFDLP LKTALFGGKIEIATWHKTTLTLTIPPNTKA MQKFRIKEKGIKNRKTSHVGDLYLQAR LILPKTETLSNELKALLEKEL	3172 ISMLLDVKLNVKVRIGQKKMILKDVVSM DIGSVVELDQLVNDPLEII.VDDKVIAKG EVVIVDGNFGIQITDIGTKKERLEQLKH	3174 KDKQEAKKAKKPSKPKATPTAKNNKS HKIDFSDARDFKGNDIYDDETDEILLFD LHEQDNFNKEEEEKEIRGNINDRVRVQ RKNPWMNESGIKRQSKIKRAFRNDNS QKVIQSTTAIPEEVRVYE"AQKANLNLA DVIKTLFNLGLMVTKNDFLDKDSIEILAE EFHLEISVQNTLEEFEVE EVLEGVKKE RPPVYTIMGHVDHGKTS LLDKIRDKRV AHTEAGGITQHIGAYMVEKNDKWVSFI DTPGHEAFSQMRNRGAQVTDIAVIVIA ADDGVKQQTIEALEHAKAANVPVIFAM NKMDKPN
3169 TTTTAGCCTTAAAATCCCTATTGGCGTGGAAGAGGGCGAAAGATTAGGGTTCGCAACAAGGGGGAAAACGGGGCGAAAACGGGGCGAAAACGGGGCGAAAACGCCAACAA	3171 ATCAGCATGCTTTTAGACGTGAAATTGAACGTTAAGGTGCGCATCGGGCAAAAAAAA	3173 AAAGACAAACAAGAGGCTAAAAAAGCCCAAAAAACCCAGTAAGCCCCAAAGCCCCCCCC
HP0406	HP0406	HP0406

	CTCTAGATT CTCTAGATT CTCCAGAA GAGCAGTTT CCCCTAGCA	3175 CATTAACGCTGAAAAACCCCAATGTGCGTTTTAATGACATGGCAGGCA
	TCTTAGCCG AGTGGATAA	CONTRACCOCACCACCOCCCCCCCCCCTTTAGCCCGAATGGATTGGTTTTGGGAGCGAAATGCGCCTGTAATTG TCTTAGCCGCAACGACCGCCCCGGAAATCTTAGATCCGCCGTTAATGCGTCCAGGGCGCGTTTGACAGGCAGG
	GTTTAGCAG	CTTTAGCAGGAAGAACCAAAAAGAAGCAGCAGCACCACATTTAAAAGAAGCAGCGTTGAAGCAGGATTGCAGG GTTAGAAAAGAAA
	CACCCTTAAC	CACCÓTTAACACGCCTGAAGAAGAATACTTGATGCAAAAGCACGAACTCATCGTGAAGGGGCATGGCGGCTTTGGGCTA CACCÓTTAACACGCCTGAAGAAAACAAATACTTGATGCAAAAGCACGAACTCATCGCTGAAATTGATGTGCTTTTAGG CGGGAGAGCGGCTGAAGATGTCTTT
HP0406	3177 GAAAAAGACA	3177 GAAAAAGACAGCTCTATTAATGATGATTTAGAGCGTTTGAGATTGAGCGCGACCACCTCACTTTTAGGTTATGATGATGATGATGATGATGATATCATGAAAAATC
	AAAGTGGGC	AAAGTGGCCGAGAAGCGCGCTTACAAGAGTTTTTATTAAAGCTAGTGGAAATGGGCTATAGCCGTAATGAAGGG GTTTGATAGGGGGGAGCTTTAGAGCGACCGGAGAGTGCGTGGATATTTTCCCGGCTTATAAAGACGTGAATTTAA
	GGATTGAATT	GGATTGAATTTTTTGGCGATGAGATAGAAAGGATTGCGGTCTTTGACGCTTTAGAAAAAAATGAAATCAAGCGCTTGG
	GATGAACTCC	ATTCLETCATECTITAAGGTTGAGATTTTTAAAGGGAGGAGGAGGAGGGTGAATTTAGCCATTAAAAGCATTGAA GATGAACTCGCTTTAAGGTTGAAATTTTTTAAAGAGCAGGATAAAATGCTTTGAATACAACCGCCTCAAACAACGACCACC
	GAGCATGATT	GAGCATGATTTAGAAATGATTAGCGCGACCGGTGTGTAAGGGCATTGAAAATTACGCGCCCCATTTCACCGGTAA
	AAGCCATGT	AGCCCATGTGAGAGAGCCCITITIGCTTGTGGGGATGTTTGGGGGTTTTTGGGGGGGGGG
1	GGTTTAGATT TTGTGTCCGCT	GGTTTTAGATTGCCTAGGGCTTTAGACAACGGCCCTTTAAAATTTGATGAATTTATCCATAAAATTGCCAGTTCCTTT TTGTGTCCGCT
HP0406	3179 TCCAAACAAG	3179 TCCAAACAAGCTGAAAAAGAAAATCAAATTCAATTGGTGGAAATATTCAGGATTAACAATAGCGACAAGTTTATTATTAG CCGCTTGTAAGTGTTGGTGATATTGATAAACAGATAGAGTTAGAAAAAAAA
	AGAGCGAAC	AGAGCGAACAAGAGTGGGATAGAACTGGAACAGGAAAAACAAAAGACATTAAAGAACAAAAAAAA
	AGTAGAAGCT	AGTAGAAGCTGAATGCAAAACCCCTAAACCTGCAAAAACCAATCAAACTTAGGAATTAAGGGTGGCATTGCTATAGA AGTAGAAGCTGAATGCCAAAACCCCTAAACCTGCAAAAACCAATCAAACCCCTATCCAGCCAAAAAAACACCCCAACT
	CCTATTCACA	CTATTCACAAAAAGCTATCGCTAAAGAGTGAATTTTTACAGGCCAAAGTTCTGTGCTTATTTGCAAAAAGAGTTAGAATCTCTGC CCTATTCACAAAAAGCTATCGCTAAACAAGTGAATTTTTACAGGCCAAGTTCTGTCGCTTATTTAGAACTAGACCCTA
	GAGATTTTAA	GAGATTTTAAGGTTACAGAAGAATGGCAAAAAGAAAATCTAAAAATACGCTCTAAAGGTCAAGGTAAAAATGCTTGGAA ATGAGAAACCCACAAGGCCCACCTTTCAACGTCTTCAAAAGCCTTTTGTTCGTTC

0.66501		FC1/E1 01/15-426	ı
3182 LKDTLTGDTLCDEKNAVVLERMEFPEP 99 VIHIAVEPKTKADGEKMGVALGKLAEE 99 DPSFRVMTGEETGGTLGGMGELHLEII 95 DPSFRVMTGEETGGTLGGMGELHLEII 95 VDRLKREFKVEAEIGQPCVAFRETIRS VDRLKREFKVEAEIGQPCVAFRETIRS SVSKEHKYAKQSGGRGCIYGHVFIKLE PKEPGSGYFFVNEISGGVIPKEYIPAVD KGIQEAMQNIQVLAGYPVVDFKYTLYD GSYHDVDSSEMAFKIAGSMAFKEASR AANPVLLEPMMKVEVEV-9EFYMGDVI GDLNRRRGQINSMDDRLGLKIVNAFVP LVEM LVEM LVEM LVEM IALNWAEAEINYGNFNNAKYLIDKVVGS NADNYSTHSESALDLLKLLKKNOMNAS	AIEIAHILLNQDDDLKAKEGALYDLGAL YARIKDFKNAHLYNLQYI.QDHAELDKA SVVRARDEKALFSMEGNTGEKIAHYDK IIQNFPNSNEALKALELKAQLIFENKRY IIQNFPNSNEALKALELKAQLIFENKRY AEVLSMQKNLPKDSPLIGXTLNVLAKT PLENHRGEEALKYLSQITTFEFSPKEEI QAFDCLYFASLKEKAQIIALNAFKTAKA PSEKLIWLYRLGRHYYRLGDFKNSTLA SKDALILAQSLNKKEFYCIIAFVLFSDYM QNNEKELALHLYAFLEK-IFKGDKRMAL VYFKLLENEKDPKSVKIYATSLLKLQDA YKDYSYTPFSEFALIDAYRTKDYLKAL ETLDKLLNRRLSLEDHQKA	ASSKNRYPKMAQIRGIEGEVLVSFTIN ASSKNRYPKMAQIRGIEGEVLVSFTIN ADGSVTDIKVVKSNTTDILNHAALEAIK SAAHLFPKP 3188 RAGAFERFTNRKKRFRENAQKNAEYS NHEASSHHKKEHRPNKKPNNHHKOKH NHEASSHHKKEHRPNKKPNNHHKOKH NHEASSHHKELRKGVEANNHHKOKH HYKMNLNSKASVKITPLGGLGEIGGNM MVIETPKSAVVIDAGMSI-PKEGLFGVDI MVIETPKSAVVIDAGMSI-PKEGLFGVDI HGLKKYRSYFKIVEKRCPISVGFFIIEWI HITHSIIDSSALAIQTKAGTIIHTGDFKID HTHSIIDSSALAIQTKAGTIIHTGDFKID HTHVDNLPTDLYRLAHYGEKGVMLLLS DSTNSHKSGTTPSESTIAPAFDTLFKEA	
(D)	3183 AATCGCGCTTAAT HEGGC LEANGE CATAGE CONTRACT GACTTGCTCAAGTTATTGAAAAAACCAAGTTTTTCAAGTTTATTCTACGCGCTTTTTCAAGTCCTAAGGCCAAGCGCTTTTCCAAGGCCAAGCGCTTTTTTCAAGAGCCAAGGCGCTTTTTCCAAGGCCAAGGCGCTTTTTTCCAAGGCGATTGCAAGGCCTTTTAAAAGCCCCTTTTTCCATGCAAGGCGATTGCAAGGCCTTTTTCCATGCAAGGCGAAGCGCTTTTTTCCATGCAAGGCGAAGCGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGAAG	3185 GGAAGCTAAAGAAAAGCGCTCCTAAACAAGTTAAGATTATGTCAAAGAAAAAGGACAAGGAAGAAAAAGAGAAGAAAAGAGAAGA	CCAACTCCCATAAATCCGGGACTACGCCGAGTGAAAGCACCATAAACCACATAAATCCGGGGACTACGCCGAGTGAAAGCACCATAAACCACATAAAACCACAATAAAACCACAAATAAAAAA
HP0406	HP0406	HP0406 HP0406	

HPO400 TAAGCACGAACCCTCCAAGGTTGGAA TAAGCACGCACCCTCCAAGTTTCATGATG TAAGCACGAACCCTCCTTTCATGGAATTACTAATAAAAAAAGAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAAAATTCAATTCAAAATTCAAAAATTCAAAAGAAATTCAAAAGAAATTCAAAAGAAATTCAAAAGAACCTTATTAAAGCCCTAAATTCAAAAGAACCTTAATCAAAAATTCAAAAGAACCTTAATCAAAAATTCAAAAGAAATTCAAAAGACCTTAATCAAAAGACCTTAATCAAAAGACCTTAATCAAAAGACCTTAATTAA	ACAMA I CCAGGO I AMAMAMAMA CATIGGAATT ATTA A GACTTATA A GAGAGA COTTATA TATTA A A CAMA	
3193	GAATACAAAAGCTTGCTTTCTAGCGTGGAATTAGCCAAGGAAAACTTAAAACTCCAAGACAGGCTTTTTTACAAGGCTTTTTACAAGGCTTTTTTACAAGGCTTTTTACAAGGCTTTTTTACAAGGCTTTTTAGCAACTGCTGGAACTCGTTCTATCGTTGGAATTTTATTAAGGCTTAGCGCTTAATTAA	3190 SEQIQAKKNMELLVNKTYKETLSYLKE YKSLLSSVELAKENLKI.QEQAFLQGLS TNAQVIDARNTLSSIVVEQKSVAYKYIV SLANLMALSDHIDLFYEFVY
3193	GCCCAAGCCAACATGCCTAATCTAGTGATGAACAAGACACTGCGGCTAGGGGGGACTATCTAT	3192 AGANMPNLVMSKQDTAARGTIYSQDN YSLATSOTLFKLGFDTRFLNPDKEDFFI DFLSIYSNIPKKSLKDAINTKGYIILAYDL TPNMAANIRDLNKKFLAFGVFQNFKDA HDKVWQKQGLNIEVSGVSRHYPYQNS LEPIIGYVQKQEEDKLTLTTGKKGVEKS QDHLLKAQQNGIRTGKRDVSFNFIQNH SYTEVERLDGYEVYLSVPLKLQREIETL LDKTKDKLKAKEILVGIINPKSGEILSLA SSKRFNPNAIKTSDYESLNLSVAEKVF EPGSTIKPIVYSLLLDKNLINPKERIDLN HGYYQLGKYTIKDDFIPSKKAVVEDI
	1993 TGAAACCCCCGAATACACCGCTAACGCTGATGGTTTGGCCACGCTAACGATTTTAGAAGCCCTGCGGATTTTAGGAAATTACAGAGAGGAGAATTACAGAGAGAATTACAGAGAGAG	3194 ETPEYTANADGIGTLRILEAMRILGLEK KTRFYQASTSELYGEVLETPQNENTPF NPRSPYAVAKMYAFYITKNYREAYNLF AVNGILFNHESRYRGETFYTRKITRAAS AVNGILFNHESRYRGETFYTRKITRAAS AVNGILFNHESRYRGETFYTRKITRAAS AVNGILFNHESPOROYJATGKTTSVR DFVKMSFEFIGINLEFQNTGIKEIGLIKS VDEKRANALKLNLSHLKKGQIVYRIDER YFRPTEVDLLLGÖPTKAEKELÖWVREY DLKELVKDMLEYDLKECQKNLYLQDG GYILRNFYE
HP0287 3195 ACTCAAGATAGGAACGCCAAACAAGGGGGTTTTAAAAGCCAACCGAGAATGGGCCCAACCGAGAATGGGCCCCAACCGAGAATGGCTCCATGGAATGGCTTTGAAGATGGATAGCGGATAAGGAAGG	ACTCAAGATAGGAACGCCAAACGAGGGGGATACCACITTACCCAAACCACTCCTTTAAAAAGGGAAAGCGATACCGA TITITATTTTAAAAGCGAGGAATGGGCTAAAAAAGTGCGGGGAAAATGCGTAACGCTCCTATTTTAGAGCTTTA CCCAGAGATTGGATGGGAGGTTTGAAGATCCTAATCTAACCCCTTTAGAAGTCTTTGATAGAATCCATCATAAAAAAA CCCAGAGAGTTTAGCGGATAAGGAAGCGATTTTAAAAGCCCTAGAAGTCTTTGATAGAATCCATCATAAAAAAA CGCTAGCCTGCATTTAGCGGATAAGGAAGCGATTTTAAAAGCCCTAGAAGTGGCTAAAAGCGATAAGAGCGGTTTCA	3196 TÖDRNAKÖSGHTTYPNIHSFKNESDTD FILKANREWAKKVREKMRNAPILELYP EMDGRFEDPNLTPLEVFDRIHHKKIAS VHLADKEAILKALEVAKSDKSRFSQKS FTEHAI MSOTAOI EDE

66501			P01/15428
319B SEYLLRLEDVKRTCEMLGIELLEGDYEL EKFLDKAKGKELLGEK.SERCFECFDLR LEASALKAFELGEEKFTTLITSPKKDP NOLIAKGOSIAORHNLEFVVFRNDNFE HFKSELDLNLQALARENELYRONYCG CQFALKIQKESQNRSPFELYSPLKR 3200 NKNAQEAHEAIRPTSIII.EPNALKDYLK	PEELRI YTLYKRFLASIJMGDALFESU SVVVACEKGEFKASGFKLLFDGYYKIL GNDDKDKLLPNLKENDPIKLEKLESNA HYTEPPARYSEASLIKVLESLGIGRPST YAPTISLLQNRDYIKVE KKOISALESAF VIEILEKHFEEIVDSKFSASLEEELDNIA QNKADYQOVLKDFYYFFMDKIEAGKK NIISOKVHEKTGOSCPKCGGELVKKNS RYGEFIACNNYPKCKYVKQTESANDEA DQELCEKCGGEMVQKFSRNGAFLACN NYPECKNTKSLKNTPNAKETIEGVKCP ECGGDIALKRSKKGSFYGCNNYPKCN	GDEEIKEFKKSVLYFILSGRYATLHON GDEEIKEFKKSVLYFILSGRYATLHON PNEFSDLVFSNPLGAARKILSYGNTKR VFYTGENESPNFNLFDYAIGFDELDFN DRYLRMPLYYAHLHYKAELVNDTTAPY KLKDNSLYAHCHYKAELVNDTTAPY KLKDNSLYAHCHYKAELVNDTTAPY KLKDNSLYAHCHYKAELVNDTTAPY KLDAYESHTIPIYWGSI-SSVAKDFNPKS FVNVHDFNNFDEAIDY-KYLHTHPNAYL DMLYENPLNTLDGKAYFYQDLSFKKIL DFFKTILENDTIYHKFSTSFMWEYDLHK PLYSIDDLRVNYDDLRVNYORLLGNAS PLLELSQNTTFKIYRKAYGKSPLRAV	SZUG INFLINENTAL IN LEGACISTAL DICKNALDY DEFRACTORYNRILKFLDICKNALDN ALTHELEGPLNSEGONLAKELLNE PVDKKENFESLCGEIAI)HTHGEYTKRL KLVEFLMLLAYADGILCSKEKELFLDV
3197 TAGCGAATACTTGTTGCGTTTAGAAGACGTGAAACGCACTTGTGAGATGCTAGGAATTGAATTGCTTGAGGGCGATT ATGAATTAGAAAAATTTTTAGATAAAGCTAAGGGTAAGGAATTGTTAGGGGAAAAAAGCGAACGCTGTTTTGAGTGCT ATGAATTAGAAAAATTTTTAGATAAAGCTTTGAAAGCCTTTGAATTAGGGGAAGAAAAATTCACCACCTTACTCACAAA GCCCTAAAAAAAGACCGTAACCAGCTCATCGCTAAGGGGCAGAGCAACGCGCAAAGGCCAATTTGCAAA GTTTAGAAAACGATAATTTTGAACATTTTAAGAGCGAGTTTGAAATTCCAAAAGCGCTTTGAGAAAACGATTTTGAAAACGATTTTGAAAATTCGCTTTTAAAATCGCTTTTAAAATCGCTTTTAAAAACGCTTTTAAAAACGCCTTTAAAAACGCCTTTAAAAACGCCTTTAAAAACGCCTTTAAAAACGCCAAAAGCGCTTTAAAAACGCCAAAACGATTAAAAAAAA	CCTTAAGCCTGAAGATTAAGGCTCTATACCTTAATTTACAAACGCTTTTTAGCTTCTCAAATGCAAGACGCTCTTTTT GAAAGCCGAAGCGTGGTTGTGCGAAAAAGGCGAGTTTAAAGCGAGTGCGAAAAGCGTTTTTTAGAAGCTTTTTTAGAATTTTAGAAAAAGCGAAAAGCGAGTTGAAAGCGAGTTAAATTAGAAAA ATTATAAAATTTTAGGCAATGACGATAAGGACAATTGCTCCCCCAATTTGAAGCGAGAAAGGTTTTAGAAAAGTTTTAGAAAAGTTTTAGAAAAAGTTTTAGAAAAAA	3201 GGCCTTTATAGAAAGCGCTTCCATTGAAAAATGGCCTCTAAATCTCCCCCCCC	3203 AACCCCTAAAACCCAAAACCGAAGAATACGACTTGAAAATGACCCTATTTGTTAGCGCAATTTGGCCCCTATTTGTTAGCCCAATTTGGCCCCTATTGGCCCAATTTGGCCCCTATTGGCCAAATTGGCCCTTTGGCCCTTTGGCCTTTGGCCTTTGGCCTTTGGCCAAACGGCGCGGCGGTGTTTTGGCCGTTTGGCCTTAAGAACGCCTTAAGCGCAAAGTTTGGCCTTAAACGCCAAAGAAATTTGGCTTTGGCCTTAAGCGCAAAGAAGGGGGAACAGCCGATGGGGGAACATTGTCTTGGTTGAACGCTGGGGGAAATTGGCCGATTGGGGGAAATTGGCCGATTGGGAAAATTGGAAAAAAAA
HP0287		HP0287	HP0287

		_	
t	2	_	3
ż	:		-
٩	ú	ĸ	d

2/066501	-	PCT/EP0 <u>1/1</u> 5
3206 MKEGEWDLSALFENKESAEFLKTLQT EAGEFESAYONNLKNLDATGFANALK HYENLSEKISRVMAYAQLLFAKNTKEA KFYSQCEMACANIQQHLLFFEIEFKNL DAKKQLAFIKKCKDHAFYLNNLIERKKH TLNLDEEKIALALSPVGVGAFSRLFDEH FSSLKIPFEEQNLSEEILALLHNPKRKI RKKSQKAFSKALEKSRPLLTYILNMVR KDLIETRLRKYDKKESFRHIDNQISQE SVDSMIEIVNANFSLVHRYYHQKAQILG HKLKOYDRYAPLNDESITMTYSQALE VLKTLKAFSPEFHKIASKAIKEGWVDSH PKDFKQGGAFSHGGVPSAHPYVLLNY TGNRRDAFTIAHEFGHMIHQELSKKQG VLNIMDTPLTTAETASVFSEMLFFEHLK KGLKSDELLFML	3208 EREIYDLDYAIVKAKDLKPSFTTGGTQK RTDMNEEQIKSIAENFDPKKIFGSGGF EDLPIILHDGQVIAGNHRIQGMLNFTPK SRFSYERAIKEYYHIDLKPDELLVRVPH KRLNNTEINNLAASSNQGRFNSESDHA IAVLSHYEAKLKELDQKLDADSIYSLKNI VAKNLNPDKATHPNYTDSNLALLMFNM PRTKTQGIELLNRWKKEFSNDIKSYEK VKKMFVDNAGSFHNLIHDLNFPKVSLN AYLSDIMDRSFANLKNYQSTSESLKÖL SEKFYKTSSLEMFEKSDQSTSDISEILG GAIARFARFDDPSKALFEALRSDNIKKG LKDYKIADVTKDMFNADSKEFKDIDIYD FT	3210 KFNERKRAYAQKFAQSQNTHASERLS H
3205 ATGAAAGAGAATTTAAAGCGCTTTATTTGAAATAAAGAAAG	3207 GGAACGAGAGTTTACGATCTAGACTATGCGAAAGATTTAAAAACCAAGGCTTTACCACAGGCGGGA CGCAAAAGAGAACGGACATGAACGAAGAGTTAAAAGCATTGCTGAAAATTTTGATCCTAAAAAGATTTTGGTA CGCAAAAGAGATTTACCGATCATTCTACGAGGCAGTTGCTGAAAATTTTGATCCTAAAAGGATATTTGGTA GCGGAGGGTTTGAAGATTTACCGATCATTTTTTTACGGGCAAGTGATCATACAAAAGATTAAAAAACCGGA GCGAGTTTAATGCGAAAGCCGTTTTACGAGAGAGCGATTAAACAAATTTAAGCCAATTTAAAAAAATTAAGCGATTAAAAAAATTAAGCGATTAAAAAAAA	3209 GGAAATTTAATGAACGCAGCCTACCGCACAAAGTTCGCACAAAGTCAAAAGTCACAAACGCCCAGTGAGGCGGTTA TCACATTGAAGATTTACGCACCTACCCTAC
HP0287	HP0287	HP0287

_PCT/EP01	/15428
-----------	--------

Transpace of the control of the
1 1

WU	UZ/	U	00	วบ
	- 1.	٠.	4	~

/066501		PCT/EP01/15428
3220 AFAKQARIKNIMCEYKDLVHEANEDYE HFWGDLAKQKLTWFKPFDKVLNSDNA PFFKWFENGKINVSYNCIDRHLKDKKN KVAIIFEGEMGDYNVITYRKLHSEVNKT ANLLKNEFNVKKGDRVIIYMPMIVESVY MMLACTRIGAIHSIVFAGFSPEALRÖRI NDAQAKLVITADGTFRKGKPYMLKPAL DKALENNACPSVEKALIVIRNAKEIDYV RGRDFVYNEMVNYQSDKCEPEMMDS EDPLFLL	3222 NRMÖKNMGGGIFGMGSAKKLINAEKP NVRFNDMAGNEEAKEEVVEIVDFLKYP ERYANLGAKIPKGVLLVGPPGTGKTLL AKAVAGEAHVPFFSMGGSSFIEMFVGL GASRVRDLFETAKKÖAPSIIFIDEIDAIG KSRAAGGVVSGNDEREOTLNOLLAEM DGFGSENAPVIVLAATNRPEILDPALM RPGRFDROVLVDKPDFNGRVEILKVHI KGVKLANDVNLQEVAKLTAGLAGADLA NIINEAALLAGRNNQKEVROQHLKEAV ERGIAGLEKKSRRISPKEKKIVAYHESG HAVISEMTKGSARVIVKVSIIPRGMAAL GYTLNTPEENYTLMÖKHELIAEIDVLLG GRAABSVSGLMVLEKÖRNAFLG GGYGSSREFSEKTAEEMDLFIKNLLEE RYKHVKQTLSDYREAIEIMVKELFDKEV ITGERVREIISEYEVANNLESRLIPLEED AS	3224 DLDYAIVKAKDLKPSFTTGGTQKRTDM NEEQIKSIAENFDPKKIFGSGGFEDLPII LHDGQVIAGNHRIQGMLNFTPKSRFSY ERAIKEYYHIDLKPDELLVRVPHKRLNN TEINNLAASSNQGRFNSESDHAIAVLS HYEAKLKELDQKLDADSIYSLKNIVAKN LNFDKATHPNVTDSNLALLMFNWPRTK TQGIELLNRWKKEFSNDIKSYEKVKKM FVDNAGSFHNLIHDLNFPKVSLNAYLS DIMDRSFANLKNYQSTSSLKDLSEKF YKTSSLEMFEKSDQSTSDISEILGGAIA RFARFDDPSKALFEALRSDNIKKGLKD YKIADVT
	ATTITIGGCATGGGGAGCGGAAAAACTCATTAACGCTGAAAAAC TGAAGAAGCCAAAGAAGTGGTAGAAATCGTAGCATTTCTTAAAAT AATCCCTAAAGGCGTGTTATTAGTAGGGCCTCCAGGAATTCTTAAAAT AATCCCTAAAGGCGTGTTATTAGTAGGGCCTCCAGGAACCGGTAAA SCGCATGTGCCGTTTTTCTCTATGGAGGGCGCTTTCATTGAAAT SGATTTATTGAAACCGCTAAAAAACAAGCCCTAGCATTTTTA SGATTTTTGGGAGCGTGTAATTGTCTTAGCCGCAACGAAC GTCCAGGGCCTTTGCTAATGTCTTAGCCGCAACGAAC GTCCAGGCCCTTTGCTAATGTTTTAGTCGAACGAAC TTGGCGAATATTACAAGGCGCTGTTTTAGCAGGAAGCGC TTGGCGATTTTTTGCGAACGAACGAAC TTGGCGATTTAGCAGGAACGAACGAAC TTGGCGATTTTTTTTTT	3223 GATCTAGACTATGCGATCGTCAAAAGGATTTAAAACCAAGCTTTACCACAGGCGGGACGAAAAGAAAG
HP0287	HP0287	HP0287

V	٧	(

02/06650	1	G., 10 CG. 2 = 5 = 5	PCT/EP01/15428
3226 RFDKQNHKIFEILADKVSAKDNVITASGS NAILLNYDVYILADKVRYDTKTKEALLE S GNIKVYRGEGLLVKTDYVK SLNEKYEIS IFPFYVQD	3228 SNPDYISTHSESALDLLKLLKKNGMNA 'SAIEIAHLL'LNQDDLKAKEJALYDLGA LYARIKDFKNAHLYNLQYLCIDHAELDK ASVVRARDEKALFSMEGN"QEKIAHYD KIIQNFPNSNEALKALELKAJLLFENKR YAEVLSMQKNLPKDSPLIQICTLNVLAK TPLENHRCEEALKYLSQITTFEF	3230 KKEHRPNKKPNNHHKQKHAKTRNYAQ EELDSNKVEGYTEILHVNERGTLGFHK ELKKGVEANNKIQVEHLNPHYKMNLNS KASVKITPLGGLGEIGGNMMVIETPKSA IVIDAGMSFPKEGLFGVDILIPDFSYLHQ IKDKIAGIIITHAHEDHIGATPYLFKELGF PLYGTPLSLGLIGSKFDEHGLKYRSY FKIVEKRCPISVGEFIIEWIHITHSIIDSSA LAIQTKAGTIIHTGDFKIDHTIPVDNLPTD LYRLAHYGEKGVMLLLSDSTNSHKSGT TPSESTIAPAFDTLFKEAGGRVIMSTFS SNIHRYYQAIQYGKYNRKIAVIGSTS SNIHRYYQAIQYGKYNRKIAVIGSTS FRUDARELGYIHLPYQSFIEANEVAKY	3232 DNAPLLDNTPALDNTPKKSCMIVLESA APLSAFLEKLEKTNARVFAFLVLDKEK KVLALAFLYEDQGYFLPLEFALFSPFSL EFLQNAFFKMLQHAQIIGHDLKPLLSFL KAKYQVPLENIRIQDTQILAFLKNPEKV GFDEVLKEYLKEELIPHEKIKDFKTKAE KLELLSVELNALKRLCEYFEKGGLEEN LLSLAREIETPFMKVLMGMEFQGFKID APYFKRLEGEFKNELHVLEFGOLELIGV DFNLNSPKQLSEVLYDKLGIPKNKSHS TDEKSLLKILDKHPSIALILEYRELNKLF NTYTTPLLKLKKDDKIHTTFIQTGTAT GRLSSHSPNLQNIPVRSPKGLLGYRGL KDLMEAFLKGRDIHLETSKALFGEYLA KEKRSIAKSINFGLVYGMGSKKLSETLN ISLNEAKSYIEAYFKRFPSIKDYLNRMK
	(5 ()()	0.44400	
3225 CGATTTGACAAACCAAAACCATAAGATTTTTGAAATCCTTGCGGATAAAGTGAGCGCTAAAGACAATGTGATAACCGCA TCAGGGAATGCGATCTTATTGAATTATGATGTGTATATTCTAGCGGACAAGGTGCGTTATGACACTAAAACCAAAGAA GCGTTATTAGAGGGGAATATCAAGGTTTATAGGGGCGAGGGTTTGCTCGTTAAAACCGATTACGTGAAATTGAGTTT GAATGAAAATATGAAATCATTTTCCCCTTTTATGTCCAAGACA	3227 ATCCAACCCTGATTATATTTCTACGCATAGCGAATCAGCCCTAGACTTGCTCAAGTTATTGAAAAAAACCAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGCCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTTGCAGGACCATGATTATGAATTTAGGAGCGTTTATGTGAAAGGGGGATGATATTGCAGGACCATGAAGAAGAATGGAAAAGGTTGTTGTGTTGTTGTTAGGGGGG	AGAAGAATTCGCCCTAACAAAAACCAAACCACCACCACAAACAA	3231 GACAACGCCCCCTATTAGACAACACGCCCGCTTAGACAACACCCCTAAAAAATCATGCATG
HP0287	HP0287	HP0287	HP0287

02/066501			PCT/EP01/15428
3234 RNDENQVDAIMIKKASILYEGGGKDEA LHLFDKAASFSQGIASHNLGVIKFKEKD FNGALDLFDSSIASKENASVSAIDALVS AYHLQDEDLYYHYLKIARDTLYKOYKK SFYSYAYALKSYYAGEYFEALSPLMHP NSNAFLKPNTRLASKLFLMFKDETNAY EQLQKSANAQDELALGLLQARLGHYK QALEHLQHYLHNYPKDLNALMALELVS LKKGDTLKASEALKLASHTKEDTLLAN SFYPIKPTIN	3236 KDANEVYŘÍKKLSTFŘELVŠVYYGMVI NAEVAETLEEVEKGHYKHFONALKMÓ KVGČIARVETLGAČVAYĎKAHIASVKA KDVLEVSČLSFNSILSSKĎDLVPSSKLE IRTEKNLPĎLSFVSSTLNSYPVLKTLE NOJOJSKENTKLOJAKFLPOVSFČSY MKČNNSVFEĎMIPSWFVGVAGRMPIL SPTGRIQKYČASKLAELQVSSEČJOAK KNMELLVNKTYKETLSYLKEYKSLLSS VELAKENLKLOEQA	3238 HSYTEVERLDGYEVYLSVPLKLGREIE TLLDKTKDKLKAKEILVGIINPKSGEILSL ASSKRFNPNAIKTSDYESLNLSVAEKV FEPGSTI	3240 LÁEFEWVVSNLKYĞSLÁKVEIKRNHKV KEVTLKVNKRYGGFLLKDTFLERYGIAL DERFIITKIGAHLPKGLDFLKLGDRILWV NYKSVASNPKALREALSAPKIELLVLRK GFEFYIKV
3233 CGAAACGATGAAAATCAAGTGGGATGCGATCATGAAAAAAGCGAGCCTTTTGTATGAGCAAGGGGCAAAAAGTGAAGG TTTGCATTTGTTTGACAAAGCCGCTTCTTTTTCGCAAGGGATTGCGAGCCCTAATTTAGGGGTGAGCTTTAAGGA AAAGGATTTTAATGGGGCGTTGGATTGTTTGAGTTCTAGCATTGTTATCATATGTGAAAATTGCGAGAGACACTTTGTA AAAGGATTTAAAAAAGTCTTTTTGCAAGAAGATTGTATTATCATTATCATAAAAAATTGGAGAGACACTTTGTA TAAAGACTATAAAAAGTCTTTTTATTCCTACGCTTACGCGCTCAAATCCTTATACGCCGGGGGGGTATTTTGAAGCCCT TTCGCCCTTAATGCACCCTAATTCCAACGCCTTTTTTAAAGCCTAATACGCGCGGGGGGGTTTTTGATTTTGAAGTTTTTGAAGTTTTTGAAGTTTTTT	3235 AAAGATGCTAATGAAGTGTTTGAAAAAGCTTTTCCACTTTTCAAGAGCTTGTGAGCGTGTATTACGGCGATGGTG TTAAACGCAGAAGTGGCTGAAACTTTAGAAGAGGTGGAAAAAGGCCATTATAAGCATTTCCAAAACGCTTTGAAAATG CAAAAAGTGGGGCAAATCGCTAGGGTAGAAACCTTAGGCGCTCAAGTGGCTTATGATAAGGCCCATATCGCTAGCG TTAAGGCTAAAGATTAGAAGTTTCGCAGCTCTCGTTCAATTCCATTTTATCTAGCAAGGACGATTTAGTGCCTT CAAGCAAATTAGAGATTCGCAGGAGAAAAATCGCAGCTCTTATTTTTTTT	3237 CACTCTTATACAGAGGTTGAACGCCTTGATGGCTATGAGGTGTATTTGAGCGTTCCTTTAAAAGCTCCAAAAGAGTTGAAATTTGAACCCTATTGGAGAGAGA	3239 CATTAGCGGAGTITGAATGGGTGGTGAGCAATCTTAAATACCCAAAGCCTTGCCAAAGTGGAAATCAAACGAAACCAT AAAGTCAAAGAAGTAGCGTGTTTTATATCATAAGCGGTTTTTGCCCAAAGGCTTTTTTAGAGCGCTAT GGCATCGCTTTAGATGAGCGTTTTATTATCATAAAATAGGCGCCTCATTGCCCAAAGGCTTTAAGAGCGCTT GGGGATAGGATTTTATGGGTGAATTATAAAAGCGTGGCGTCCAAAGGCTTTAAGAGCGTTAAGCGCGC CTAAAATTGAATTG
HP0287	HP0287	HP0287	нР0975

3242 NLNAPKPL FECFVGVNI AKAKYYSKKE 0 BREKEKMILNFCKIFEIIL FEAIQKOPKP 9 DFKNKDELLGDYPNLKNLDSLREVRECS FLKRAFKNDEASLGAYVLVILSCKYFE 0 SVFEKVQEWLDFIARI JALRG	3244 PEDNSIELSPSUSAWKI INTERACTION OF THE COSSUIEELKKREEAKROKELIKGENL NTTAYINKWMASNESIINKEKIREEKO KIILDOAKALETQYYHIALKRNPVPRNY NYYQAPEKRSKHIMPSEIFDDGTFTYF GFKNITLQPAIFVVQPISGKLSMTDAAID PNMTNSGLRWYRVNEIAEKFKLIKDKA LVTVINKGYGKNPLTKNYNIKNYGELER VIKKLPLVRDK	3240	
3241 CAAACTTAAACGCACCCAAACCCTTATTTGAATGTTTTGTAGGAGTTAATCTGGCCAAAGCCAAATATTTATT	3243 GCCTGAGGATAACTCCATAGAATTATCTCCTAGCGATAGCGCTTGGAGAACTAATCTTGTTGTGCGGACTAATAAAG CCTTGTATCAATTGAGAATTATCTCCAAAAAGACAATTTTGCTTCAGCGTATCTACCAACGGAACTAACAACGCGTATCTAACAACGAAGAATTGAACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	3245 GGCGGTTTTTTTTTTTTTTTTTTTTTTTTAGCCCGTAGGAAGGCAAGGCAAGGCGAAGGCCTTAAAAATCGCTAAAATTTTTAAAGGCTTTAA 3245 GGCGGTTTTTTTTTTTTTTAGCCCGTGGTTTTTTTTTTGAAAGGCCCGCACCGATTGTTGGAAGAAAAACCCCGGTGGTTTAA TGCGTATTTGGAAAAAAACCCCGGTGGTTTTTTTTTATGAAGCCCGCACCGATTGTTGGAAGAAAAAAGGCATGCCTATAAGGCTTAAGGACAAAAAAAA	CATTIGAAGCTGTAATCGGGCTAGAAGTCCAAGTGTCCAACCAAAAGCCAAAATCAAAAGCTTTGAAGGAATTGAAGGAAG
HP0975	HP0975	HP0975	HP0975

02/066501		
3250 GYGEHFYTNEETLYGVLALGYADGLM RALGNRIQVAINNQLAPLIGKVCMDQC FVKLNNIQAKEGDEVILFGDKSAKAND ASEIXALLNTIAYETISTLSKRLERXYI	3252 GHVIGKEGKMVSAIKAFISGVKAKDGF SYKIVVFASKNGDKNPHVLGDQTP	3254 QEYAIHYNTDHSQRVSSVTKYWEDSS SVTINAFFTNQDENETFHTEMATFILSN NILFTIYYGTLEIFDSIQKKVLASPKKFE DGFDILTKIFEVYFEKGVECLEWINKQT SLLRKNIIFKETSTHDDILVRLSNLQEFN VT
3249 TGGCTATGGCGAGCATTTTATACCAATGAAGACTTTAGTGGGTGTTTTAGCTCTAGGGTATGCAGACGGGTTAA TGCGCGCTTTAGGCAATCCAATGAGTGGCATCAATAACCAATTAGCCCCCCTGATTGGCAAGGGTGCAGGGT CAATGTTTGTCAAACTCCAATAATATTCAAGCCGAAGAGGGCGATGAGGTCATTTTGTTTG		3253 CCAAGAATATGCTATCCACTACAACAGACCATTCCCAACGAGTCTCATCAGTTACCAAATATTGGGAAGACGCTC CAGCGTTACGATCATCACGCTTTTTCACCAACCAGGATGAAAATGAGACTTTCCACACGGAAATGGCGACCTTTATTTT GTCTAATAACATTCTTTTCACGATCTATTATGGGACTTTAGAAAATCTTTGATTCTATCCAAAAAAAGGTTTTGGCTAGC CCTAAAAAAATTTGAAGACGGGTTTGATATTCTAACTAAAAAATCTTTGAAGTGTATTTTGAAAAAAGGCTAGAAGAAGCCTAGAAAAAGGCTTGAACTACTAGAAAAAGGCTAGAAGAAAAGGCTAGAAGAAAAGGCTAGGAAGAAAAAGAAAAGAAAAGAAAAGAAAG
HP0975	HP0975	HP0975

l		٠	۰	
ï	٠	,	٠	
۰	_	1	_	
•	ς	3	ľ	

wc	3256 DVDLSNRVALEEILALKPSLLSFSADKFORSAGIIMGGKERVEALKNHPLYRV9 LRVGKITLTLFCSLKAWINHGEDITIHAS LLNGTKDALLGKALK-YALLKPLELNVSC IASSFSKIGNLFGRELESFCVKIGPKNT RALNSEKLYLKLFGKGVIARISCEFVCF EVFSLNEKDFEKIALVLEEILNKA
46/	3255 GGGATGTGGATTTGTCAAACAGAGTGGCTTTGGAAGAATTTTAGCCCTAAAACCATCGCTTTTAAAAAACACCACC GATAAATTCTTTAACAGTGCGCAAGCGGGCATTATTATGCGGGTTGAAAACCACCACC GATAAATTCTTTAACAGTGCGTAAACAGCAACTAAATTATTGCAGCGTTAAAAAGCATCACCTTCATCACCTTTATATTGCAAAAAAAA
-	HP0975

TARI, F.

	_	_	_	_	_	_		_																					
	3265)	3266)	3267)	3268)	3269)	3270)	3271)	3272)	3273)	3274)	3275)	3276)	3277)	3278)	3279)	3280)	3281)	3282)	3283)	3284)	3285)	3286)	3287)	3288)	3289)	3290)	3291)	3292)	32931
	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEO ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NÓ.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEO ID NO
		-								-	-										•	·.							
-	CUACUACUACTCAATTCAAGGGTTTTTGAG	CUACUACUATTTTAACCCTTGAGAGTTTGG	CUACUACUATTCCTTTAAAATAAATTTTGG	CUACUACUAGGGGTTTTTGTTTTAGAAGTT	CUACUACUATTAACAATCCTTTAAAAGCTC	CUACUACUAAAACTACACCCATAAATTATC	CUACUACUATCAGCTGGTAGAGCAATTCCC	CUACUACUACTAATAAGATTTGTTAGATCT	CUACUACUAGGGGCTTACATCATGCCACCC	CUACUACUAAATAATGTTTTTAGTGTTTTT	CUACUACUAATCTTTTTCATATGGCGACTA	CUACUACUATICAAGCGAACAAATATICCC	CUACUACUACTATICTACGATTIGATAGAC	CUACUACUAAATCATTAAAAAATTCCCATA	CUACUACUAACATTCTACGCTCTATAACAT	CUACUACUACTAGCTCCTCAAAAGTTTCTC	CUACUACUATGAAATCATTTTAAACGACTC	CUACUACUATCATGCTAATTCCAAAAATTG	CUACUACUATTAGITICIGITITIATAGIC	CUACUACUATTAAGGCTTTTTGGGGCTTGT	CUACUACUATGTTATTTTACTCTTTTTGT	CUACUACUATTATTTGGATTTGCCCCATAT	CUACUACUATTAGCGTTTCATCAAAACAC	CUACUACUACTTTTAGTAAGCAAACACATA	CUACUACUAAGCCTTAATCCCCTACATAGA	CUACUACUAGCTCTTTCACATGTTTTCAAT	CUACUACUATTAATGAGCTTTGCTCTTAAA	CUACUACUACGTTCTGTTTGCACTTTATTT	CUACUACUAATGGTTTAAACTTTAAAGTGG
	1SA1_HP0001	1SA2_HP0002	1SA3_HP0003	1SA4_HP0004	1SA5_HP0005	1SA6_HP0006	1SA7_HP0007	1SA8_HP0008	1SA9_HP0010	1SA10_HP0011	1SA11_HP0012	1SA12_HP0013	1SB1_HP0014	1SB2_HP0015	1SB3_HP0016	1SB4_HP0017	1SB5_HP0018	1SB6_HP0019	1SB7_HP0020	1SB8_HP0021	1SB9_HP0022	1SB10_HP0023	1SB11_HP0024	1SB12_HP0025	1SC1_HP0026	1SC2_HP0027	1SC3_HP0028	1SC4_HP0029	1SC5 HP0030

			0	
1SC6_HP0031	CUACUACUACTACTTGGCGATCACAACAGG	٠.	(SEQ ID NO.	3294)
1SC7_HP0032	CUACUACUATTATTTTATCTTCTACCAA		(SEQ ID NO.	3295)
1SC8 HP0033	CUACUACUATCAAAGTCATTTTCTTTCAC		(SEQ ID NO.	3296)
1SC9_HP0034	CUACUACUAATCCATCTCTAACCCTTTTCT		(SEO ID NO.	3297)
1SC10 HP0035S3	4 CUACUACUATGAAACATCACAATTTAGCAA		(SEQ ID NO.	3298)
1SC11 HP0036S35	Ŋ		(SEQ ID NO.	3299)
1SC12 HP0037S36			(SEQ ID NO.	3300)
1SD1 HP0038S37	CUACUACUAGCATCAATCACCCCTATTAGT		(SEQ ID NO.	3301)
1SD2 HP0039S38	_		(SEQ ID NO.	3302)
1SD3 HP0040S39	_		(SEQ ID NO.	3303)
1SD4 HP0041S40	CUACUACUAATGCGAGCGGCTAGTAATCC	-	(SEQ ID NO.	3304)
1SD5 HP0042841			(SEQ ID NO.	3305)
1SD6_HP0043S42	CUACUACUATTTATTAGGCGTTTTGATTTT		(SEQ ID NO.	3306)
1SD7 HP0044S43	CUACUACUAATAATCTCATTCATAAAATT		(SEQ ID NO.	3307)
1SD8 HP0045S44	CUACUACUATTCAAACCTCTAAAAGCTTCA		(SEQ ID NO.	3308)
1SD9 HP0046S45	CUACUACUAGITTGTTTTAATGCAAAGA		Ω	3309)
1SD10 HP0047S46	6 CUACUACUATTAACAAATCCTAGGCAATAA		(SEQ ID NO.	3310)
1SD11 HP0048S47	7 CUACUACUATTTATCCTTTTTTGATGATTG		(SEQ ID NO.	3311).
1SD12_HP0049S48	8 CUACUACUATCAATAAAGTTGCATCGTTAC		(SEQ ID NO.	3312)
1SE1 HP0050S49	CUACUACUAAATAGCGTTTTTAAAACAGAT		(SEQ ID NO.	3313)
1SE2_HP0051S50	CUACUACUATCATTTTCTTAAGCTTTTTAA	-	(SEQ ID NO.	3314)
1SE3 HP0052S51	CUACUACUAAGTAGGGCAAAGTTTAGCAAG		(SEQ ID NO.	3315)
1SE4_HP0053S52	CUACUACUAACTTATTAAAATTTTAGCTTG		(SEQ ID NO.	3316)
1SE5 HP0054S53	CUACUACUACTITICATAAGCTACTCCTTAA			3317)
1SE6_HP0055S54	CUACUACUATTAATGTTTCAAGCTCTCAAT		(SEQ ID NO.	3318)
1SE7_HP0056S55	S CUACUACUATTATTTTCAGCACAGCATGA		(SEO ID NO.	3319)
1SE8_HP0057S56	S CUACUACUAATAAACCCCTAGAATGTAGAA		(SEQ ID NO.	3320)
1SE9_HP0059S57	CUACUACUATTATGGTTTTGGTTGTTTTGA			3321)
1SE10 HP0060S58	58 CUACUACUAGTCATCATAATTTTTCTGCCT		(SEQ ID NO.	3322)
1SE11 HP0061S59	59 CUACUACUATTTAAAAATTTTCTTCATCAA			3323)
1SE12_HP0062S60	50 CUACUACUACCACCCTTAATAATCTTCCT		(SEQ ID NO.	3324)
1SF1_HP0063S61	L CUACUACUAAATTCAGTTCTGAGTTTGCAG		(SEQ ID NO.	3325)

ľ	-	ī	3
1		J	١
	_	ì	
7	٠,	7	

	1SF2_HP0064S62	CUACUACUATTAACCCCTTGATTCCAGTTT	(SEQ ID NO.	332
	1SF3_HP0065S63	CUACUACUATCATCATTTTTTATCCTTAGA	(SEQ ID NO.	332
	1SF4_HP0066S64	CUACUACUACCCCTTTTTTGACCCTATAA	(SEQ ID NO.	332
	1SF5_HP0067S65	CUACUACUATTTCAAACCTTTTGCGTGGTG	(SEQ ID NO.	332
	1SF6_HP0068S66	CUACUACUAAGTGTTCATCAATCTTCCAAT	(SEQ ID NO.	333
	1SF7_HP0069S67	CUACUACUAGAGATTAAAATTCAAGACATA	(SEQ ID NO.	333
	1SF8_HP0070S68	CUACUACUATCTTTTCTATTTTACGACCAC	(SEQ ID NO.	333
	1SF9_HP0071S69	CUACUACUATCACACCCAGTGTTGGATAAA	(SEQ ID NO.	333
	1SF10_HP0072S70	CUACUACUACTCCTAAAAAATCCTAGAAAA	(SEQ ID NO.	333
	1SF11_HP0073S71	CUACUACUATTACTCCTTAATTGTTTTTAC	(SEQ ID NO.	333
	1SF12_HP0074S72	CUACUACUATTATGCCTTAATTTTGTTTTG	(SEQ ID NO.	333
	1SG1_HP0075S73	CUACUACUATTAGCACAAATGCCCTTCAAA	(SEQ ID NO.	333
	1SG2_HP0076S74	CUACUACUAAAACTAAGCGAGAGCGAGAG	(SEQ ID NO.	333
	1SG3_HP0077S75	CUACUACUAAGTAATGGTCTTATTCAAACT	(SEQ ID NO.	333
	1SG4_HP0078S76	CUACUACUAACTICCITCTIATITITICAT	(SEQ ID NO.	334
٠	1SG5_HP0079S77	CUACUACUATTAGAAGTTGATCATGTAGTT	(SEQ ID NO.	334
	1SG6_HP0080S78	CUACUACUTTTGATATTGGGGTTAATCT	(SEQ ID NO.	334
	1SG7_HP0081S79	CUACUACUATTACCTTAAAAGAATCATTTT	(SEQ ID NO.	334
	1SG8_HP0082S80	CUACUACUAAAATCAAAATTTCTTCCTGCT	(SEQ ID NO.	334
	1SG9_HP0083S81	CUACUACUAGATTACCTTTTGGAGAATTGT	(SEQ ID NO.	334
	1SG10_HP0084S82	CUACUACUATTCTCATTTAGCGTCCTTTTT	(SEQ ID NO.	334
	1SG11_HP0085583	CUACUACUACTTTTTTATTTTTGCTCCTGA	(SEQ ID NO.	334
	1SG12_HP0086S84	CUACUACUATTAATTTTCCAATTCTTCTGG	(SEQ ID NO.	3348
	1SH1_HP0087S85	CUACUACUAAGAAAATCAATTCGCATTTA	(SEQ ID NO.	3346
	1SH2_HP0088S86	CUACUACUACATCAAATGCGCAAATAGTTT	(SEQ ID NO.	335(
	1SH3_HP0089S87	CUACUACUAACAACCCTAAAGCTCATCCA	(SEQ ID NO.	3351
	1SH4_HP0090S88	CUACUACUATCACACGIATTCTTCTAAAA	(SEQ ID NO.	3352
	1SH5_HP0091S89	CUACUACUAATTACCATTTTTGTGCCTTTG	(SEQ ID NO.	3353
	1SH6_HP0092S90	CUACUACUACTTTATTGGTGGTTTAAATCT	(SEQ ID NO.	3354
	1SH7_HP0093S91	CUACUACUACACTTTAAGCGTTATACTTTT	(SEQ ID NO.	3326
	1SH8_HP0094S92	CUACUACUATCAAAGAAAGCTTGCACTGAT	(SEQ ID NO.	3356
	1SH9_HP0095S93	CUACUACUAAATCATTTGAATTTTTTTTT	(SEQ ID NO.	3357

9	
4	

<u></u>	(69	()	31	32)	33)	34)	92)	(99	97)	38)	(65	(02	71)	(2)	73)	74)	(22	(92	(2)	(8)	(62	80)	81)	82)	83)	84)	82)	3386)	87)	3388)	3389)
3328)	3359	3360	3361	3362	3363	3364	3365	3366	3367	3368	3369	3370	3371	3372	3373	3374	3375	3376	3377	3378	3379	3380	3381	3382	3383	3384	3385	ကိ	3387	33	m m
(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	SEQ ID NO.	(SEQ ID NO.	SEC ID NO.	SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	SEO ID NO.	(SEQ ID NO.	SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	SEQ ID NO.		(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.
SE)	SE SE	SE)	BS)	BS)	SE)	SE)	as)	SE SE	SE SE	SE SE	S)	SE)	SE)	SE)	SE SE	SE)	S)	SE.	SE SE	SE (SE	S)	S)	S)	SS)	SE)	SE)	S)	S)	S)	SE SE	S)
٠.																					٠										
CUACUACUATTTTTTGCGTTTATTTTGAG	CUACUACUACGATTACATCTTAGAAATATC	CUACUACUAGGGCTTAAAAAAAGATTTAATG	CAUCAUCAUAGGGTTAAAATGGCGACACGA	CAUCAUCAUATGCAAATCATAGAAGGGAAA	CAUCAUCAUGGAAAAGTCATGAAAACTTCT	CAUCAUCAUTAAAGAGTGAAAGCGTTTTTA	CAUCAUCAUGGGCTTTCATGCAATTATGTG	CAUCAUCAUAGCTTTTAAAGGATTGTTAAA	CAUCAUCAUACGATGCTCATGGTGACCCGT	CAUCAUCAUGATGCGTTTTTTTTTTTGGTT	CAUCAUCAUATGGCAAAAGAAATCAAATTT	CAUCAUCAUTATGAAGTTTCAGCCATTAGG	CAUCAUCAUTGAAAATGATTCTTAAAAGT	CAUCAUCAUAGTCGCCATATGAAAAAGATT	CAUCAUCAUAGGTTTGCATGCAAGAGTTTT	CAUCAUCAUTTTTGATGTCCGCTCATTTTT	CAUCAUCAUATTTTTAATGATTATCCTGT	CAUCAUCAUTTATAGAGCGTAGAATGTTAG	CAUCAUCAUTTAGATTGAAAATATTCGTTC	CAUCAUCAUGGGAAGTCATGGCTGATAGTT	CAUCAUCAUATGAAAAAATACAGCACTATC	CAUCAUCAUACACGCATGAAAAAATTCTTA	CAUCAUCAUCGTGTTTGGCATCATTATTCC	CAUCAUCAUATGGTTTATTTAAAGTGGAAA	CAUCAUCAUATGAAGTGTAAAAGTGGCAAA	CAUCAUCAUAGGAGAAAACATGAAGAAAAA	CAUCAUCAUAATGTCTGTCACTTTAGTCAA	CAUCAUCAUAGTGGCTTACAACCCTAAAAT	CAUCAUCAUAGGAATGAAGTTGATAAAATT	CAUCAUCAUGTTAAACCATGCTCTTTATCA	CAUCAUCAUATGCTATTGAATTACGATTTT
1SH10_HP0096S94	1SH11 HP0097S95	1SH12_HP0098S96	1RA1 HP0001R1	1RAZ HP0002R2	1RA3 HP0003R3	1RA4 HP0004R4	1RAS HP0005RS	1RAG HP0006R6	1RA7 HP0007R7	1RA8 HP0008R8	1RA9 HP0010R9	1RA10 HP0011R10	1RA11 HP0012R11	1RA12 HP0013R12	1RB1 HP0014R13	1RB2_HP0015R14	TRB3_HP0016R15	1RB4_HP0017R16	1RB5_HP0018R17	1RB6_HP0019R18	1RB7_HP0020R19	1RB8_HP0021R20	1RB9_HP0022R21	1RB10 HP0023R22	1RB11_HP0024R23	1RB12 HP0025R24	1RC1 HP0026R25	1RC2 HP0027R26	1RC3 HP0028R27	1RC4_HP0029R28	1RCS_HP0030R29

- •	1RC6_HP0031R30	CAUCAUCAUGGTTGGTTCTTATGAATATTT	(SEQ ID NO.
•	1RC7_HP0032R31	CAUCAUCAUATAAGCGGCATGAAAATGTAT	(SEQ ID NO.
• •	1RC8_HP0033R32	CAUCAUCAUAGATAAATAATGGCTAAATT	(SEQ ID NO.
	IRC9_HP0034R33	CAUCAUCAUATGACTTTTGAAATGCTTTAT	(SEQ ID NO.
	1RC10_HP0035R34	CAUCAUCAUGGTTAGAGATGGATTTTAGTC	(SEQ ID NO.
	1RC11_HP0036R35	CAUCAUCAUATGTTTCACAAAGCCCTTATT	(SEQ ID NO.
••	1RC12_HP0037R36	CAUCAUCAUTGATGAAAAATGACGCTTATG	(SEQ ID NO.
•	1RD1_HP0038R37	CAUCAUCAUATGAAAGAAAAGCCTTTCAAT	(SEQ ID NO.
	1RD2_HP0039R38	CAUCAUCAUGGTGATTGATGCGTAAGGTTT	(SEQ ID NO.
	1RD3_HP0040R39	CAUCAUCAUATGGCGACCTTATTGTTTTT	(SEQ ID NO.
••	1RD4_HP0041R40	CAUCAUCAUAAAAAGGCTAAAGATGAATAA	(SEQ ID NO.
••	1RD5_HP0042R41	CAUCAUCAUATGGATAACCCTAAAGGCATT	(SEQ ID NO.
• •	1RD6_HP0043R42	CAUCAUCAUATGAAAATTTAAAAATATCTTA	(SEQ ID NO.
••	1RD7_HP0044R43	CAUCAUCAUATGAAAGAAAAAATCGCTTTA	(SEQ ID NO.
• •	1RD8_HP0045R44	CAUCAUCAUATGAATGAGATTATTTTAATC	(SEQ ID NO.
-	IRD9_HP0046R45	CAUCAUCAUTTAAAAGGGATTTTGGTGTGTG	(SEQ ID NO.
	1RD10_HP0047R46	CAUCAUCAUATGGATAGCGTAACTCTAGCA	(SEQ ID NO.
	IRDII_HP0048R47	CAUCAUCAVAGAAGTGATAGGGGTTGATTG	(SEQ ID NO.
П	1RD12_HP0049R48	CAUCAUCAUGGATATTTTGAATGAAAGAA	(SEQ ID NO.
П	1RE1_HP0050R49	CAUCAUCAUGCTTAAGAAAATGATACAAAT	(SEQ ID NO.
П	IREZ_HP0051R50	CAUCAUCAUGAAAGCTTGAAATGAATTATA	(SEQ ID NO.
	1RE3_HP0052R51	CAUCAUCAUTTTAATTTAGGGGTGTTGTTG	(SEQ ID NO.
П	1RE4_HP0053R52	CAUCAUCAUAGCTTATGAAAGAGCAATCAA	(SEQ ID NO.
	1RE5_HP0054R53	CAUCAUCAUTATGCTCTTTGATCAAACCTT	(SEQ ID NO.
	1RE6_HP0055R54	CAUCAUCAUATGGGACATGTTGTTTTAAGT	(SEQ ID NO.
П	1RE7_HP0056R55	CAUCAUCAUAGGTAAGCTCATGCAAAAAAT	(SEQ ID NO.
-	1RE8_HP0057R56	CAUCAUCAUATGAAAACAATTAAAAATGGT	(SEQ ID NO.
-	1RE9_HP0059R57	CAUCAUCAUATGGGAACATTCATTGAAAAA	(SEQ ID NO.
П	1RE10_HP0060R58	CAUCAUCAUATGGTAACACCCTTAAAAAGT	(SEQ ID NO.
-	IRE11_HP0061R59	CAUCAUCAUAGAAAATTATGATGACTAAG	(SEQ ID NO.
7	1RE12_HP0062R60	CAUCAUCAUCGATGAGCAGAGTGCAAATGG	(SEQ ID NO.
Н	1RF1_HP0063R61	CAUCAUCAUTGGTTTATGGCTGAATGGAAA	(SEQ ID NO.

3390)
3391)
3392)
3393)
3394)
3395)
3396)
3398)
3398)
3398)
3399)
3401)
3402)
3405)
3406)
3407)
3408)
3411)
3412)
3411)
3412)
3414)
3416)

	~	7	ì
,	Ċ	h	
	₹	t	•

3453	(SEQ ID NO.	CAUCAUCAUATGCCAAAACCCAAGAAAAC	1RH9 HP0095R93
3452	(SEQ ID NO.	CAUCAUCAUTGAATGGCTTTTAAGGTGGTG	TRHE HP0094R92
3451	(SEQ ID NO.	CAUCAUCAUAGGCGCTTGAGTATATGGCAA	1RH7 HP0093R91
3450	(SEO ID NO.	CAUCAUCAUATGGTAATCGCGCATTCTAAT	1RH6 HP0092R90
3449	(SEQ ID NO.	CAUCAUCAAAAATGAAAAACCATCTGC	1RH5_HP0091R89
3448	(SEQ ID NO.	CAUCAUCAUATGCAATACGCGCTATTATTT	1RH4 HP0090R88
3447	(SEQ ID NO.	CAUCAUCAUGGGAGAAAATGGTGCAAAAAA	1RH3 HP0089R87
3446	(SEQ ID NO.	CAUCAUCAUATGAAAAAAAAGCTAACGAA	1RH2 HP0088R86
3445	(SEQ ID NO.		1RH1 HP0087R85
3444	(SEQ ID NO.	CAUCAUCAUGGAGAAAGACAATGAGTATGG	1RG12 HP0086R84
3443	(SEQ ID NO.		1RG11_HP0085R83
3442	(SEQ ID NO.		1RG10 HP0084R82
3441	(SEQ ID NO.	CAUCAUCAUAAATGAGAAAAATCTATGCTA	1RG9 HP0083R81
3440	(SEQ ID NO.	CAUCAUCAUATGAAATCTACAAGAATTGGT	1RGB HP0082RB0
3439	(SEQ ID NO.	CAUCAUCAUAAGAAATGCCCATGCAGGCTT	1RG7_HP0081R79
3438	(SEQ ID NO.	CAUCAUCAUTATCAATGAAAGCTATAAAAA	1RGK HP0080R78
3437	(SEQ ID NO.	CALICALICATION DA PARAGECATECARARA	7500000 3001
3436	(SEQ ID NO.	CALICALITABATGABAAAGGTTTTTTA	ACA HOOOTBRAG
3435	(SEQ ID NO.	CAUCAUCAUATGTCCATTCTAGCCGAAAAG	1RG3 HP0077R75
3434	(SEQ ID NO.	CAUCAUCAUGCTATGGCAAATCATAAGTCC	1RG2 HP0076R74
3433	(SEQ ID NO.		1RG1 HP0075R73
3432	(SEQ ID NO.		1RF12 HP0074R72
3431	(SEQ ID NO.		1RF11 HP0073R71
3430	(SEQ ID NO.		1RF10 HP0072R70
3429	(SEQ ID NO.	CAUCAUCAUGGCAATGCTAGGACTTGTATT	1RF9 HP0071R69
3428	(SEQ ID NO.	CAUCAUCAUATGATCATAGAGCGTTTAGTT	1RF8 HP0070R68
3427	(SEQ ID NO.	CAUCAUCAUATAACAAATGGATAAAGGAAA	1RF7_HP0069R67
3426	(SEQ ID NO.	CAUCAUCAUATGGTAAAATTGGAGTTTGT	1RF6_HP0068R66
3425	(SEQ ID NO.	CAUCAUCAUTGGAAGATTGATGAACACTTA	1RF5 HP0067R65
3424	(SEQ ID NO.	CAUCAUCAUCGTGAAGCCAAAGAGCATGAA	1RF4_HP0066R64
3423	(SEQ ID NO.	CAUCAUCAUATGTTTTCTCATGAAGTTTAT	1RF3 HP0065R63
3422	(SEO ID NO.	CAUCAUCAUATGGAAACAATTCCTGCAAAC	1RF2 HP0064R62

(SEQ ID NO. 3454	Ω NO.	ID NO.	₽	ID NO.	ID NO.	Š.	ID NO.	ID NO.	ID NO.	ID NO.	ID NO.	ID NO.	ID NO.	ID NO.	ID NO.	\Box	ID NO.	ID NO.	ID NO.	Ō	D NO.	EÓ ID	EQ ID	EQ ID NO.	EQ ID	ന	EQ ID	EQJÍD NO. 3	SEQ ID NO. 348
						• •			_		_	_	<u> </u>		_		_	_			Ÿ			•	<u> </u>	•	<u>ت</u>	:	~

CUACUACUATTTATCCTTTTTAGCTTTTTA CUACUACUACCCTTTTTAAGCGTATGTGTC CUACUACUATTACCATTCTTTAAAGCCAT

CUACUACUACTTTAGCCATTATCTTCCTCT CUACUACUAAGGTTAAAACGCGCAATAAAA CUACUACUATATCAATGTTCAGTTAAGCCA CUACUACUACAAACCTTAAAATTTAGCAAT

> 2SB7_HP0117S115 2SB8_HP0121S119 2SB9_HP0122S120

SB6_HP0116S114

CUACUACUATTAAGCCCTGCAAAGCAACGA CUACUACUACCAATAGAGATTAAAGATGCT CUACUACUACTTAAAAGCTTACAATGTAAC CUACUACUAGATTTTTCAAAGATTTGTTTG

2SC1_HP0126S124 2SC2_HP0127S125 2SC3_HP0128S126

CUACUACUACCGCGATTAGTCTTCATTTT

25B10_HP01235121 25B11_HP01245122 25B12_HP01255123 CUACUACUACTAATGCTTATGATGGCTTGG

CUACUACUATACTATTTTTCAGACTTACTA

2SC4_HP0129S127 2SC5_HP0130S128

CUACUACUAGTTATTGTAAAAGCCTTAAGA

CUACUACUACATCTTTCATTATTCCTCCTC

124

CUACUACUAAGCATTAAAACTGCTTTTTAT CUACUACUACTTACAGCAAATAAAACACT

CAUCAUCAUATTTTATGCCTTTTGTCCCCA

CAUCAUCAUAATGAAAAAATCGTTTTAGT

1RH11_HP0097R95 1RH12_HP0098R96

1RH10 HP0096R94 CAUCAUCAUATAGAGATGAAACATTCAAA

CUACUACUAAATCTTTCTTTAATCGTTTCG

2SA4_HP0102S100

2SA2_HP0100S98 2SA3_HP0101S99

2SA1 HP0099S97

2SA6_HP0104S102 2SA7_HP0105S103 2SA8_HP0106S104

SSAS_HP0103S101

CUACUACUACCCTGATTAAGTTTTAAACAA CUACUACUATTATTTAACTTCACTCTCTTT

CUACUACUACTAAAACGAAACGATTAAAGA

CUACUACUATCAAACCCCCACTTCAGACCA
CUACUACUATGTAATGAAACTTTAGCCTAT
CUACUACUATTATAAATAAATAACTTTTGA
CUACUACUATTCAAGATGGGCTTTTTAAAT
CUACUACUATTCAAGATGGCCTTTTTCAAC
CUACUACUATGCTTTTAAAT

SA10 HP0108S106

2SA9_HP0107S105

2SA11_HP0109S107 2SA12_HP0110S108

2SB1_HP0111S109

2SB2_HP0112S110 2SB3_HP0113S111 2SB4_HP0114S112 2SB5_HP0115S113

2SC6 HP0131S129	CUACUACUATCTGCTTTGATATTCTTAAAA	· (SEQ ID NO.	3486)	
2SC7_HP0132S130	CUACUACUATCCCTTAGCATTTTAAGGTTT	(SEQ ID NO.	3487)	
2SC8_HP0133S131	CUACUACUAGCCATTAAAATAGTCCTAAAA	(SEQ ID NO.	3488)	
2SC9_HP0134S132	CUACUACUATTTTAACTAAGCGTGCTGTT	(SEQ ID NO.	3489)	2
2SC10_HP0135S133	CUACUACUAACAATTTTTTTTTTTTTCAG	(SEQ ID NO.	3490)	
2SC11_HP0136S134	CUACUACUAAAACTACAAACTCTCTAAAAC	(SEQ ID NO.	3491)	
2SC12_HP0137S135	CUACUACUATCTTATCCTTTAGTAGAGAAT	(SEQ ID NO.	3492)	
2SD1 HP0138S136	CUACUACUAAGCTCTTTACTCATAAATCA	(SEQ ID NO.	3493)	
2SD2_HP0139S137	CUACUACUATTAAAGCCCAAGTCTTGAGGC	(SEQ ID NO.	3494)	
2SD3 HP0140S138	CUACUACUATTATTAGGAATGAGGGAT	(SEQ ID NO.	3495)	
2SD4_HP0141S139	CUACUACUAATCTAAAATGGCCCTACTTTA	(SEQ ID NO.	3496)	
2SD5 HP0142S140	CUACUACUAAGGGTTTAACCCCCAAATAAA	(SEQ ID NO.	3497)	
2SD6_HP0144S141	CUACUACUACCTCCCCTATCTAGACATAGG	(SEQ ID NO.	3498)	
2SD7_HP0145S142	CUACUACUACCCTTATTTAGCGTTTTGATT	(SEO ID NO.	3499)	
2SD8_HP0146S143	CUACUACUACATTTCAACTTTCCTTTATGC	(SEQ ID NO.	3200)	
2SD9_HP0147S144	CUACUACUATTAGCGATTGGATAAATTCAG	(SEQ ID NO.	3501)	
2SD10_HP0148S145	CUACUACUATCATTTTTACTCCCTTGATT	(SEQ ID NO.	3502)	
2SD11_HP0149S146	CUACUACUACCTCTTAAGATTTTTTAAAAA	(SEQ ID NO.	3503)	
2SD12_HP0150S147	CUACUACUATITITIAAATGCGITGCTTGA	(SEQ ID NO.	3504)	
2SE1_HP0151S148	CUACUACUATTCTTAATCCAATTCCAATTT	(SEQ ID NO.	3505)	
2SE2_HP0152S149	CUACUACUAGATTAAGAAAAGCGGTATTTT	(SEQ ID NO.	3206)	
2SE3_HP0153S150	CUACUACUAAATCCTTTTTATTCCATTTCT	(SEQ ID NO.	3507)	
2SE4_HP0154S151	CUACUACUACACTAGCCATGCTTAAACAAC	(SEQ ID NO.	3508)	
2SE5_HP0155S152	CUACUACUACTACCATTTCCTTAAATCTA	(SEQ ID NO.	3209)	
2SE6_HP0156S153	CUACUACUAGCTTTTATTTCAATTTTAATT	(SEQ ID NO.	3510)	
2SE7_HP0157S154	CUACUACUATTATGCGATGAATTGTAGCAC	(SEQ ID NO.	3511)	
2SE8 HP0158S155	CUACUACUACTCTTAGCGTTCTCGTTTGGG	(SEQ ID NO.	3512)	
2SE9_HP0159S156	CUACUACUAGAGAACGCTAAGAGTTAAAAA	(SEQ ID NO.	3513)	
2SE10_HP0160S157	CUACUACUAGCTTTAACTTATTGCATATCA	(SEQ ID NO.	3514)	
2SE11_HP0161S158	CUACUACUACCTAAGACCACTTTAAAAAAT	(SEQ ID NO.	3515)	
2SE12 HP0162S159	CUACUACUAGCATTTCACTCAATATTGGTA	(SEQ ID NO.	3516)	
2SF1 HP0163S160	CUACUACUAGICCCATICAATICCITIGIA	(SEQ ID NO.	3517)	

	_	•
¢	3	١
•	-	•
	٧.	

2SF2_HP0164S161	11 CUACUACUAACTTCTCTCAAATTTTCGGGG	(SEQ ID NO.	3518)
2SF3_HP0165S162	32 CUACUACUACAACTCACGCTTTTATCCCCT	(SEQ ID NO.	3519)
2SF4_HP0166S163	33 CUACUACUATCAGTATTCTAATTTATAACC	(SEQ ID NO.	3520)
2SF5_HP0167S164	4 CUACUACUATCGTTTTTCACTCTGTGTTTT	(SEQ ID NO.	3521)
2SF6_HP0168S165	5 CUACUACUATITITCAATICCATICIACCA	(SEQ ID NO.	3522)
2SF7_HP0169S166	6 CUACUACUAGCCATTTTTAGACTCTGACTT	(SEQ ID NO.	3523)
2SF8_HP0170S167	7 CUACUACUAACTACTTGGCTCCAAAAGAAG	(SEQ ID NO.	3524)
2SF9_HP0171S168	8 CUACUACUAGCACTTAAGCTTTAGCAATCA	(SEQ ID NO.	3525)
2SF10_HP0172S169	69 CUACUACUAATTTTAATTTTCAAACCTTAA	(SEQ ID NO.	3526)
2SF11_HP0173S170	70 CUACUACUACCTTTAAAAGATTTTGCTAAT	(SEQ ID NO.	3527)
2SF12_HP0174S171	71 CUACUACUATGAATAAAATCTAGCATTCTT	(SEQ ID NO.	3528)
2SG1_HP0175S172	2 CUACUACUATCAATTACTTGTTGATAACAA	(SEQ ID NO.	3529)
2SG2_HP0176S173	3 CUACUACTITCCTIGITGATTAAATTI	(SEQ ID NO.	3530)
2SG3_HP0177S174	4 CUACUACTCACTTCACCTTTTCAAGAT	(SEQ ID NO.	3531)
2SG4_HP0178S175	5 CUACUACUACTACAATGAGCGTTCTATATC	(SEQ ID NO.	3532)
28G5_HP0179S176	6 CUACUACUATTATTTCTCCTTAATCAAAC	(SEQ ID NO.	3533)
2SG6_HP0180S177	7 CUACUACUATITAATCATGATCGTTTCCTA	(SEQ ID NO.	3534)
2SG7_HP0181S178	8 CUACUACUATTTATAGGGGTTCTTTATTAG	(SEQ ID NO.	3535)
2SG8_HP0182S179	9 CUACUACUAATTATTCTTCACTCTCCACAT	(SEQ ID NO.	3536)
2SG9_HP0183S180	0 CUACUACUATTAAAAATAGGTTGGTGGTA	(SEQ ID NO.	3537)
2SG10_HP0184S181	81 CUACUACUACCTTTCAAAAATGGTTATAAA	(SEQ ID NO.	3538)
2SG11_HP0185S182	82 CUACUACUACTACCGCGCTTCTATGACAAC	(SEQ ID NO.	3539)
2SG12_HP0186S183	83 CUACUACUATTAGTGGGCGGCGAAATCCTT	(SEQ ID NO.	3540)
2SH1_HP0187S184	4 CUACUACUATCAAAACTTCAAAAAGATTTT	(SEQ ID NO.	3541)
2SH2_HP0188\$185	5 CUACUACUATCITACAGATCCCIAAAATTC	(SEQ ID NO.	3542)
2SH3_HP0189S186	6 CUACUACUAAAACTTTTAATGCGCTTTATT	(SEQ ID NO.	3543)
2SH4_HP0190S187	7 CUACUACUATTAAAGCTCTCTTTCAGGAAG	(SEQ ID NO.	3544)
2SH5_HP0191S188	B CUACUACUAAAGAAATTAGCGGCTTTTACC	(SEQ ID NO.	3545)
2SH6_HP0192S189	9 CUACUACUACATTATCACTCATGGTGTTCT	(SEQ ID NO.	3546)
2SH7_HP0193\$190	_	(SEQ ID NO.	3547)
2SH8_HP0194S191	٠.	(SEQ ID NO.	3548)
2SH9_HP0195S192	2 CUACUACUACCTTATTGTTCTTTATGCAAA	(SEQ ID NO.	3549)

٠	٠	۰	

(SEQ IC (SEQ IC (SEQ IC	CAUCAUCAUCTCTTTATGGCCTTTTATGAT CAUCAUCAUATGAAAAATTAGCGGTTTCT CAUCAUCAUTTGGTGTGAAACGGATTTTAT	2RC3_HP0128R126 2RC4_HP0129R127 2RC5_HP0130R128
(SEQ ID (SEQ ID		2RB12_HP0125R123
(SEQ ID		2RB10_HP0123K121 2RB11_HP0124R122
(SEQ ID		2RB9_HP0122R120
OEQID (SEQID	CAUCAUCAUTGTGCGATATATCAAGTTTTT	2RB8_HP0121R119
(SEO ID	CAUCAUCAUTAATGGCTAAAGAAAATCCGC	2RB7_HP0117R115
(SEQ ID	CAUCAUCAUCGTTCCATGAAGCACCTTATT	2RB5_HP0115R113
(SEQ ID	CAUCAUCAUTTATAAGTTAGAALGALGAL	2RB4_HP0114R112
(SEQ ID	CAUCAUCAUACATGACCATCAACACCCATT	2RB3_HP0113R111
GI DES)	CAUCAUCAUATGGIGALIGACGAGALLTTT	2RB1_HP0111R109
(SEQ ID	CAUCAUCAUGGAATAATGAAAGATGAACAC	2RA12_HP0110R108
(SEQ ID	CAUCAUCAUATGGGAAAAGTTATTGGAATT	2RA11 HP0109R107
(SEQ ID	CAUCAUCAUATGCCTAAACTCGTTAAATGG	2RA9_HP010/KLUS
(SEQ ID	CAUCAUCAUCATGCCATGCAAACCAAAAAAAAAAAAAAAA	2RA8_HP0106R104
(SEC ID	CAUCAUCAUACATGAAAACACCAAAAATGA	2RA7_HP0105R103
(SEQ ID	CAUCAUCAUCAATGAAAAATTGGTTTTAG	2RAS_HP0103K101
(SEQ ID	CAUCAUCAUTGGATTGTTAAAAGTTTCTT	2RA4_HP0102R100
(SEQ ID.)	CAUCAUCAUTITGAAAACTCTATITAGTAT	2RA3_HP0101R99
(SEQ ID I	CAUCAUCAUATGCTCATTCATATTTGCTGC	2RA2 HP0100R98
(SEQ ID I	CAUCAUCAUTIGICIAAAGGITIGAGIAIC	2SH12_HPU1985155
(SEQ ID N	CUACUACUACITAAATCITAAAGATCICTA	2SH11_HP0197S194
(SEQ ID N	CUACUACUAGCTTATTATAGCTTATTICAT	
(SEQ ID N	TACATHA CHIPATA CHIPATA CATA	

51)	52).	53)	54)	55)	26)	22)	28)	29)	(09	61)	562)	3563)	(64)	(29)	3566)	(199	(899	(699	3570)	571)	572)	573)	574)	575)	276)	577)	578)	579)	ထ္ထ	581)
355		35	. 355			, 3557					က									က	ന	က	ന	ന	က	က	o.	က		
0	ID NO	0	\Box	<u>∩</u>	9	₽	₽	9	₽	ON DI W	므	=	\sqsubseteq	므	Q ID N	=	=	=	=	=	=	=	=	<u></u>	_ g	ā	<u>a</u>	ō	ON OI O	ø
(SEQ		(SEQ	(SEQ	ш	(SEQ		(SEQ	(SEQ	(SEQ	(SEC	(SEQ	(SEQ	(SEQ	(SE(Ш	(SE	(SEQ	(SE	(SE	(SE	(SEQ	SE.	SE (SE	(SE	(SE	(SE		SE (SE		
															-	-	•										•			
	•														_			٠.	٠.		E	rn		ריז	4	ы	_ ⊲	F-4	ы	E

	2RC6_HP0131R129	CAUCAUCAUATGCCCTATCCTTTTATGAGT	(SEQ ID NO.	3582
	ZRC7_HP0132R130	CAUCAUCAUATGGCTAGTTTTTCTATTTTA	(SEQ ID NO.	3583
	2RC8_HP0133R131	CAUCAUCAUATGGCACAAGAAAAAGCAGTT	(SEQ ID NO.	3584
	2RC9_HP0134R132	CAUCAUCAUAAAGGATTATAGAAATGTCAA	(SEQ ID NO.	3585
	2RC10_HP0135R133	CAUCAUCAUTGAAATGAGAATTTCTCTTTT	(SEQ ID NO.	3586
	2RC11_HP0136R134	CAUCAUCAUAGAATGGAAAAATTAGAAGTA	(SEQ ID NO.	3587
	2RC12_HP0137R135	CAUCAUTAGAAGGGGTGATTTATGAGT	(SEQ ID NO.	3588
	2RD1_HP0138R136	CAUCAUCAUATGATCATGGAAAAATACCAT	(SEQ ID NO.	3589
	2RD2_HP0139R137	CAUCAUCAUGCCTTCTTTGAAAGTCAATTT	(SEQ ID NO.	3590
	2RD3_HP0140R138	CAUCAUCAUTTATGGAATTTTATCAAGTCT	(SEQ ID NO.	3591
	2RD4_HP0141R139	CAUCAUCAUGTGCTAGAATTTCATCAAATT	(SEQ ID NO.	3592
	2RD5_HP0142R140	CAUCAUCAUTGTAGCTGGAAACTTTACACA	(SEQ ID NO.	3593
	2RD6_HP0144R141	CAUCAUCAUTATTGCATGCAAGAAATGTG	(SEQ ID NO.	3594
	2RD7_HP0145R142	CAUCAUCAUGGAGGTTGGAAATGTTTAGTT	(SEC ID NO.	3595
	2RD8_HP0146R143	CAUCAUCAUGGTGAATGATGTTTAGAAA	(SEQ ID NO.	3596
	2RD9_HP0147R144	CAUCAUCAUATGGATTTTTTAAACGACCAT	(SEQ ID NO.	3597
	2RD10_HP0148R145	CAUCAUCAUAAAGAGATGAAATTTTTAAAC	(SEQ ID NO.	3598
•	2RD11_HP0149R146	CAUCAUCAUTGTTTAGCACATGAGAATCTT	(SEQ ID NO.	3599
	2RD12_HP0150R147	CAUCAUCAUAGAGGGAAAATTAATGAAAGA	(SEQ ID NO.	3600
	2RE1_HP0151R148	CAUCAUCAUATGATAAAAGCCTAAATTCC	(SEQ ID NO.	3601
	2RE2_HP0152R149	CAUCAUCAUTTGATTAGTGTCGCTCATAGC	(SEQ ID NO.	3602
	2RE3_HP0153R150	CAUCAUCAUGTAATTTAATGGCAATAGATG	(SEQ ID NO.	3603
	2RE4_HP0154R151	CAUCAUCAUTITGATGCTAACCATTAAAGA	(SEQ ID NO.	3604
	2RES_HP0155R152	CAUCAUCAUGTTGTTTAAGCATGGCTAGTG	(SEQ ID NO.	3605
	2RE6_HP0156R153	CAUCAUCAUATGGTAGTGTTAAAAAAAAGATG	(SEQ ID NO.	3606
	2RE7_HP0157R154	CAUCAUCAUCATGCAGCATTTAGTCTTAAT	(SEQ ID NO.	3607)
	2RE8_HP0158R155	CAUCAUCAUGCCTTTTGATGTTAAGTAGAG	(SEQ ID NO.	3608)
	2RE9_HP0159R156	CAUCAUCAUAATGAGTATTATTATTCCTAT	(SEQ ID NO.	3609)
	2RE10_HP0160R157	CAUCAUCAUGAATGAGATGATAAAGAGTTG	(SEC) ID NO.	3610)
	2RE11_HP0161R158	CAUCAUCAUCCTATGATTAGGGACGCAGAG	(SEQ ID NO.	3611)
	2RE12_HP0162R159	CAUCAUCAUTACAAAGGAATTGAATGGGAC	(SEQ ID NO.	3612)
	2RF1_HP0163R160	CAUCAUCATGTTCAAACGATTGAGAAG	(SEQ ID NO.	3613)

0	١
ℸ	٠

			7777
2RF2_HP0164R161	CAUCAUCAUGGATAAAAGCGTGAGTTGTAA	(SECTIONO.	3014)
2RF3 HP0165R162	CAUCAUCAUTTTGCGTTTCTCTATCTTTT		3615)
2RF4 HP0166R163	CAUCAUCAUATGATAGAAGTTTTAATGATA	(SEQ ID NO.	3616)
2RF5 HP0167R164	CAUCAUCAUAAATGGCTGGTAGAATGGAAT	(SEQ ID NO.	3617)
200 HD01688165	CAUCAUCAUACGCATGCCCTTAGAAACGAT	(SEQ ID NO.	3618)
2017 2017 2017 2017 2017 2017 2017 2017	CAUCAUCAUTITGAACCAAGTIGAATIACT	(SEQ ID NO.	3619)
SOLE TO TO TO TO TO TO TO TO TO TO TO TO TO	CAUCAUCAUAACGACAATGACACAAGAAGA	(SEQ ID NO.	3620)
2012 III 01/2015)	CAUCAUCAUGGTTCTGTTTGTGGATAACTA	(SEQ ID NO.	3621)
2RF10 HP0172R169	CAUCAUCAUAACATGATTAGTTTAAAGAA	(SEQ ID NO.	3622)
2PF11 HP0173R170	CAUCAUCAUGAATGCTAGATTTTATTCAAG	(SEQ ID NO.	3623)
2RF12_HP0174R171	CAUCAUCAUGACTTTGCGCTTAAATTACCC	(SEQ ID NO.	3624)
2RG1 HP0175R172	CAUCAUCAUAACACACAATGAAAAAAAATA	(SEQ ID NO.	3625)
2RG2_HP0176R173	CAUCAUCAUATGTTAGTTAAAGGCAATGAA		3626)
2RG3_HP0177R174	CAUCAUCAUACATGGCAATTGGGATGAGCG	(SEQ ID NO.	3627)
2RG4_HP0178R175	CAUCAUCAUAGAAATGTTACAACCCCCTAA	(SEQ ID NO.	3628)
2RG5 HP0179R176	CAUCAUCAUTCATGATTAAAGCGATTAATA	(SEQ ID NO.	3629)
2RG6 HP0180R177	CAUCAUCAUCATGCGTCTTCTTCTGTTCAA	(SEQ ID NO.	3630)
2RG7_HP0181R178	CAUCAUCAUGTGGTGGTGGTAGCCTTTGGG	(SEQ ID NO.	3631)
2RG8 HP0182R179	CAUCAUCAUCATGTTTTCTAACCAATACAT	(SEQ ID NO.	3632)
2RG9_HP0183R180	CAUCAUCAUGTGGAGAGTGAAGAATAATGG	(SEQ ID NO.	3633)
2RG10 HP0184R181	CAUCAUCAUAGATGACAGAAATGGAATTAA	(SEQ ID NO.	3634)
2RG11_HP0185R182	CAUCAUCAUTGAAAGGATTTTTAATGTCAG	(SEQ ID NO.	3635)
2RG12_HP0186R183	CAUCAUCAUAAATTGAGTGAAGAAGAAGTG		3636)
2RH1 HP0187R184	CAUCAUCAUATGGTTGTCGCTAAGAATGAA	(SEO ID NO.	3637)
2RH2 HP0188R185	CAUCAUCAUGAATGAAAACCACTATAAAAG	(SEQ ID NO.	3638)
2RH3_HP0189R186	CAUCAUCAUTTGAGATGTTGGAAAAATTGA	(SEQ ID NO.	3639)
2RH4_HP0190R187	CAUCAUCAUAGIGGGICGITITIGAAAAIC	(SEQ ID NO.	3640)
2RH5 HP0191R188	CAUCAUCAUAACACCATGAGTGATAATGAA	(SEO ID NO.	3641)
2RH6 HP0192R189	CAUCAUCAUGGTAGAAAATGAAAATAACAT	(SEQ ID NO.	3642)
2RH7 HP0193R190	CAUCAUCAUATGCAACAAGAAGAGATTATA	(SEQ ID NO.	3643)
2RH8 HP0194R191	CAUCAUCAUAAGGATCGTTCAATGACAAAA	(SEO ID NO.	3644)
2RH9_HP0195R192	CAUCAUCAUTCATGGGATTTTTAAAAGGTA	(SEQ ID NO.	3645)

	٩
	:
	i
	1
·	ı

•			
3677)	(SEQ ID NO.	CUACUACUATCATGCAATCCCTTTAGATTT	3SC5_HP0228S224
3675)	(SEQ ID NO.	CUACUACUATTACCCCATAATGAGCTTGTG CUACUACUATTAGTAAGCAAACAAATT	3SC3_HP0226S222 3SC4_HP0227S223
3674)	(SEQ ID NO.	CUACUACUAAATCATTTAAGGCGGTTTTTA	3SC2_HP0225S221
3673)	(SEQ ID NO.	CUACUACUAACCCCTTAATGCGACTTTTTA	3SC1_HP0224S220
3672)	(SEQ ID NO.	CUACUACUATCCAATCACATCCATTCAACA	3SB12_HP0223S219
3671)	(SEQ ID NO.	CUACUACUATTACTCTATTTTTTTAAAGC	3SB11_HP0222S218
3670)	(SEQ ID NO.	CUACUACUAAAAAAGTTCAAATCGGTAACA	3SB10_HP0221S217
3669)	(SEQ ID NO.	CUACUACUATTAATAAGAGCTTGAAATATT	3SB9_HP0220S216
3668)	(SEQ ID NO.	CUACUACUATTAAGGTTTTTTAAGGGGTCT	3SB8_HP0219S215
3667)	(SEQ ID NO.	CUACUACUAAACCTATTTCCTCACAAACTG	3SB7_HP0218S214
3666.)	(SEQ ID NO.	CUACUACUACTATCTTTCCGCTAAATTGAA	3SB6_HP0217S213
3665)	(SEQ ID NO.	CUACUACUACTACACTCCCGCTACATTTTT	3SB5_HP0216S212
3664)	(SEQ ID NO.	CUACUACUAAACCATTCAATCCCCTAAAAA	3SB4_HP0215S211
3663)	(SEQ ID NO.	CUACUACUATAATCAATTAAATATTAACGA	3SB3_HP0214S210
3662)	(SEQ ID NO.	CUACUACUATTAAGAGTTTTTCCGCAAATG	3SB2_HP0213S209
3661)	(SEQ ID NO.	CUACUACUATTGTTTATTTTATGCCTCACT	3SB1_HP0212S208
3660	(SEQ ID NO.	CUACUACUAȚTAAAGTTCTATTTTAATTC	3SA12_HP0211S207
3659	(SEQ ID NO.	CUACUACUACCCCTACAACGCTTTCAATAG	3SA11_HP0210S206
3658	(SEQ ID NO.	CUACUACUAGTTTTAATTTTTAAAAACGAT	3SA10_HP0209S205
3657	(SEQ ID NO.	CUACUACUAACCCTTTTTAAACTAATGCGA	3SA9_HP0207S204
3656	(SEQ ID NO.	CUACUACUATCCTTTAAATTATCTCTTTAG	3SA8_HP0206S203
3655	(SEQ ID NO.	CUACUACUAAATCCTTTCACTTTATAACAT	3SA7_HP0205S202
3654	(SEQ ID NO.	CUACUACUATTTATTTGGAAAATTTATGGT	3SA6_HP0204S201
3653	(SEQ ID NO.	CUACUACUAGGCTTGCTCTAAAGCCATTTG	3SA5_HP0203S200
3652	(SEQ ID NO.	CUACUACUACCTAACTTCCTCCAAAATACA	3SA4_HP0202S199
3651	(SEQ ID NO.	CUACUACUATAGTCATCTTTAAGCGTCTTG	3SA3_HP0201S198
3650	(SEQ ID NO.	CUACUACUAACTAGTATTCTTTAGTAAATT	3SA2_HP0200S197
3649	(SEQ ID NO.	CUACUACUATTTCAATCTGCATAATGGTAG	3SA1_HP0199S196
3648	(SEQ ID NO.	CAUCAUCAUGGAGTTTAAATTGAAACAAAG	2RH12_HP0198R195
3647	(SEQ ID NO.	CAUCAUCAUAAGGACAATCAATGAAAGATA	2RH11_HP0197R194
3646	(SEQ ID NO.	CAUCAUCAUTGATGAAATTAAGCGAATTGT	2RH10_HP0196R193

1	=	-
	7	Ξ
	4	

3SC6_HP0229S225	CUACUACUATGAGAACCGATTCAATATCAA	(SEQ ID NO.	3678)
3SC7_HP0230S226	CUACUACUATTCACCGCTCAAGGAGATCGG	(SEQ ID NO.	3679)
3SC8_HP0231S227	CUACUACUATATATCATGCCTTATAATGGT	(SEQ ID NO.	3680)
3SC9_HP0232S228	CUACUACUATGAATCAATTAAATTATGAGT	(SEQ ID NO.	3681)
3SC10_HP0233S229	CUACUACUAGCTCATTATTGCAACCTATGG	(SEQ ID NO.	3682)
3SC11_HP0234S230	CUACUACUAACCCTACAAAGACCAATAGAT	(SEQ ID NO.	3683)
3SC12_HP0235S231	CUACUACUAGGGGGTTGATTAAATTTTCAA	(SEC) ID NO.	3684)
3SD1_HP0236S232	CUACUACUAGATTAAGGCTTÄGGAGAATCC	(SEQ ID NO.	3685)
3SD2_HP0237S233	CUACUACUAAACAAACGCATTAAAACAACT	(SEQ ID NO.	3686)
3SD3_HP0238S234	CUACUACUACTTATTCGCTTTCTAACATTT	(SEQ ID NO.	3687)
3SD4_HP0239S235	CUACUACUAATTATTCCTCGTAATATTCGC	(SEQ ID NO.	3688)
3SD5_HP0240S236	CUACUACCATTAAAAAGTCCTATAAAT	(SEO ID NO.	3689)
3SD6_HP0241S237	CUACUACUATTCCTTAAGGCTCTTTAGGAG	(SEQ ID NO.	3690)
3SD7_HP0242S238	CUACUACUAGCGGATAAGCTCATTCATTCC	(SEO ID NO.	3691)
3SD8_HP0243S239	CUACUACUATGGTCGCTTAAGCCAAATGGG	(SEQ ID NO.	3692)
3SD9_HP0244S240	CUACUACUACCAAATTAAGAAGCGTTAAGA	(SEQ ID NO.	3693)
3SD10_HP0245S241	CUACUACUAATTTTTTCATGGTTTTTTGTTT	SEQ ID NO.	3694)
3SD11_HP0246S242	CUACUACUATGTTTATCATAGTATCTCCAT	(SEQ ID NO.	3695)
3SD12_HP0247S243	CUACUACUATTAACGGCGTTTGGGTTTTTT	(SEQ ID NO.	3696)
3SE1_HP0248S244	CUACUACUACGTTTTTAAGGCTCTTTAGTC	(SEQ ID NO.	3697)
3SE2_HP0249S245	CUACUACUATTATAAACAAAACAAAGAAAC	(SEQ ID NO.	3698)
3SE3_HP0250S246	CUACUACUATTAAAGCCTGGATTCTAACAA	(SEQ ID NO.	3699)
3SE4_HP0251S247	CUACUACUACCCCCTTATTTGAGCATGTTA	(SEQ ID NO.	3700)
3SE5_HP0252S248	CUACUACUATCCTTAAAAACCGACTGAATA	(SEQ ID NO.	3701)
3SE6_HP0253S249	CUACUACUACGCCACGCTTAAAGGAAGGCT	(SEQ ID NO.	3702)
3SE7_HP0254S250	CUACUACUATTAAAAACCTATCGTGTAATT	(SEQ ID NO.	3703)
3SE8_HP0255S251	CUACUACUATACAGAAGCGAATTTTTTCAT	(SEQ ID NO.	3704)
3SE9_HP0256S252	CUACUACUACAGACCCAATAACAAGATTTT	(SEQ ID NO.	3705)
3SE10_HP0257S253	CUACUACUACGCTACAATGAACATCATAC	(SEQ ID NO.	3706)
3SE11_HP0258S254	CUACUACUATTTTATAGCAAACGAGTGAGA	(SEQ ID NO.	3707)
3SE12_HP0259S255	CUACUACUATCAAACCCCTACACCCTATCC	(SEQ ID NO.	3708)
3SF1_HP0260S256	CUACUACUATTTATCTTAAAATTTCGTATT	(SEQ ID NO.	3709)

	١.
7	ζ
r	
	7

3SF2_HP0261S257	CUACUACUAACTTTATGCAAGATAATTTTC	(SEQ ID NO.	3710)
3SF3_HP0262S258	CUACUACUACTAGCCTTTAGGCTTGTCTTT	(SEQ ID NO.	3711)
3SF4_HP0263S259	CUACUACUAGCTCACACTAACGACAAACTC	(SEQ ID NO.	3712)
3SF5_HP0264S260	CUACUACUAACAAACCTCACTTAATCTTA	(SEQ ID NO.	3713)
3SF6_HP0265S261	CUACUACUACCTCCTATTTTTGCAAGAAT	(SEQ ID NO.	3714)
3SF7_HP0266S262	CUACUACTATGATTTCTTGCATGCATT	(SEQ ID NO.	37.15)
3SF8_HP0267S263	CUACUACUAAATTAGATCACCCTTTTCCCC	(SEQ ID NO.	3716)
3SF9_HP0268S264	CUACUACUATTAAATAATGTGCAATTCATA	(SEQ ID NO.	3717)
3SF10_HP0269S265	CUACUACUATATTTTATTAGTTGCCTTTA	(SEQ ID NO.	3718)
3SF11_HP0270S266	CUACUACUCCTTAAGCACCCAAACCCC	(SEQ ID NO.	3719)
3SF12_HP0271S267	CUACUACUACTAAAACGCATGCTTTTCATT	(SEQ ID NO.	3720)
3SG1_HP0272S268	CUACUACUATCATTTAATAGACTCCGGATT	(SEQ ID NO.	3721)
3SG2_HP0273S269	CUACUACUAATCCTATTGGAGATCAATACT	(SEQ ID NO.	3722)
3SG3_HP0274S270	CUACUACUAAATTTTAGCGCACTTTAGTTT	(SEQ ID NO.	3723)
3SG4_HP0275S271	CUACUACUACCTATTTCTTGCATTCTTGAA	(SEQ ID NO.	3724)
3SG5_HP0276S272	CUACUACUATTAAAATTCAATCTAAAAAGA	(SEQ ID NO.	3725)
3SG6_HP0277S273	CUACUACUATAGCCTTTAATCTTGCTCTTT	(SEQ IĎ NO.	3726)
3SG7_HP0278S274	CUACUACUATCAAGCAAACTCTATCGTCAA	(SEQ ID NO.	3727)
3SG8_HP0279S275	CUACUACUATCTTTGTAAGTCATTCTTTT	(SEQ ID NO.	3728)
3SG9_HP0280S276	CUACUACUACTATCTTTGATAAATCTCAGG	(SEQ ID NO.	3729)
3SG10_HP0281S277	CUACUACUATTCAATGAGAGCGGGAGTTGT	(SEQ ID NO.	3730)
3SG11_HP0282S278	CUACUACUACATTCTTTCACTCCGCTACAG	(SEQ ID NO.	3731)
3SG12_HP0283S279	CUACUACUTAATGCCATTTTTCTAAC	(SEQ ID NO.	3732)
3SH1_HP0284S280	CUACUACUATTTCATTTTTTTTTTTTTTTTTTTTTTTTT	(SEQ ID NO.	3733)
3SH2_HP0285S281	CUACUACUATTTTAGAAAACGGCATGATT	(SEQ ID NO.	3734)
3SH3_HP0286S282	CUACUACUATCACCCGTTCAATAAATCATA	(SEQ ID NO.	3735)
3SH4_HP0287S283	CUACUACUACTICCACCITITITAAGAITT	(SEQ ID NO.	3736)
3SH5_HP0288S284	CUACUACUAAAGGGACTAAAGCACATTTTT	(SEQ ID NO.	3737)
3SH6_HP0289S285	CUACUACUAGAACGAAGCATTATAGCAAAA	(SEQ ID NO.	3738)
3SH7_HP0290S286	CUACUACUATCAAACCCCTTTTAAGCCTTC	(SEQ ID NO.	3739)
3SH8_HP0291S287	CUACUACUTTTTTTTTTTTAACTCTTT	(SEQ ID NO.	3740)
3SH9_HP0292S288	CUACUACUAAAATCCCCAAAAATCATTTA	(SEQ ID NO.	3741)

		עטבע
3SH10_HP0293S289	CUACUACUAGCTCTGTTTTTATAGTTATT	ייייייייייייייייייייייייייייייייייייי
3SH11 HP0294S290	CUACUACUACCICCITITIGCCCTITIAITIC) (SE)
38H12 HP0295S291	CUACUACUAACCACCAAAAGATTACAAGTA)as)
38A1 HP0199R196	CAUCAUCAUATGCAATTTGAAATGCGTAAA	(SEC
3RA2 HP0200R197	CAUCAUCAUTTTATGGCAGTACCTGATAGA	(SEC
HP0201R198	CAUCAUCAUCGCATGATGAAAATTGTAATA	SE(
	CAUCAUCAUATGGAATTTTACGCCTCTCTT) SE(
3RA5 HP0203R200	CAUCAUCAUATGAAAAGGTTGTTTTTTA	(SE(
3RA6 HP0204R201	CAUCAUCAUTTTTGATGTTTAAAAAAATGT	(SE(
3RA7 HP0205R202	CAUCAUCAUTTGAGCGAGCTTGTAACTGAA	(SE(
3RA8 HP0206R203	CAUCAUCAUATGGAATTTTATAAGCGTGTT	(SE(
3RA9 HP0207R204	CAUCAUCAUAAATGGTGCAATTTCAAAACA	SE(
3RA10 HP0209R205	CAUCAUCAUAGGGTGCTTAATCAAAAAGTT	(SE(
3RA11 HP0210R206	CAUCAUCAUGGAAAAGATCAATGTCTAATC	(SE(
3RA12 HP0211R207	CAUCAUCAUATGCTAGGAAACGTTAAAAAA	(SE(
3RB1 HP0212R208	CAUCAUCAUGCATGGACGCTTTAGAAATCA	SE(
	CAUCAUCAUGAGTGGTAAAAGAAAGTGATA	(SE
3RB3 HP0214R210	CAUCAUCAUAATAAAATGGAAAATCATTCG	(SE
3RB4 HP0215R211	CAUCAUCAUGGAAAAAGTGAAAGAAGAGT	(SE
3RB5 HP0216R212	CAUCAUCAUTAGGGGATTGAATGGTTGTTT	(SE
3RB6_HP0217R213	CAUCAUCAUTATGGGGTTAAAAAATAAAAT	(SE
3RB7 HP0218R214	CAUCAUCAUAAAAGGGCTTAAAAATGAAAAC	SE)
3RB8 HP0219R215	CAUCAUCTTTTTTTGGTGGTTAGTAT	(SE
3RB9 HP0220R216	CAUCAUCAUACCTTGTTACAACGAATTTAT	SE SE
3RB10 HP0221R217	CAUCAUCAVAAATGGCAAAACATGATTTAG	SE)
3RB11 HP0222R218		(SE
3RB12 HP0223R219	CAUCAUCAUGIGATITIAAAAAAAGAGIGGI	SE)
3RC1 HP0224R220	CAUCAUCAUCAATGAAGGTATTATCTTATT	SE)
3RC2 HP0225R221	CAUCAUCAUATGAGGGGTTTAAGCGTTTGG	SE)
3RC3 HP0226R222	CAUCAUCAUTTTTTTATGGAAGAATCAACA	SE)
3RC4_HP0227R223	CAUCAUCAUAACATGAAAAAATCCCTCTTA	es)
3RC5_HP0228R224	CAUCAUTAATGAGAAAGAAAGGCATGT	S)

	-	
TTATAGTTATTT	(SEQ ID NO.	3742)
GCCTTTATTTC	(SEQ ID NO.	3743)
AGATTACAAGTA	(SEQ ID NO.	3744)
GAPATGCGTAAA	(SEQ ID NO.	3745)
GTACCTGATAGA	(SEQ ID NO.	3746)
AAAATTGTAATA	(SEQ ID NO.	3747)
TACGCCTCTCTT	(SEQ ID NO.	3748)
GTTGTTTTTA	(SEQ ID NO.	3749)
TTAAAAAATGT	(SEQ ID NO.	3750)
CTTGTAACTGAA	(SEQ ID NO.	3751)
TATAAGCGTGTT	(SEQ ID NO.	3752)
AATTTCAAAACA	(SEQ ID NO.	3753)
AATCAAAAAGTT	(SEQ ID NO.	3754)
CAATGTCTAATC	(SEQ ID NO.	3755)
AACGTTAAAAAA	(SEQ ID NO.	3756)
CTTTAGAAATCA	(SEQ ID NO.	3757)
AAGAAGTGATA	(SEQ ID NO.	3758)
GAAAATCATTCG	(SEQ ID NO.	3759)
TGAAAGAAGAGT	(SEQ ID NO.	3760)
GAATGGTTGTTT	(SEQ ID NO.	3761)
PAAAATAAAT	(SEQ ID NO.	3762)
TAAAATGAAAAC	(SEQ ID NO.	3763)
GGTGGTTAGTAT	(SEQ ID NO.	3764)
CAACGAATTTAT	(SEQ ID NO.	3765)
AACATGATTTAG	(SEQ ID NO.	3766)
AGACAGAAAACA	(SEQ ID NO.	3767)
AAAAAGAGTGGT	(SEQ ID NO.	3768)
STATTATCTTATT	(SEQ ID NO.	3769)
TTTAAGCGTTTGG	(SEQ ID NO.	3770)
SGAAGAATCAACA	(SEQ ID NO.	3771)
AAAATCCCTCTTA	(SEQ ID NO.	3772)
APGREGATET	(SEQ ID NO.	3773)

2	2	L
٩	•	2
4	•	1

3RC6_HP0229R225	CAUCAUCAUTITAIGAAAAAAACGAITITIA	(SEQ ID NO.	3774)
3RC7_HP0230R226	CAUCAUCAUATGATTATCATTCCTGCTAGG	(SEQ ID NO.	3775)
3RC8_HP0231R227	CAUCAUCAUAATGATATTAAGAGCGAGTGT	(SEQ ID NO.	3776.)
3RC9_HP0232R228	CAUCAUCAUATGAAAAACCCTATAGGAAG	(SEQ ID NO.	3777)
3RC10_HP0233R229	CAUCAUCAUTAAAAATGCAAGTGATTCCT	(SEQ ID NO.	3778)
3RC11_HP0234R230) CAUCAUCAUCAATAATGAGGGCAATGATGC	(SEQ ID NO.	3779)
3RC12_HP0235R231	. CAUCAUCAUATGGGTGTCAAATTTTTAAAA	(SEQ ID NO.	3780)
3RD1_HP0236R232	CAUCAUCAUTTGTTTTAATGCGTTTGTTTA	(SEQ ID NO.	3781)
3RD2_HP0237R233	CAUCAUCAUAGTGGGAAATTTAGTGATTGG	(SEQ ID NO.	3782)
3RD3_HP0238R234	CAUCAUCAUCATGCTATTTTCAAAACTCTT	(SEQ ID NO.	3783)
3RD4_HP0239R235	CAUCAUCAUAGGACTTTTTAATGGAGTTAG	(SEQ ID NO.	3784)
3RD5_HP0240R236	CAUCAUCAUATGCAAGAAAAACAACTTAAA	(SEQ ID NO.	3785)
3RD6_HP0241R237	CAUCAUCAUTCAGCGGGAATGAATGAGCTT	(SEÓ ID NO.	3786)
3RD7_HP0242R238	CAUCAUCAUAGCCAGCATGAGAGATTACAG	(SEQ ID NO.	3787)
3RD8_HP0243R239	CAUCAUCAUGATGAAAACATTTGAAATTCT	(SEQ ID NO.	3788)
3RD9_HP0244R240	CAUCAUCAUATGAAAAATCCAAGCACTTA	(SEQ ID NO.	3789)
3RD10_HP0245R241	CAUCAUCAUGAGATACTATGATAAACAACA	(SEQ ID NO.	3790)
3RD11_HP0246R242	CAUCAUCAUTGATTGAAACGGGTGTTTTTA	(SEQ ID NO.	3791)
3RD12_HP0247R243	CAUCAUCAUCCCATGGAATTGAATCAACCA	(SEQ ID NO.	3792)
3RE1_HP0248R244	CAUCAUCAUATGCCCATTGATTTGAACGAA	(SEQ ID NO.	3793)
3RE2_HP0249R245	CAUCAUCAUAACGCATGGCATCTCTTGCCT	(SEQ ID NO.	3794)
3RE3_HP0250R246	CAUCAUCAUGTTATATGCTAGAAATCAAAA	(SEQ ID NO.	3795)
3RE4_HP0251R247	CAUCAUCAUGAGCGTGAGCAGTTTGTTTAA	(SEQ ID NO.	3796)
3RES_HP0252R248	CAUCAUCTIGAAAACCACTCCTTTAAA	(SEQ ID NO.	3797)
3RE6_HP0253R249	CAUCAUCAUATGAAAATACCAATACAAAA	(SEC) ID NO.	3798)
3RE7_HP0254R250	CAUCAUCAUGTGGCGTTAGCTGAAGACGAT	(SEQ ID NO.	3799)
3RB8_HP0255R251	CAUCAUCAUTTTTATGGCAGATGTCGTTGT	(SEQ ID NO.	3800)
3RE9_HP0256R252	CAUCAUCAUCTATGAAAAAATTCGCTTCTG	(SEQ ID NO.	3801)
3RE10_HP0257R253	CAUCAUCAUATGCGTAAAATCTTGTTATTG	(SEQ ID NO.	3802)
3RE11_HP0258R254	CAUCAUCAUGGGGTATGATGTTCATTGTAG	(SEQ ID NO.	3803)
3RE12_HP0259R255	CAUCAUCAUGGAGCTGGTGGATGTATTGAG	(SEQ ID NO.	3804)
3RF1_HP0260R256	CAUCAUCAUGGGAAAATTATCTTGCATAAA	(SEQ ID NÓ.	3805)

3806	3807	3808	3809	3810	3811	3812	3813	3814	3815	3816	3817	3818	3819	3820	3821	3822	3823	3824	3825	3826	3827	3828	3829	3830	3831	3832	3833	3834	3835	œ	3837
D NO.	ON OI C	ON QI C	Q ID NO.	ON OI O	a ID NO.	Q ID NO.	Ω	Z □	Ω	Z □	Z Q	Ω	Z <u>Q</u>	Ω	Ω	Q ID NO.	ΩN	Ω Ω	Ω	₽	Ω	Q ID NO.	Ω	O ID NO	Ž	O ID NO.	Ž	Ω	Q ID NO.	Ž Q	a ID NO.
(SE	(SE	(SE	(SE	(SE	(SE	(SE	(SE	(SE()ES)	(SEQ	(SE	(SE	(SE	SE(SE((SE	ш	ш	ш	(SE	(SE	ш	SE(ш	ш	ш	ш	Ш	SE(Ш	(SE

CAUCAUCAUAGGAGTTAGTCATGTCATTAT CAUCAUCAUGCAATGGCTAAAATCACAACC CAUCAUCAUGATAGAGTTTGCTTGAAAATA

CAUCAUCAUGAATGCAAGAAATAGGGATTT

CAUCAUCAUCTTAAACGATGGATTTTCAAC CAUCAUCAUTTTTAGGAAGTTTGGAATTGA

CAUCAUCAUATGACTTACAAAGAACGACTC

CAUCAUCAUATGGCATTAAGGGTATTGTTA CAUCAUCAUAGGGAACAAAAATGAAAAAG CAUCAUCAUATCCTTTTTTTTTTT CAUCAUCAUATGCGTTTTTTTAGTGGTTTT

3RH1 HP0284R280

3RH2 HP0285R281

3RH3_HP0286R282 3RH4_HP0287R283 3RH5_HP0288R284

CAUCAUCAUTGAAAGAATGCAAGAAATTTT

3RG11_HP0282R278 3RG12_HP0283R279

3RG10 HP0281R277

3RG8_HP0279R275 3RG9_HP0280R276 CAUCAUCAUGGTTTTTCTATGTTTAATTAT CAUCAUCAUATGCAAAAGAATTTGGATAGT CAUCAUCAUAGTTGTTATGTTTGAAAAAT

3RH9_HP0292R288

CAUCAUCAUATGAAAAAGTTTAAAAAGAAA

3RH6_HP0289R285 3RH7_HP0290R286 3RH8_HP0291R287

CAUCAUCAUGGTGCTTAAGGGGTTAAAAAA

CAUCAUCAUGATGATTGGGTTTGCGTATTT

3RF10_HP0269R265 3RF11_HP0270R266

3RF9_HP0267R263 3RF9_HP0268R264 3RF12 HP0271R267

3RG1_HP0272R268 3RG2_HP0273R269

3RG4_HP0274R270 3RG4_HP0275R271 3RG5_HP0276R272 3RG6_HP0277R273

CAUCAUCAUAGAGTCAATGAAACTAGTTTT CAUCAUCAUCTTGTATTGAAAGTTTATATT CAUCAUCAUAATGAAGCCATTGCATTTTTC CAUCAUCAUATGCAAGATTTTGATTTTAGT CAUCAUCAUATGAATATTCAAATAAAGAAA

CAUCAUCAUAGCATGCGTTTTAGTTACATT

CAUCAUCAUGACATGCAATTTTTAAATCAA
CAUCAUCAUATGGATTCTTTTTTAAGG
CAUCAUCAUATGAAACCTTATTTCAGTTTA
CAUCAUCAUAAAGGATTGATAATGAATTTA
CAUCAUCAUTTGAAAAAGGATTGATGAATGATG
CAUCAUCAUAGGGTTTGATGATTAAAAA
CAUCAUCAUATGCAAGAAATCATAAAAA

3RF2 HP0261R257

3RF3_HP0262R258 3RF4_HP0263R259 3RF5_HP0264R260 3RF6_HP0265R261 3RF7_HP0266R262

		•
0	3	_
•		_

3RH10_HP0293R289 CAUCAUCAUATGATTTTTGGGGATTTTAAA 3RH11 HP0294R290 CAUCAUCAUATATGAGACATGGAGATATA
CAUCAUCAUTCATGCGCGTTACCTTTGGCT
CUACUACUATTATGCTACAATTTTAGTGAT
CUACUACUACTACTCCCCAAAATTTTGACT
CUACUACUATITATITITCTAAATACACCI
CUACUACUAATTATGACAACCTTATTCTAG
CUACUACUACATGCAAGCTCCTTTTAAGAG
CUACUACUATCATCGCAACTCCTTTTGAAA
CUACUACUATTTATTTGGCAAATCTTTGCA
CUACUACUATTAGGGTAACGCTTCCAACAA
CUACUACUATTCATGGCGATCGGAGTTTCA
CUACUACUATTATCCCTTGATCATGCTTTC
CUACUACUAAAATTCACACACCTTTTATGA
CUACUACUATTATTTTGTTTTATTTTGTGT
CUACUACUATTGTGTCAAAACTTACCATTA
CUACUACUAGCTCCTTTTTAAGTGAATTTT
CUACUACUATCGCTATTTTTTTTTAGGGTT
CUACUACUAGGGATTTTGGGCCATCAGTGAA
CUACUACUATTATTGGGTTTCAAAACCCTT
CUACUACUATTCTATTTATGGATAGCTGTT
CUACUACUATTAAAATTTTTGGCACTTATA
CUACUACUACTAGGATTTCACAATCTCAGT
CUACUACUATCAAACGCTAAAGCATACATT
CUACUACUAAGCTTAGTAAGCGAACACATA
CUACUACUATTATTTCTTGTGAGCGAAATT
CUACUACUAGCTTAATCTCTAGCGGAAATT
CUACUACUATTAACTTTCTTGTTTGCTTTT
CUACUACUAGTTTTATAGGGTTTCGTTTTT
CUACUACUATTATGCATTAGGTTTTTTATC
CUACUACUATTTAAAACCCAACGCAACTCC
CUACUACUATTTAGAAGTGGTAATTATACC

4SC6 HP0325S321	CUACUACUATTTTAATAAGGCATTTGGGTT	(SEQ ID NO.	3870)
4SC7_HP0326S322	CUACUACUAGAATAATTTTTTTTCAAATCT	(SEQ ID NO.	3871)
4SC8_HP0327S323	CUACUACCCTAAAGTTTTAGAAGAGAT	(SEQ ID NO.	3872)
4SC9_HP0328S324	CUACUACUAGAGITTATAGACGTTCTTTTG	(SEQ ID NO.	3873)
4SC10 HP0329S325	CUACUACUATCATTCAGGGTTAAATCGTTT	(SEQ ID NO.	3874)
4SC11 HP0330S326	CUACUACUATGATTTATTTTTATGATTGA	(SEQ ID NO.	3875)
4SC12_HP0331S327	CUACUACUACTCATGAAATATCCCTTTTA	(SEQ ID NO.	3876)
4SD1 HP0332S328	CUACUACUACTATTABATATATATCTC	(SEQ ID NO.	3877)
4SD2 HP0333S329	CUACUACUAAATCACGCTAACACCACAATG	(SEQ ID NO.	3878)
4SD3 HP0334S330	CUACUACUATCCCTAATGATTTTTTCAAAAC	(SEQ ID NO.	3879)
4SD4_HP0335S331	CUACUACUATTCACACGCTTTAACATAGTA	(SEQ ID NO.	3880)
4SD5 HP0336S332	CUACUACUATCAAATCTAGTAGTTGTTTAA	(SEQ ID NO.	3881)
4SD6_HP0337S333	CUACUACUACTATTTCCTTGCTCATTGTC	(SEQ ID NO.	3882)
4SD7_HP0338S334	CUACUACUATTTTAATTCCCCTTATTATT	(SEQ ID NO.	3883)
4SD8_HP0339S335	CUACUACUATCCAATTTCCAAAATTTCCATA	(SEQ ID NO.	3884)
4SD9_HP0340S336	CUACUACUATTATTCCCCAAGCAAAATACA	(SEQ ID NO.	3885)
4SD10 HP0341S337	CUACUACUATTAAAGCCTCCCTAAATTACT	SEQ ID NO.	3886)
4SD11 HP0342S338	CUACUACUATTATTTTTATCCCTCTTGTT	(SEQ ID NO.	3887)
4SD12_HP0343S339	CUACUACUATCTAGACATCAGCATCAAATA	(SEQ ID NO.	3888)
4SE1_HP0344S340	CUACUACUACATCATTTCCATACTCACTC	(SEQ ID NO.	3889)
4SE2_HP0345S341	CUACUACUAATCTTTATAATATCGGTAGG	(SEQ ID NO.	3890)
4SE3_HP0346S342	CUACUACUATTATTGATTGATCTTTTGGTT	(SEQ ID NO.	3891)
4SE4_HP0347S343	CUACUACUATCAATAAAAAAGGATAGATC	(SEQ ID NO.	3892)
4SE5_HP0348S344	CUACUACUACACTACAACAACTTTTAACA	(SEQ ID NO.	3893)
4SE6_HP0349S345	CUACUACUATTGTTAGATTTAGAA	(SEQ ID NO.	3894)
4SE7 HP0350S346	CUACUACUATCGTTTAGATCTTTTGAAACA	(SEQ ID NO.	3895)
4SE8 HP0351S347	CUACUACUAACCTTCTATCTTTTAACCTTT	(SEQ ID NO.	3896)
4SE9 HP0352S348	CUACUACUACTATTCAATGACATCTTCCTC	(SEQ ID NO.	3897)
4SE10 HP0353S349	CUACUACUACAAATCACACCTTAAAATTT	(SEQ ID NO.	3898)
4SE11_HP0354S350	CUACUACUATTTCATCTCTCTTGTCCTAAA	(SEQ ID NO.	3899)
4SE12_HP0355S351	CUACUACUACGCCCTAATCGATCTTTAATA		3900)
4SF1_HP0356S352	CUACUACUAGTTATTTTATTTGCCCTATTA	(SEQ ID NO.	3901)

4SF2_HP0357S353	CUACUACUATTAAGGGTTTTTTATGGGTGGG	(SEQ ID NO.	3902)
4SF3_HP0358S354	CUACUACUATTAAAAAGCCCCTTAAGCCC	(SEQ ID NO.	3903)
4SF4_HP0359S355	CUACUACUATAGCTCAGCTGGGAGAGCGCC	(SEQ ID NO.	3904)
4SF5_HP0360S356	CUACUACUATTATTGAAACCTCAAAAGGTG	(SEQ ID NO.	3905)
4SF6_HP0361S357	CUACUACUACCTTTTGAGGTTTCAATAATA	(SEQ ID NO.	3906)
4SF7_HP0362S358	CUACUACUATCAATAACGCTTTAAAATGAA	(SEQ ID NO.	3907)
4SF8_HP0363S359	CUACUACUATTATTGCACCCCATCTACAAC	(SEQ ID NO.	3908)
4SF9_HP0364S360	CUACUACUACCTTAAAAATCATCAAAACTC	(SEQ ID NO.	3909)
4SF10_HP0365\$361	CUACUACUATAGGGCTTCAAATCTTAATCA	(SEQ ID NO.	3910)
4SF11_HP0366S362	CUACUACUAACTCATTCTATTTAAAACTC	(SEQ ID NO.	3911)
4SF12_HP0367S363	CUACUACUATCGCTATAAGCAAACTCTTTC	(SEQ ID NO.	3912)
4SG1_HP0368S364	CUACUACUAAAAATATTAATCTAATCCTA	(SEQ ID NO.	3913)
4SG2_HP0369S365	CUACUACUATTGTTCTAAGTCCATCAATTA	(SEQ ID NO.	3914)
4SG3_HP0370S366	CUACUACUAAACTTAAAAATTTTCTTCTAA	(SEQ ID NO.	3915)
4SG4_HP0371S367	CUACUACUATTAAAGCTTTTCAACTTTGAT	(SEQ ID NO.	3916)
4SG5_HP0372S368	CUACUACUATCACTTTAAAATTTTAGGCAA	(SEQ ID NO.	3917)
4SG6_HP0373S369	CUACUACUACCTAAAAATCCACCCGTAAT	(SEQ ID NO.	3918)
4SG7_HP0374S370	CUACUACUACCCCCTAAACTTGTGCGATAC	(SEQ ID NO.	3919)
4SG8_HP0375S371	CUACUACUATCAAAGGCCCCATTAACACAAC	(SEQ ID NO.	3920)
4SG9_HP0376S372	CUACUACUATACTATTCCTTGAGGTTTTTA	(SEQ ID NO.	3921)
4SG10_HP0377S373	CUACUACUAAGGCTTTCCTAGTTAGACTTG	(SEQ ID NO.	3922)
4SG11_HP0378S374	CUACUACUATGGTTATCCTTTAAGCTAATT	(SEQ ID NO.	3923)
4SG12_HP0379S375	CUACUACUACCAATTTTACAAACCCAATTT	(SEQ ID NO.	3924)
4SH1_HP0380S376	CUACUACUAGGTTTGTAAATTGGGGGTAA	(SEQ ID NO.	3925)
4SH2_HP0381S377	CUACUACUATTTATCTTAAAAAACTTTTTA	(SEQ ID NO.	3926)
4SH3_HP0382S378	CUACUACUAAAAGGGTCATTCAATTTCATA	(SEQ ID NO.	3927)
4SH4_HP0383S379	CUACUACUATTATTGGATTTTTATAAAGCCA	(SEQ ID NO.	3928)
4SH5_HP0384S380	CUACUACUACGATTACTTTTCCACCAACAC	(SEQ ID NO.	3929)
4SH6_HP0385S381	CUACUACUAATGTTTTAATGGTTTATGAC	(SEQ ID NO.	3930)
4SH7_HP0386S382	CUACUACUAGGAGCGATTAAGTGATAGAAC	(SEQ ID NO.	3931)
4SH8_HP0387S383	CUACUACUATTAAAAATATCCACAGGATC	(SEQ ID NO.	3932)
4SH9_HP0388S384	CUACUACUATTTCAAAAAACTTAAGTTTTT	(SEQ ID NO.	3933)

7	7	
ч		Ġ
	ú	۶

	4SH10 HP0389S385	CUACUACUAAAATAACGCTTAAGCTTTTTT	(SEO ID NO	3934)
	4SH11_HP0390S386	CUACUACUAGATTTCCTATTTCAACACTTT	(SEQ ID NO.	3935)
	4SH12_HP0391S387	CUACUACUAGITITIAGAAGICITITITA	(SEQ ID NO.	3936)
	4RA1_HP0296R292	CAUCAUCAUAAATGTCATACGCAATATTCA	(SEQ ID NO.	3937)
	4RA2_HP0297R293	CAUCAUCAUCAATGGCACACAAAAAAGGTC	(SEQ ID NO.	3938)
	4RA3_HP0298R294	CAUCAUCAUGACTGGCTTATGAATAATGTT	(SEQ ID NO.	3939)
	4RA4_HP0299R295	CAUCAUCAUATGCTGAGTTTTTATCATTAAG	(SEQ ID NO.	3940)
	4RA5_HP0300R296	CAUCAUCAUATGGAGTCTTTAGAGAGTTT	(SEQ ID NO.	3941)
	4RA6_HP0301R297	CAUCAUCAUGCATGATTTTAGAAGTTAAAG	(SEQ ID NO.	3942)
	4RA7_HP0302R298	CAUCAUCAUGATGAAGCTCTTAGAAATTAA	(SEQ ID NO.	3943)
	4RA8_HP0303R299	CAUCAUCAUGATTTTTAAGCTGTGTTTTGTA	(SEQ ID NO.	3944)
	4RA9_HP0304R300	CAUCAUCAUATGAAAAGATTTGTTTTTTT	(SEQ ID NO.	3945)
	4RA10_HP0305R301	CAUCAUCAUAATGAAAAAAATGGTTTTTGGT	(SEQ ID NO.	3946)
	4RA11_HP0306R302	CAUCAUCAUTCATGGAGTTGTTGCACAGCA	(SEQ ID NO.	3947)
	4RA12_HP0307R303	CAUCAUCAUAAAGGTGTGTGAATTTTTTGA	(SEQ ID NO.	3948)
	4RB1_HP0308R304	CAUCAUCAACAATCCCATGTGCCAAATCC	(SEQ ID NO.	3949)
	4RB2_HP0309R305	CAUCAUCAUGGGAGTGGATCTTGAAAACAA	(SEQ ID NO.	3950)
	4RB3_HP0310R306	CAUCAUCAUTTATGGCAAAAGAAATTTTAG	(SEQ ID NO.	3951)
	4RB4_HP0311R307	CAUCAUCAUTGGAAGATGTGCGTTTTATGC	(SEQ ID NO.	3952)
	4RB5_HP0312R308	CAUCAUCAUATGCCCAAAATCCCTATCACG	(SEQ ID NO.	3953)
	4RB6_HP0313R309	CAUCAUCAUAATGCGCGTGTTTGTTTGCTT	(SEQ ID NO.	3954)
	4RB7_HP0314R310	CAUCAUCAUATGCGATTGTTGCATTTTTT	(SEQ ID NO.	3955)
	4RB8_HP0315R311	CAUCAUCAUAAAGGTTTTGAAAATGTATGC	(SEQ ID NO.	3956)
	4RB9_HP0316R312	CAUCAUCAUAGGAATAAGCATGCCTAACAC	(SEQ ID NO.	3957)
	4RB10_HP0317R313	CAUCAUCAUAAAAACATGAAAAAAACACATC	(SEQ ID NO.	3958)
	4RB11_HP0318R314	CAUCAUCAUATGCTTAATCGTATCATAGAA	(SEQ ID NO.	3929)
•	4RB12_HP0319R315	CAUCAUCAUAGCATGCACACTCTCATTAAG	(SEQ ID NO.	3960)
	4RC1_HP0320R316	CAUCAUCAUGTATGGGCGGATTCACAAGCA	(SEQ ID NO.	3961)
	4RC2_HP0321R317	CAUCAUCAUCCTAATGCATAATGATTTTAA	(SEQ ID NO.	3962)
	4RC3_HP0322R318	CAUCAUCAUATGAAATGATTCTATTCAAC	(SEQ ID NO.	3963)
	4RC4_HP0323R319	CAUCAUCAUTGATGTTAAACAAGTTTAAAA	(SEQ ID NO.	3964)
	4RC5_HP0324R320	CAUCAUCAUATGAAACTTAACTTGCAGGAG	(SEQ ID NO.	3965)

	•
v	٦
_	•

בכימורנסמון למת		
4KC0_HFU363K361	CAUCAUCADAGGCTAGTGGATGAAAAAGC	(SEQ ID NO.
4RC7_HP0326R322	CAUCAUCAUATGAGAGCGATCGCTATTGTT	(SEO ID NO.
4RC8_HP0327R323	CAUCAUCAUTTTAGAGATTTGAAAAAAAT	(SEQ ID NO.
4RC9_HP0328R324	CAUCAUCAUCCTGAATGAAAGCGATAAAC	(SEQ ID NO.
4RC10_HP0329R325	CAUCAUCAUAGGCATGCAAAAAGATTACCA	(SEQ ID NO.
4RC11_HP0330R326	CAUCAUCAUATTTTGGCATTACCCCGTTTAT	(SEQ ID NO.
4RC12_HP0331R327	CAUCAUCAUGGAATCATATGGCAATAGTAG	(SEQ ID NO.
4RD1_HP0332R328	CAUCAUCAUTICATGAGTTTGTTTTGTTTTT	(SEQ ID NO.
4RD2_HP0333R329	CAUCAUCAUAGTGAATCAACGAATGAAAAG	(SEQ ID NO.
4RD3_HP0334R330	CAUCAUCAUTGTGGTGTTAGCGTGATTTTG	(SEQ ID NO.
4RD4_HP0335R331	CAUCAUCAUGGGGGGTTAATGGCAGAGCCA	(SEQ ID NO.
4RD5_HP0336R332	CAUCAUCAUCGATGGTAGGGGGTGGAACGG	(SEQ ID NO.
4RD6_HP0337R333	CAUCAUCAUAAAACGGATAACCATGAAAAT	(SEQ ID NO.
4RD7_HP0338R334	CAUCAUCAUCGACAATGAGCAAGGAAAATA	(SEQ ID NO.
4RD8_HP0339R335	CAUCAUCAUGTGGATTCAGAGGGGTTTTCG	(SEQ ID NO.
4RD9_HP0340R336	CAUCAUCAUCAAGGAATATGGAAATTTTGA	(SEQ ID NO.
4RD10_HP0341R337	CAUCAUCAUATGCTAAAGAATTTCAAAAAG	(SEQ ID NO.
4RD11_HP0342R338	CAUCAUCAUGTGAGCGTGGAATTTGCTTCT	(SEC) ID NO.
4RD12_HP0343R339	CAUCAUCAUATGTCTTATTTTTTAAAATC	(SEQ ID NO.
4RE1_HP0344R340	CAUCAUCAUGGGGTTTGTTTTTGCACTAT	(SEQ ID NO.
4RE2_HP0345R341	CAUCAUCAUGAGTGAGTATGGAAAATGATG	(SEQ ID NO.
4RE3_HP0346R342	CAUCAUCAUTGTGGATAAGTTCTTGGATTG	(SEQ ID NO.
4RE4_HP0347R343	CAUCAUCAUTGTTGTAGTGCCTTTTTGTTGA	(SEQ ID NO.
4RE5_HP0348R344	CAUCAUCAUAAATCCTAATCTAACAAATGA	(SEQ ID NO.
4RE6_HP0349R345	CAUCAUCAUTATGGATAGAGCCAAATTTAT	(SEQ ID NO.
4RE7_HP0350R346	CAUCAUCAUTAAATAATGGCTGAAAATTCT	(SEQ ID NO.
4RE8_HP0351R347	CAUCAUCAUTAATATTGGATTTTAAAGGTAT	(SEQ ID NO.
4RE9_HP0352R348	CAUCAUCAUAATGGCAACCAAGCTTACCCC	(SEQ ID NO.
4RE10_HP0353R349	CAUCAUCAUATGTCATTGAATAGCCGTAAG	(SEQ ID NO.
4RE11_HP0354R350	CAUCAUCAUGTGATTTTGCAAAATAAAACT	(SEQ ID NO.
4RE12_HP0355R351	CAUCAUCAUGACAAGAGAGATGAAAACAAA	(SEQ ID NO.
4RF1_HP0356R352	CAUCAUCAUCTICTATGGCAAAACATAAGA	(SEQ ID NO.

					-																										
3300)	3967)	3968)	3969)	3970)	3971)	3972)	3973)	3974)	3975)	3976)	3977)	3978)	3979)	3980)	3981)	3982)	3983)	3984)	3985)	3986)	3987)	3988)	3989)	3990)	3991)	3992)	3993)	3994)	3995)	3996)	Č
ב ב ב	E0 ID	EQ ID	EQ 1D 1	₽	000	EQID	0.00	<u> </u>	0 0 E	10103	O O	ig p	O D	d di	d o	~	N QI O	Q ID	O ID	N QI O	N OI O	N O O	N O	N Q Q	NOO	N O O	EO ID N	EQ ID N	EO ID N	(SEQ ID NO.	
																														•	

CAUCAUCAUAAAATCTCATCATGTTCTATC CAUCAUCAUATGAAAGACACTCTGTTTAAT

> 4RH9_HP0388R384 4RH8_HP0387R383

4RH5_HP0384R380

4RH3_HP0382R378 4RH4_HP0383R379

1RH2_HP0381R377

4RH1 HP0380R376

1RH7 HP0386R382

4RH6_HP0385R381

CAUCAUCAUCCAATGGATTTAATCAATGAA

4RG11_HP0378R374 4RG12_HP0379R375

4RG10_HP0377R373

4RG7_HP0374R370 4RG8_HP0375R371 4RG9_HP0376R372

4RG6_HP0373R369 4RG5_HP0372R368

CAUCAUCAUCATGCTAAGATTCGTTAGTAA CAUCAUCAUATGCGTTTTGTCTATCACCCT CAUCAUCAUAAGAAGTTAATGTTAGAGATG

CAUCAUCAUTCCATGAATAAAGTGAATAAA CAUCAUCAUAGGAATAGATCGTTATGAACC CAUCAUCAUAGGCTTTGTGCGTATGGGATT

CAUCAUCAUGIGAAGITAITAAAAAATACG CAUCAUCAUGIGCITAACGCIAIAGAIGGA

CAUCAUCAUGGAACAAAATGGAAGTTTCAC CAUCAUCAUGAAGTGGCGAAATTGGTAGAC CAUCAUCAUTIGAAAGAGTTTGCTȚATAGC CAUCAUCAUATGTCTAAGATTTCAAATAAT

4RF10_HP0365R361

4RF8_HP0363R359 4RF9 HP0364R360

4RF7_HP0362R358

4RF5_HP0360R356 4RF6_HP0361R357

4RF3_HP0358R354 4RF4_HP0359R355

1RF2_HP0357R353

4RF12_HP0367R363

4RG1_HP0368R364 4RG2_HP0369R365 4RG3_HP0370R366 4RG4_HP0371R367

4RF11_HP0366R362

CAUCAUCAUGGGCTTGTTTGAATAGTATTA

CAUCAUCAUAGGGGTTTTATGGCATTATTA CAUCAUCAUCGTTATTGAATGCGTTGTTTT CAUCAUCAUTAAAGCATGATTAAACACTAT

CAUCAUCAUATGGTGGAGAATAGCGGGATC CAUCAUCAUATGAAAAAACTTCTTTATACC CAUCAUCAUAATGGCGCACATTTTAGTTAG

4RH10_HP0389R385	5 CAUCAUCAUCATGTTTACATTACGAGAGTT	(SEQ ID NO.	4030)
4RH11_HP0390R386	S CAUCAUCATGCAAAAGTTACTTTTAA	(SEQ ID NO.	4031)
	7 CAUCAUCAUAATCGTGAGCAACCAATTAAA	(SEQ ID NO.	4032)
5SA1_HP0392S388	CUACUACTCACGATTGGTCTCCTTCTA	(SEQ ID NO.	4033)
5SA2_HP0393S389	CUACUACUAATTACGCATTCTTGTCTAAAA	(SEO ID NO.	4034)
5SA3_HP0394S390	CUACUACUAATTTAGGCGTCCTTATTTTGA	(SEQ ID NO.	4035)
5SA4_HP0395S391	CUACUACUAGCATCTTACTCTTTGAACAAA	(SEQ ID NO.	4036)
5SA5_HP0396S392	CUACUACUATTCTTTATAGATCTTCTTTGT	(SEQ ID NO.	4037)
5SA6_HP0397S393	CUACUACUAACCTTAAATAACCACATAATG	(SEO ID NO.	4038)
5SA7_HP0398S394	CUACUACUATGAATTTAAAAAACAGCATGA	(SEQ ID NO.	4039)
5SA8_HP0399S395	CUACUACUTTTAGAGTTTTTCTTTAAGA	(SEQ ID NO.	4040)
5SA9_HP0400S396	CUACUACUAGIGITAAAICGIGCIGAITIT	(SEQ ID NO.	4041)
5SA10_HP0401S397	CUACUACUATTAATTTCCATTAAGACTCCC	(SEQ ID NO.	4042)
5SA11_HP0402S398	3 CUACUACUATCIATCACATATTATCCTTTA	(SEQ ID NO.	4043)
5SA12_HP0403S399	OUACUACUAATTAAAAGCTCTCCAACACTC	(SEQ ID NO.	4044)
5SB1_HP0404S400	CUACUACUACGCTTTTAATGTTTGTCTCCG	(SEQ ID NO.	4045)
5SB2_HP0405S401	CUACUACUATAGCTTAACGCAATTTTTAA	(SEQ ID NO.	4046)
5SB3_HP0406S402	CUACUACUTAATTTAAAACTACTTTT	(SEQ ID NO.	4047)
5SB4_HP0407S403	CUACUACUAACTCTTTTAAGCCCCAATAA	(SEQ ID NO.	4048)
5SB5_HP0408S404	CUACUACUATCATCGCTCATTCTTTATTTT	(SEQ ID NO.	4049)
5SB6_HP0409S405	CUACUACUATCATTCCCATTCAATCGTTCC	(SEQ ID NO.	4050)
5SB7_HP0410S406	CUACUACUAACTACTTTCGTTTTTTTTTTT	(SEQ ID NO.	4051)
5SB8_HP0411S407	CUACUACUATTAAATGAGATGGGGTGGAAG	(SEQ ID NO.	4052)
5SB9_HP0412S408	CUACUACUATCAATCTTTAGAAAAAAAAA	(SEQ ID NO.	4053)
5SB10_HP0413S409	CUACUACUATTIGITITAGACTTITAACACCT	(SEQ ID NO.	4054)
5SB11_HP0414S410	CUACUACUACTAATTTAATGCGGTGTTTCT	(SEQ ID NO.	4055)
5SB12_HP0415S411	CUACUACUATCTACCAATAATTTCAGATTT	(SEQ ID NO.	4056)
5SC1_HP0416S412	CUACUACUATCTGAAATTATTGGTAGATGT	(SEQ ID NO.	4057)
5SC2_HP0417S413	CUACUACUATTAGCTGATCAAACTTCCTGC	(SEQ ID NO.	4058)
5SC3_HP0418S414	CUACUACUAAAATGAGCATGATTTACCATA	(SEQ ID NO.	4059)
5SC4_HP0419S415	CUACUACUATTATTTAACGCTTGCTTGGTT	(SEQ ID NO.	4060)
5SC5_HP0420S416	CUACUACUACTACTCTTTAAAATTGAA	(SEQ ID NO.	4061)
			1,

. 00	4062)	4063)	1064)	4065)	4066)	4067)	4068)	4069)	4070)	4071).	4072)	4073)	4074)	4075)	4076)	4077)	4078)	4079)	4080)	4081)	4082)	4083)	4084)	4085)	4086)	4087)	4088)	4089)	4090)	4091)	4092)	4093)
٠.	(SEC ID NO. 4	(SEQ ID NO. 4	(SEQ ID NO. 4	(SEQ ID NO. 4	Š.	(SEQ ID NO. 4	ò.	(SEQ ID NO. 4	(SEQ ID NO. 4	(SEQ ID NO. 4	(SEQ ID NO. 4	(SEQ ID NO. 4	(SEQ ID NO. 4	(SEQ ID NO. 4	(SEO ID NO. 4	Ö.	Š.		Ö.	Š.	9	(SEQ ID NO. 4	9	(SEQ ID NO. 4	(SEQ ID NO. 4	D NO.	ò.	(SEQ ID NO. 4	9	0		(SEQ ID NO. 4
	CUACUACUATTATGATAAGGTTTTTAAAGAG	CUACUACUATTAAGAAATCGTGCGCAAATA	CUACUACUAGAGTGGGGGGGGTTTTATTCTA	_	1 CUACUACUATTATAAGGCTTGTAAGCTTTT	_	m	_			CUACUACUACTICTAACTCCATAAACTACC		CUACUACUAACTCAGCATTTTTGAACCTTA	CUACUACUATTAGGATTGGCGCTTCAAACC	CUACUACUACACGCATAGAAGAATTAAAAA	CUACUACUATACTCATAGGGTTTTTTATAGT	3 CUACUACUAATTAACCTTGATTTTCTATAT	4 CUACUACUAAACCGCTAAAGCGATTGGCTT	5 CUACUACUAGGAGCTATGAAGCAAGAAAAA	CUACUACUATCATTTCTTTGTCTTTTTTGTG	CUACUACUACCTACTCCTTTGTCAAGTAAA	CUACUACUAATTTTCTCAAGCATAATAATT	CUACUACUATCTAAAATAACCATTGACTTA	CUACUACUATTTGTTTTCATCTTTCATGTC	CUACUACUAACTTCAATCGCGGTCTACTAC	CUACUACUACTTTATGATGCTAAAATTTCC	_	CUACUACUAACATCAGCCTAGGAAGCCCAA	5 CUACUACUACTCATCGTTTCTCCTTTAGAT	6 CUACUACUATITIAGATAAACTITITITIT	7 CUACUACUATGCTACTTTTAAGAAGTTTT	CUACUACUATGATTTATTCATCCTCTTCTG
	5SC6_HP0421S417	5SC7 HP0422S418	5SC8 HP0423S419	5SC9 HP0424S420	5SC10 HP0425S421	5SC11_HP0426S422	5SC12 HP0427S42	5SD1 HP0428S424	5SD2 HP0429S425	5SD3_HP0430S426	5SD4_HP0431S427	5SD5_HP0432S428	5SD6_HP0433S429	5SD7_HP0434S430	5SD8 HP0435S431	5SD9_HP0436S432	5SD10_HP0437S433	5SD11_HP0438S434	5SD12 HP0439S43	5SE1_HP0440S436	5SE2_HP0441S437	5SE3 HP0442S438	5SE4_HP0443S439	5SE5 HP04448440	5SE6_HP0445S441	5SE7 HP0446S442	5SE8_HP0447S443	5SE9 HP0448S444	5SE10 HP0449S445	5SE11 HP0450S446	5SE12 HP0452S447	5SF1_HP0453S448

0	1
- Z	:
₽	!
O	(
S	(
<i>:</i> -	•

CUACUACUATTAGGTTTTAATGTCTTTGCC CUACUACUAGCGTGAATTTTAAAACAACAT CUACUACUATCACACAGAACTTGGATAATA CUACUACUATCCTTTTAAGCGTAAAATGAA

5SF2 HP0454S449 5SF3 HP0455S450

NSDOCID: <WO

5SF5 HP0457S452 5SF6_HP0458S453 5SF7_HP0459S454 5SF8_HP0460S455 5SF9 HP0461S456

5SF4 HP0456S451

4096) 4097 SEQ ID NO

SEQ ID NO

1098) 4099) 4100)

SEO ID NO. SEQ ID NO

> CUACUACUAGTTTTCATTTAAGCACCTTT CUACUACUATCAAATTTGCGAGCTTAAAGC

CUACUACUATTAGCCTTTGTGTGTTCTTTT CUACUACUATTTTCATTGGGGTTTGACTTG CUACUACUACAGGGTTTAGAGAATAATTTT CUACUACUATTAGGCATGCGGATTTCCTTG CUACUACUATGTAAAAATAAAATCATGGT CUACUACUATTAGGAGTCTTTTAAATCATT CUACUACUACCTTTATGAGTATTTTTCAT CUACUACUAATCTTAAATGAAAGTAACCTT

> 5SF11_HP0463S458 5SF12-HP0464S459

5SG1 HP0465S460

5SG2 HP0466S461

5SF10_HP0462S457

CUACUACUATTAAGGGCGCTTTCTAACATT

SEQ ID NO SEQ ID NO

4102)

4103 4104

4101

SEQ ID NO

SEC ID NO SEQ ID NO

4105 4106

SEQ ID NO

SEO ID NO. SEQ ID NO

4108 4109

4107

SEQ ID NO

SEQ ID NO SEQ ID NO

4111

4110

SEQ ID NO SEQ ID NO

CUACUACUATTAGAAAGTAAAGACATAATC

CUACUACUATTATCATAAAAACGAGCTTTG CUACUACUATTCTAAAATTTTTTTTTTTGA

5SG10 HP0474S469 5SG11_HP0475S470 5SG12_HP0476S471

5SG9 HP0473S468

5SG8 HP0472S467

58G7

CUACUACUATTAATCCACAATATAGCCGTA

CUACUACUACCTAAAACTATAAACGTAAC

5SH1 HP0477S472

5SH2: HP0478S473 5SH3_HP0479S474 5SH4 HP0480S475

CUACUACUAAGAGCCAATTTTTTAGTTTTT

CUACUACUAATTATCCCCTAAAGCCAAAAG CUACUACUAGAAGTATAACACAATATTATA CUACUACUATTATTTTTCGCCCTTTTCCT

CUACUACUACTTGTTATTTAAAAGCCTTAA CUACUACUATTATTTTTAGCCGGCTCATT

5SG6 HP0470S465 HP0471S466

5SG5 HP0469S464

CUACUACUACTTTAGCTTTTGTGCAGATTT

4113)

4112

4114)

SEQ ID NO SEC ID NO

SEQ ID NO

4115 4116

4117 4118 4119) SEQ ID NO SEQ ID NO SEQ ID NO

4120 4121 SEQ ID NO SEQ ID NO.

CUACUACUAATTTTAGAATTTTCTAACACA

5SH5 HP0481S476

5SH6 HP0482S477 5SH7_NP0483S478 5SH8 HP0484S479 5SH9_HP0485S480

CUACUACUACTAATCTTTGCCCTGCTCTTG

CUACUACUACATCTTACCCCTTTAAAAGT

CUACUACUATTTATGAAAGCGGCTTATTAG

CUACUACUATTTATTGCCTTCTGCTAAAAG

4122:) SEO ID NO. SEQ ID NO SEQ ID NO

514

5SG4 HP0468S463

5SG3 HP0467S462

1	K K H D C H K K K K K K K K K K K K K K K K K K	CEO ID
5SH11_HP0487S482	CUACUACUATAAATGCTAGTAAATCCTAA	בי לבי היים לי
5SH12 HP0488S483	CUACUACUATITAATITITIGIGGIAGGAT	(SEQ ID
5RA1 HP0392R388	CAUCAUCAUATGGATGATTTGCAAGAAATA	(SEQ ID
	CAUCAUCAUATGGCAGAAAAAAACAGCTAAC	(SEQ ID
5RA3 HP0394R390	CAUCAUCAUCAAAGAGTAAGATGCTAGAAA	(SEQ ID
	CAUCAUCAUATGTTAGATTATCGCCAAAAA	(SEQ ID
5RA5 HP0396R392	CAUCAUCAUGGTAGTTGGATGCGAGATTTT	(SEQ ID
5RA6 HP0397R393	CAUCAUCAUAATGTATCAAGTAGCCATTTG	(SEQ ID
5RA7 HP0398R394	CAUCAUCAUATGAGATTTAAGGGTGTTGTT	(SEQ ID
5RA8 HP0399R395	CAUCAUCAUCAATGAGCAAGATAGCAGAGC	(SEQ ID
5RA9_HP0400R396	CAUCAUCAUATGGAAATTAAAATGGCTAAG	(SEQ ID
5RA10 HP0401R397	CAUCAUCAUTGTGATAGAGCTTGACATTAA	(SEQ ID
5RA11 HP0402R398	CAUCAUCAUAATGAAACTGAGCATTAATGA	(SEQ ID
5RA12 HP0403R399	CAUCAUCAUCGTTATTGCACACCTTAATAG	(SEQ ID
5RB1 HP0404R400	CAUCAUCAUATGAATGTGTTTGAAAAAAA	(SEQ ID
SRB2_HP0405R401	CAUCAUCAUGTGCAAGCGTTTTTAAATAGG	(SEQ ID
SRB3 HP0406R402	CAUCAUCAUAATTTGGATATTTAGATTTG	(SEQ ID
5RB4_HP0407R403	CAUCAUCAUATGTCCATTTCACGCAGAAGT	(SEQ ID
5RB5 HP0408R404	CAUCAUCAUTATAAGGATAAAAGATGAATA	(SEQ ID
5RB6_HP0409R405	CAUCAUCAUCGATGATTTTAGTATTAGATT	(SEQ ID
5RB7 HP0410R406	CAUCAUCAUAGGAATTTAATGAAAAAAGGT	(SEQ ID
5RB8 HP0411R407	CAUCAUCAUTGAGTGCCGCTTTTGATTTTA	(SEQ ID
SRB9_HP0412R408	CAUCAUCAUGGAGTTATGGATTCTTTAGAG	(SEQ ID
5RB10 HP0413R409	CAUCAUCAUTTCTATGAAAGTCAATAAGGG	(SEQ ID
5RB11 HP0414R410	CAUCAUCAUGGICIAIGAAAAAAAIIGAIG	(SEQ ID
SRB12 HP0415R411	CAUCAUCAUATGCGTTTATTATTGTGGTGG	(SEQ ID
5RC1 HP0416R412	CAUCAUCAUGATGATTTCAAAATTTTTGCT	OEO ID
5RC2 HP0417R413	CAUCAUCAUGATTATAAAGATGCAAAAATC	(SEQ ID
5RC3 HP0418R414	CAUCAUCAUATGCGATTAGGGGTGAATGAA	(SEQ ID
5RC4_HP0419R415	CAUCAUCAUGGTAAATCATGCTCATTTGTA	OSEO ID
5RC5 HP0420R416	CAUCAUCAUAAGATAGTGCAAGAATCAGTC	(SEQ ID

		4128)	4129)	4130)	4131)	4132)	4133)	4134)	4135)	4136)	4137)	4138)	4139)	4140)	4141)	4142)	4143)	4144)	4145)	4146)	4147)	4148)	4149)	4150)	4151)	4152)	4153)			~	4157)
	O O	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEO ID NO.	(SEQ ID NO.	Ž Q Ø	(SEQ ID NO.
) !) ! ; ;	ATCCTAA	3TAGGAT	AGAAATA	AGCTAAC	CTAGAAA	CCAAAAA	AGATTTT	CCATTTG	TGTTGTT	ġcagagc	GGCTAAG	ACATTAA	TTAATGA	TTAATAG	AAAAATA	AAATAGG	AGATTTG	CAGAAGT	ATGAATA	TTAGATT	AAAAGGT	GATTTTA	TTTAGAG	ATAAGGG	ATTGATG	GTGGTGG	TTTTGCT	AAAAATC	GAATGAA	ATTTGTA	ATCAGTC

	5RC6_HP0421R417	CAUCAUCAUAGAAGAGTAGTTAAATGGTTA	(SEQ ID NO.	4158)
	5RC7_HP0422R418	CAUCAUCAUATGCAAGAAGTCCATGATTAT	(SEQ ID NO.	4159)
	SRC8_HP0423R419	CAUCAUCAUTATGGGTTTTCAAAATGAAAA	(SEQ ID NO.	4160)
•	5RC9_HP0424R420	CAUCAUCAUATGTTATTGGATTATGATTTT	(SEQ ID NO.	4161)
	5RC10_HP0425R421	CAUCAUCAUATGCCTAAAAAAAGAGCTATTA	(SEQ ID NO.	4162)
	5RC11_HP0426R422	CAUCAUCAUATGATGGCAAAAATAGATGTA	(SEQ ID NO.	4163)
	5RC12_HP0427R423	CAUCAUCAUATACCCCATGTCATCTTTTT	(SEQ ID NO.	4164)
	5RD1_HP0428R424	CAUCAUCAUATGAGTGCGTCTTTGGGTGAT	(SEQ ID NO.	4165)
	5RD2_HP0429R425	CAUCAUCAUCTATGAATGAAAATGGGAAAA	(SEQ ID NO.	4166)
		CAUCAUCAUTIGITGITGAGCGATGGGCAT	(SEQ ID NO.	4167)
	5RD4_HP0431R427	CAUCAUCAUCGATTAAGCAATGAGAGATTT	(SEQ ID NO.	4168)
	5RD5_HP0432R428	CAUCAUCAUTTATGGAGTTAGAAGAAATTG	(SEQ ID NO.	(4169)
	5RD6_HP0433R429	CAUCAUTTGAAACGCCCTACTATGCCC	(SEQ ID NO.	4170)
	5RD7_HP0434R430	CAUCAUCAUGGTTCAAAAATGCTGAGTTTT	(SEQ ID NO.	4171)
	5RD8_HP0435R431	CAUCAUCAUACGATGGATGAAGTCTTAAAA	(SEQ ID NO.	4172)
	5RD9_HP0436R432	CAUCAUCAVAAATGAGAGCTTTTTTTAATT	(SEQ ID NO.	4173.)
	5RD10_HP0437R433	CAUCAUCAUGGATAGAGGAATGAGGAAAAA	(SEQ ID NO.	4174)
	5RD11_HP0438R434	CAUCAUCAUATITITGCTITAACGCTATCAA	(SEQ ID NO.	4175)
	5RD12_HP0439R435	CAUCAUCAUCATAGGCTAGTTGATGTCAAA	(SEQ ID NO.	4176)
	5RE1_HP0440R436	CAUCAUCAUAAGGAGTAGGAATGAAAGATA	(SEQ ID NO.	4177)
	SRE2_HP0441R437	CAUCAUCAUTATGCTTGAGAAAATTTTTAA	(SEQ ID NO.	4178)
	5RE3_HP0442R438	CAUCAUCAUAGATGGCATTGCATATTGTTT	(SEQ ID NO.	4179)
	5RE4_HP0443R439	CAUCAUCAUTGAAAGATGAAAACAAACAT	(SEQ ID NO.	4180)
	5RES_HP0444R440	CAUCAUCAUTATGGCTTATATCGCTAATTT	(SEÓ ID NO.	4181)
	SRE6_HP0445R441	CAUCAUCAUAATGCAATTCCCACTCAAAAA	(SEQ ID NO.	4182)
	5RE7_HP0446R442	CAUCAUCAUGGACCATGCAAGAAAGAGTTT	(SEQ ID NO.	4183)
	5RE8_HP0447R443	CAUCAUCAUCCCAACGAAGAAGTAGTGTCC	(SEQ ID NO.	4184)
	5RE9_HP0448R444	CAUCAUCAUTATGAAAATTATTAGCTTTGA	(SEQ ID NO.	4185)
	5RE10_HP0449R445	CAUCAUCAUAGTGGAGTTTTTTGCAGACTC	(SEQ ID NO.	4186)
	5RE11_HP0450R446	CAUCAUCAUAACGATGAGCGGGAATGAAGA	(SEQ ID NO.	4187)
	5RE12_HP0452R447	CAUCAUCAUAAATGGCAGATGAAACGAACG	(SEQ ID NO.	4188)
	5RF1_HP0453R448	CAUCAUCAUTGCAATGGATCTAGAAGAACT	(SEQ ID NO.	4189)

r	-
3	_
7	_
u	_

SRF2 HP0454R449	CAUCAUCAUGGTGTTGGAATTGAAATTAAT	(SEQ ID NO.	4190)
SRF3 HP0455R450	CAUCAUCAUAAAATGTTTTTGCAAGTTGTA	(SEQ ID NO.	4191)
	CAUCAUCAUAAAGGAAAACAATGATTAAAC	(SEQ ID NO.	4192)
5RF5 HP0457R452	CAUCAUCAUCCATGCAATTAGTTGGTATTT	(SEQ ID NO.	4193)
5RF6 HP045BR453	CAUCAUCAUATGCAAAAAAAGAAGTCTTAGTA	(SEQ ID NO.	4194)
5RF7_HP0459R454	CAUCAUCAUGAAAGTCTTCTTAATGTTAGA	(SEQ ID NO.	4195)
5RF8_HP0460R455	CAUCAUCATGTCTAATTTGCAAGAACT	(SEQ ID NO.	4196)
5RF9 HP0461R456	CAUCAUCAUGTTAAATGAAGTTTTTATTCAA	(SEQ ID NO.	4197)
5RF10 HP0462R457		(SEQ ID NO.	4198)
SRF11 HP0463R458		(SEQ ID NO.	4199)
SRF12 HP0464R459		(SEQ ID NO.	4200)
5RG1 HP0465R460		(SEQ ID NO.	4201)
5RG2 HP0466R461	CAUCAUCAUAATGGAAATCATTTTTATTGAT	(SEQ ID NO.	4202)
5RG3 HP0467R462	CAUCAUCAUATGCGCATTATCATAAGGTTA	(SEQ ID NO.	4203)
5RG4_HP0468R463	CAUCAUCAUGATGAGCGTTTTGAAATTGCA	(SEQ ID NO.	4204)
5RG5 HP0469R464	CAUCAUCGCATGCAAAGAGAATTAAGG	(SEQ ID NO.	4205)
5RG6 HP0470R465	CAUCAUCAUCATGAAAGAGCAAGAATGGGA	(SEQ ID NO.	4206)
5RG7 HP0471R466	CAUCAUCAUATGGAAAACAGCACACTTTAT	(SEQ ID NO.	4207)
5RG8 HP0472R467	CAUCAUCAUGAAGGATTTATTATGATTAAA	(SEQ ID NO.	4208)
5RG9 HP0473R468	CAUCAUCAUAGGGAGTTCTATGAAAAATAC	(SEQ ID NO.	4209)
5RG10 HP0474R469		(SEQ ID NO.	4210)
5RG11 HP0475R470	CAUCAUCAUATGATAAAAGCGCGGTTTAAA	(SEQ ID NO.	4211)
5RG12 HP0476R471		(SEO ID NO.	4212)
5RH1 HP0477R472		(SEQ ID NO.	4213)
	CAUCAUCAUGGGGGTAAATGCCTTCAAACG	(SEQ ID NO.	4214)
5RH3 HP0479R474	CAUCAUCAUAATCATGCATGTTGCTTGTCT	(SEQ ID NO.	4215)
5RH4 HP0480R475	CAUCAUCAUAGGACATTTATGAAAAATATT	(SEQ ID NO.	4216)
	CAUCAUCAUGAATGCATGCCAATTTATTCA	(SEO ID NO.	4217)
	CAUCAUCAUATGCATATTAGCGAAGTCAAA	(SEQ ID NO.	4218)
	CAUCAUCAUTTTCTATGCACCCTTATTT	(SEQ ID NO.	4219)
	CAUCAUCAUAGGGGTAAGATGTTTAACAAT	(SEQ ID NO.	4220)
5RH9 HP0485R480	CAUCAUCAUCAAGAATGAAAAAAATTGGTT	(SEQ ID NO.	4221)

				٠
	SRH10_HP0486R481	CAUCAUCAUGAATGAAATTAAAGAAACGAA	(SEQ ID NO.	422
	5RH11_HP0487R482		(SEQ ID NO.	422
	5RH12_HP0488R483	CAUCAUCAUAGGAGTGAAGTTACCCAAAGC	(SEQ ID NO.	422
	6SA1_HP0489S484	CUACUACUACTCAAATCCTTGACTTTCTTC	(SEQ ID NO.	422
	6SA2_HP0490S485	CUACUACUACAATCACAATGAAATGTAATC	(SEQ ID NO.	422
	6SA3_HP0491S486	CUACUACUAAAAACCCTAAACGGCTAAGC	(SEQ ID NO.	422
	65A4_HP0492S487	CUACUACUAACTACTTTTTTTGAGGCATAG	(SEQ ID NO.	4228
	6SA5_HP0493S488	CUACUACUATTTTCATTTTAACGCACCTTC	(SEQ ID NO.	422
	6SA6_HP0494S489	CUACUACUACGCTTTAATCCTTTAAAACAA	(SEQ ID NO.	423(
	6SA7_HP0495S490	CUACUACUAGATTAAAGCGTTTGAACCACT	(SEQ ID NO.	4231
	6SA8_HP0496S491	CUACUACUATCAGATGGCATTGAGCAGCTC	(SEQ ID NO.	4232
	6SA9_HP0497S492	CUACUACUATTAATAAATCTTGCTCAACCA	(SEQ ID NO.	4233
	6SA10_HP0498S493	CUACUACUATATTTCACTTAAATTGCAAGA	(SEQ ID NO.	4234
	6SA11_HP0499S494	CUACUACUATTAAGGGTTTAAGCGTATTCC	(SEQ ID NO.	423£
	6SA12_HP0500S495	CUACUACUATCAGCCTTTATAGTGTGATTG	(SEQ ID NO.	4236
	6SB1_HP0501S496	CUACUACUAAAAATCCCTTACACATCTAGT	(SEQ ID NO.	4237
	6SB2_HP0502S497	CUACUACUATCAATATCCGCTCCTATTTT	(SEQ ID NO.	4238
	6SB3_HP0503S498	CUACUACUACACTAAATTCAAACTCA	(SEO ID NO.	4239
	6SB4_HP0504S499	CUACUACUATTTTAAACTAAAAGGGATTTT	(SEQ ID NO.	4240
	6SB5_HP0505S500	CUACUACUATGTTAATTTTGAAGTATTTTT	(SEQ ID NO.	4241
	6SB6_HP0506S501	CUACUACUAATAAGACATTAAAAACCCTCT	(SEQ ID NO.	4242
	6SB7_HP0507S502	CUACUACUATCCTTTTAAACATTTTTAAAC	(SEQ ID NO.	4243
	6SB8_HP0508S503	CUACUACUATIGGICTAACAIGTIAITITI	(SEQ ID NO.	4244
	6SB9_HP0509S504	CUACUACUATCCTTGCTTTAAATCTTACAA	(SEQ ID NO.	4245
	6SB10_HP0510S505	CUACUACUAAAAACATTCAACCAAACATCT	(SEQ ID NO.	4246
	6SB11_HP0511S506	CUACUACUATGTGCTTCTTTTCTATAAAC	(SEQ ID NO.	4247
	6SB12_HP0512S507	CUACUACUACATTGTTTTAGCATGAATAAG	(SEQ ID NO.	4248
	6SC1_HP0513S508	CUACUACUATTATTGCCTATTCCTACCACC	(SEQ ID NO.	4249
	6SC2_HP0514S509	CUACUACUACTACTCAGCCACCACATCAAT	(SEQ ID NO.	4250
	6SC3_HP0515S510	CUACUACUATTAAAGCTCCAAAATTTTAAT	(SEQ ID NO.	4251
•	6SC4_HP0516S511	CUACUACUACATCATAAAATATACTTCACC		4252
	6SC5_HP05175512	CUACUACUATCAATCCCTATTCCTTCTATG	(SEQ ID NO.	4253

4254)	4255)	4256)	4257)	4258)	4259)	4260)	4261)	4262)	4263)	4264)	4265)	4266)	4267)	4268)	4269)	4270)	4271)	4272)	4273)	4274)	4275)	4276)	4277)	4278)	4279)	4280)	4281)	4282)	4283)	4284)	4285)
(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEO ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	. (SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	. (SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.
CUACUACUATTTTTCTTATTTTTCCATTAT	CUACUACUACTACAGAGCTTCCATGGCTTT	CUACUACUAGTTTTGCCTCAATCTTTAGTC	CUACUACUAAACTTACTTTGAATCTTTCAG	CUACUACUACTACTCGTTATATCGCACTTG	CUACUACUATTGTCTTAATCACAGTTCACT	CUACUACUAACTACCTGTGTTTGATATAAA	CUACUACUATCTTATTCCAAATTTAATTTT	CUACUACUACTTGAATTAATTGCCACCTTT	CUACUACUAACGCCTTTTTATTTTATCTCTG	CUACUACUAGGCTTATCCTTTAAACATAGA	CUACUACUATTCTTATTTAATGCCTT	CUACUACUATCATTCTGCACCGCCTTGTTT	CUACUACUACCTTTTCTTTCAATCACTTAC	CUACUACUACACTCATCTTTTTTAATTCT	CUACUACUAATTTTACACTCCTTTTTCTTT	CUACUACUAAATACACTACTAGAGTCTTAC	CUACUACUATCATAAGAACCAATTTTGCCA	CUACUACUATCCTATTCAAAGGGATTATTC	CUACUACUACGCTATTTTTTCCCATGAGCG	CUACUACUAAAAAATCATTTAACAATGATC	CUACUACUAAGTGTTTTCATTTGACAATAA	CUACUACUATTCCTCACTTCACGATTATTT	CUACUACUAGTTAATACCCTAAGATCGGTG	CUACUACUATTAACGCCACTCAATCGTTAC	CUACUACUACATTTTAATACTCCTTTATTT	CUACUACUACCCCTCTCTTTATAGATATAC	CUACUACUATCAATTTAGCTAGCTCCTCCG	CUACUACUAATCCTTTAAGATTTTTGGAAA	CUACUACUACGITACAAITIAAGCCAITCI	CUACUACUATAGGGATTTTTATTTTTCATTC	CUACUACUAAAGAGTTACTTCAAGTTGTAG
6SC6_HP0518S513	6SC7_HP0519S514	6SC8_HP0520S515	6SC9_HP0522S516	6SC10_HP0523S517	6SC11_HP0524S518	6SC12_HP0525S519	6SD1_HP0526S520	6SD2_HP0527S521	6SD3_HP0528S522	6SD4_HP0529S523	6SD5_HP0530S524	6SD6_HP0531S525	6SD7_HP0532S526	6SD8_HP0533S527	6SD9_HP0534S528	6SD10_HP0535S529	6SD11_HP0536S530	6SD12_HP0537S531	6SE1_HP0538S532	6SE2_HP0539S533	6SE3_HP0540S534	6SE4_HP0541S535	6SE5_HP0542S536	6SE6_HP0543S537	6SE7_HP0544S538	6SE8_HP0545S539	6SE9_HP0546S540	6SE10 HP0547S541	6SE11_HP0549S542	6SE12_HP0550S543	6SF1_HP0551S544

				:	
	6SF2_HP0552S545	CUACUACUACTTTTATTGATTTTTTTTTC	(SEQ ID NO.	4286)	
	6SF3_HP0553S546	CUACUACUACCTAGITGAITITIAICCAITA	(SEQ ID NO.	4287)	
	6SF4_HP0554S547	CUACUACUATTTTCATCGCTGGAGTTCTTT	(SEQ ID NO.	4288)	
	6SF5_HP0555S548	CUACUACUATTAAGGCATCGCATCAAAAAC	(SEQ ID NO.	4289)	
	6SF6_HP0556S549	CUACUACUAAAAAAAAAGAGGGCCTTAATAA	(SEQ ID NO.	4290)	
	6SF7_HP0557S550	CUACUACUATCTAATTCATGCTCTCCACAA	(SEQ ID NO.	4291)	
	6SF8_HP0558S551	CUACUACUACTAGGCTTTTTTGAAAATCAC	(SEQ ID NO.	4292)	
-	6SF9_HP0559S552	CUACUACUATTAAGCCAGTTTATTATCCTC	(SEQ ID NO.	4293)	
	6SF10_HP0560S553	CUACUACUATTCGTTGGAGCGTTTATTTTT	(SEQ ID NO.	4294)	
	6SF11_HP0561S554	CUACUACUATTGTTTAGGACTACATATAAA	(SEQ ID NO.	4295)	
	6SF12_HP0562S555	CUACUACUAGTCTATTATAGTCTTGACTCA	(SEQ ID NO.	4296)	
	6SG1_HP0563S556	CUACUACUATCACTTTTTTCTGGCAATTTT	(SEQ ID NO.	4297)	
	6SG2_HP0564S557	CUACUACUATTAAAGCCTACTAGAAGAATC	(SEQ ID NO.	4298)	
	6SG3_HP0565S558	CUACUACUATCAGCTCTTAAGAGCAGCACC	(SEQ ID NO.	4299)	
	6SG4_HP0566S559	CUACUACUAAATGATCAAAAACACCCATTT	(SEQ ID NO.	4300)	
	6SG5_HP0567S560	CUACUACUACCATAGGGCTTATATCATTCG	(SEQ ID NO.	4301)	
	6SG6_HP0568S561	CUACUACUATTATTTTTAAACGAATGAG	(SEQ ID NO.	4302)	
	68G7_HP0569S562	CUACUACUAATAAGACAGACTAGATATTGA	(SEQ ID NO.	4303)	
	6SG8_HP0570S563	CUACUACUACAGACAAGCCCATTTCAAGCC	(SEQ ID NO.	4304)	
•	6SG9_HP0571S564	CUACUACUACTCTAGCGGTTTTTCTTACTA	(SEQ ID NO.	4305)	
	6SG10_HP0572S565	CUACUACUACCCTTATTCTAGCACTCTAAC	(SEQ ID NO.	4306)	
	6SG11_HP0573S566	CUACUACUATTTAAAGGAGAGCTTCTATTT	(SEQ ID NO.	4307)	
	6SG12_HP0574S567	CUACUACUAAGGTTTATGATTTCAGCGATT	(SEQ ID NO.	4308)	
	6SH1_HP0575S568	CUACUACUAAAAGATTAAGAGAGGAGTAAA	(SEQ ID NO.	4309)	
	6SH2_HP0576S569	CUACUACUATTAATGCGTTGCGTTTTCTTT	(SEQ ID NO.	4310)	
	6SH3_HP0577S570	CUACUACUATTAAAATCCCTTCCTTTGTTG	(SEQ ID NO.	4311)	
	6SH4_HP0578S571	CUACUACUATAGTTTGTCAATCTTTAAGAT	(SEQ ID NO.	4312)	
	6SH5_HP0579S572	CUACUACUAAGCGTTAATACAACCTTTTTT	(SEQ ID NO.	4313)	
	6SH6_HP0580S573	CUACUACUACGTTAATCACTTGAGGAGGGA	(SEQ ID NO.	4314)	
	6SH7_HP0581S574	CUACUACUATTAGGCGATTTCTTGAAGGTT	(SEQ ID NO.	4315)	
	6SH8_HP0582S575	CUACUACUATTTTAATTGCCCCCTAAGTAA	(SEQ ID NO.	4316)	
	6SH9_HP0583S576	CUACUACUATTAGAATTTTCCGGCATATAA	(SEQ ID NO.	4317)	

6SH10_HP0584S577	CUACUACUATCATGAATTTTTAGCGAGATA	(SEQ ID NO.	4318)
6SH11_HP0585S578	CUACUACUACCACTACGCTTTAAAGCTAGC	(SEQ ID NO.	4319)
6SH12_HP0586S579	CUACUACUAGCGTCATTTTACTTCCTTTTT	(SEQ ID NO.	4320)
6RA1_HP0489R484	CAUCAUCAUACAATGATCAATTACCCTAAT	(SEQ ID NO.	4321)
6RA2_HP0490R485	CAUCAUCAUTTGTTTGAAAAGTTGAAATTT	(SEQ ID NO.	4322)
6RA3_HP0491R486	CAUCAUCAUAGGATACACAATGGCAAAAAG	(SEQ ID NO.	4323)
6RA4_HP0492R487	CAUCAUCAUTITATGGAGCGTTCGCTTATT	(SEQ ID NO.	4324)
6RA5_HP0493R488	CAUCAUCAUTTTATGCTCTATTCTTTACTA	(SEQ ID NO.	4325)
6RA6_HP0494R489	CAUCAUCAUAGGTGCGTTAAAATGAAAATC	(SEQ ID NO.	4326)
6RA7_HP0495R490	CAUCAUCAUATGCCATCTGATTCAAAAAA	(SEQ ID NO.	4327)
6RA8_HP0496R491	CAUCAUCAUATGCGCTGTAGGGTATATTAC	(SEQ ID NO.	4328)
6RA9_HP0497R492	CAUCAUCAUGGTAGTTAAGAATGGGTAATC	(SEQ ID NO.	4329)
6RA10_HP0498R493	CAUCAUCAUGCATGGGAAAATTTTCTAAAT	(SEQ ID NO.	4330)
6RA11_HP0499R494	CAUCAUCAUATGAAAAGCATTTTGCTCTTT	(SEQ ID NO.	4331)
6RA12_HP0500R495	CAUCAUCAUAACTATGAAAATCAGTGTTAG	(SEQ ID NO.	4332)
6RB1_HP0501R496.	CAUCAUCAUGCTGATTTGAATGCAAAATTA	(SEQ ID NO.	4333)
6RB2_HP0502R497	CAUCAUCAUCGTGAATTTAGGGGTTTATTA	(SEQ ID NO.	4334)
6RB3_HP0503R498	CAUCAUCAUGTGGGAAATCCCCCCTATAAC	(SEQ ID NO.	4335)
6RB4_HP0504R499	CAUCAUCAUTGTGAGTTTGATTAAAGTTAG	(SEQ ID NO.	4336)
GRBS_HP0505R500	CAUCAUCAUTTGAGTGAAATGATTGATTAC	(SEQ ID NO.	4337)
GRBG_HP0506R501	CAUCAUCAUCATGGTATTTTTTCATAAGAA	(SEQ ID NO.	4338)
6RB7_HP0507R502	CAUCAUCAUAGAGGGTTTTTAATGTCTTAT	(SEQ ID NO.	4339)
GRBB_HP0508R503	CAUCAUCAUATGTTAAGGCTTTTGATAGGA	(SEQ ID NO.	4340)
6RB9_HP0509R504	CAUCAUCAUACATGTTAGACCAACAACACA	(SEQ ID NO.	4341)
GRB10_HP0510R505	CAUCAUCAUCATGAAAATCGGTGTTTATGG	(SEQ ID NO.	4342)
GRB11_HP0511R506	CAUCAUCAUTATAAATGAAAACCATTAGA	(SEQ ID NO.	4343)
6RB12_HP0512R507	CAUCAUCAUTAATGATAGTAAGAACTCAAA	(SEQ ID NO.	4344)
GRC1_HP0513R508	CAUCAUCAUAATGATAAGATGAACGGACAT	(SEQ ID NO.	4345)
6RC2_HP0514R509	CAUCAUCAUGGGATATGATGAAAGTTCTAT	(SEQ ID NO.	4346)
GRC3_HP0515R510	CAUCAUCAUAAATGTTTGAAGCGACGACGA	(SEQ ID NO.	4347)
6RC4_HP0516R511	CAUCAUCAUTTAATGTCTAAATTGAATATG	(SEQ ID NO.	4348)
6RCS_HP0517R512	CAUCAUCAUAGTATATTTTATGATGAAAAC	(SEQ ID NO.	4349)

	1
C	ı
Y)

4350) 4351) 4352) 4353) 4354)	4356) 4357) 4358) 4359) 4360) 4361)	4364) 4365) 4366) 4366) 4368) 4369)	4371) 4372) 4373) 4374) 4375) 4376) 4378) 4378) 4378)
		9 9 9 9 9 9 9 9	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

٠.	
0	0
Z	Z
$\dot{\Box}$	$\dot{\Box}$
_	
Œ	Ø
Ū	Ш
n	'n

4385

6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
(SEQ ID N (SEQ I	(SEQ
	<i>5</i>
	,
	AA CT TTA
TTTY AAAT TAGG TAGG TAGG TAGG TAGG TAGG	AGP TTC TAAL
TAAT FRAA FRAA GGAA GGAA GGAA GGAA FRAA FRAA	2 5 5 5
CAUCAUCAUTGGCTTTTTGTGCTGTATTTT CAUCAUCAUTGGAACGGAATAAAAAA CAUCAUCAUTGAATGGAACCTTTTTTTTAGCT CAUCAUCAUATGAAAACCTTTTTTTTTAGCT CAUCAUCAUATTGAATGGCGTTTATTTTAG CAUCAUCAUATTGGTGCTTTATTTTAGT CAUCAUCAUATTGGTGCTTTATTTTAGT CAUCAUCAUAATGCAATTCACAGGGAAAAA CAUCAUCAUGAGGTAACAAGTTAGA CAUCAUCAUGTGACTTTTTATCTCTCTTAAA CAUCAUCAUGAGGGTAAAAATCCAAUCAUCAUCAUCATGAAAGGTTTAAAAATC CAUCAUCAUCATGAAAGGTTTAAAAATTTT CAUCAUCAUCATGAAAGCTTTTTTTTTTTTTTTTTTTTTT	CAUCAUCAUTATCTTGGAACCTTCAAGAAA CAUCAUCAUATGGAAATCACGCTTTTTGAC CAUCAUCAUTATGCCGGAAAATTCTAAACT CAUCAUCAUATGAGATTGTTATTCTTGTTA
COT COLOR OF	GAA GAA TGT
TTTT SGA/ SGA/ SAAC SACT TTTT TTTT TGC SGC SGC TGC SGC TGC TGC TGC TGC TGC TGC TGC T	TTG AAA CCG GAT
CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	ATC TGG ATG TGA
TGG PATC PATC PATC TTT TTT TATC TATC TATC T	AUT AUT AUT AUD
CAU CAU CAU CAU CAU CAU CAU CAU CAU CAU	AUC. AUC. AUC.
CAU CAU CAU CAU CAU CAU CAU CAU CAU CAU	AUC.
	5 5 5 5
E 4 2 2 L B B O L 2 E 4 B B C O L Z	573 574 575 576
6RF2_HP0552R545 6RF3_HP0553R546 6RF4_HP0554R547 6RF6_HP0558R549 6RF7_HP0558R550 6RF7_HP0559R552 6RF10_HP0560R553 6RF11_HP0561R554 6RG1_HP0563R556 6RG1_HP0563R556 6RG2_HP0564R557 6RG3_HP0568R561 6RG3_HP0568R561 6RG4_HP0568R562 6RG4_HP0568R561 6RG4_HP0568R561 6RG4_HP0568R561 6RG4_HP0568R561 6RG4_HP0568R561 6RG1_HP0577R569 6RG1_HP0573R566 6RG1_HP0573R566 6RG1_HP0573R566 6RG1_HP0573R566 6RG1_HP0573R567	6RH6_HP0580R573 6RH7_HP0581R574 6RH8_HP0582R575 6RH9_HP0583R576
5521 5531 5531 5531 5531 5531 5531 5531	058 058 058
SRF2_HE GRF4_HI GRF5_HI GRF5_HI GRF7_HI GRF10_ GRF11_ GRF11_ GRG1_H GRG4_H GRG5_H GRG5_H GRG5_H GRG5_H GRG7_I GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_ GRG1_	6RH6 6RH7 6RH8 6RH9
6RF2 6RF3 6RF6 6RF7 6RF11 6RF11 6RF11 6RG1 6RG3 6RG3 6RG3 6RG4 6RG3 6RG4 6RG4 6RG7 6RG9 6RG1 6RG	,

4399)

4397) 4398)

4395)

BNSDOCID: <WO____02066501A2_L:

6RH10_HP0584R577	CAUCAUCAUAGITITIAIGICAGAAACAGAA	(SEQ ID NC
6RH11_HP0585R578	CAUCAUCAUGAAAGCGTGTGAAAATGGGTT	(SEQ ID NC
6RH12_HP0586R579	CAUCAUCAUTGATGAATAAAAGAAACATG	(SEQ ID NO
7SA1_HP0587S580	CUACUACUACTTAAAAATGATTATTAGAAA	(SEQ ID NC
7SA2_HP0588S581	CUACUACUAGCATTATTTGTCTCTCCCTTC	(SEQ ID NC
7SA3_HP0589S582	CUACUACUAGCCATTTTAAAGCTCCTTCAA	(SEQ ID NC
7SA4_HP0590S583	CUACUACUTCCATTATTGTTTTCCTTG	(SEQ ID NC
7SA5_HP0591S584	CUACUACUAGCCATTAAGCCCTAACTTTCA	(SEQ ID NC
7SA6_HP0592S585	CUACUACUATCTGTCATGGCGTTTCCTTTA	(SEQ ID NC
7SA7_HP0593S586	CUACUACUATCAATACACCACGCTTAAACG	(SEQ ID NC
7SA8_HP0594S587	CUACUACUACCCCTTATAGATTCATGTTAG	(SEQ ID NO
7SA9_HP0595S588	CUACUACUAAGTTTAAAATTAAGGGTGTA	(SEQ ID NO
7SA10_HP0596S589	CUACUACUACCTACATGGCTATAGGGACTT	(SEQ ID NO
7SA11_HP0597S590	CUACUACUATTAGAACAACAAGCGTTCCTC	(SEQ ID NO
7SA12_HP0598S591	CUACUACUATTAACCACTCTTAAAAGAAGA	(SEQ ID NO
7SB1_HP0599S592	CUACUACUAATCATTCGCCTTTTTGAATTT	(SEQ ID NÓ
7SB2_HP0600S593	CUACUACUATTAGTATTGCTGCTTCAAAAA	(SEQ ID NO
 7SB3_HP0601S594	CUACUACUAACTAAGATTAAAAGCCTTAAGA	(SEQ ID NO
7SB4_HP0602S595	CUACUACUAAAATCAAAGTTTTAATTCCAA	(SEQ ID NO
7SB5_HP0603S596	CUACUACUATTACCCTAAAAATCTCGTAAA	(SEQ ID NO
7SB6_HP0604S597	CUACUACUACCTATCGTCTGGTTTTAGCAT	(SEQ ID NO
7SB7_HP0605S598	CUACUACUATTAATGCACATAGTCGTCTAT	(SEQ ID NO
7SB8_HP0606S599	CUACUACUAACATCAAAATATCCTATTATT	(SEQ ID NO
7SB9_HP0607S600	CUACUACUATITICATICIPAAGITITITG	(SEQ ID NO
7SB10_HP0608S601	CUACUACUATCTCTTAAAACATATAGCTAT	(SEQ ID NO
7SB11_HP0609S602	CUACUACUATGTTGTTATCCGCTCTTAATA	(SEQ ID NO
7SB12_HP0610S603	CUACUACUATGGCTCAAAAAAGGGGTAAGC	(SEQ ID NO
7SC1_HP0611S604	CUACUACUACTTTAACGCATGCGTTCTTTG	(SEQ ID NO
7SC2_HP0612S605	CUACUACUAACAAGAATATATTATGCGATT	(SEQ ID NO
7SC3_HP0613S606	CUACUACUACCCACTAAATATCCTTTAGTA	(SEQ ID NO
7SC4_HP0614S607	CUACUACUAGTTATTGGTTTTATGGGTGTT	(SEQ ID NO.
7SC5_HP0615S608	CUACUACUATAATTTTAATCCAATTCTTTA	(SEQ ID NO.

4414)
4415)
4416)
4417)
4418)
4420)
4421)
4428)
4428)
4428)
4423)
4431)
4431)
4431)
4443)
4443)
4443)
4444)

7SC6_HP0616S609	9 CUACUACUAATTTATGAAAGCGTTTTTTA	(SEO ID NO.	4446)
7SC7_HP0617S610	0 CUACUACUATTATTTTCTCAAGCGAATGTG	(SEQ ID NO.	4447)
7SC8_HP0618S611	1 CUACUACUATTAATTACCGAAAGACAAGAT	(SEQ ID NO.	4448)
7SC9_HP0620S612	.2 CUACUACUATTAGCCTTGATAGGCTTTTAT	(SEQ ID NO.	4449)
7SC10_HP0621S61	113 CUACUACUAAACTACAATTTAACGATTTTA	(SEQ ID NO.	4450)
7SC11_HP0622S614	114 CUACUACUATCATTAGGGTTGGATTAAGGG	(SEQ ID NO.	4451)
7SC12_HP0623S615	115 CUACUACUATTACATTTCGCCTCTTAATTG	(SEQ ID NO.	4452)
7SD1_HP0624S616	6 CUACUACUATCAAGCATGATTTTCTCGATA	(SEQ ID NO.	4453)
7SD2_HP0625S617	7 CUACUACUACTAATCCTTTAAACTTTTTC	(SEQ ID NO.	4454)
7SD3_HP0626S618	8 CUACUACUATTAATGCAGGTTTTGATTCAA	(SEO ID NO.	4455)
7SD4_HP0627S619	9 CUACUACUATACCCCATTAGCATACATCGC	(SEQ ID NO.	4456)
7SD5_HP0628S620	O CUACUACUAAATTAGGGTATATCATAAGAA	(SEQ ID NO.	4457)
7SD6_HP0629S621	1 CUACUACUACTTGTTTATTCCACAATAAAG	(SEQ ID NO.	4458)
7SD7_HP0630S622	2 CUACUACUAGAAATGGGGGGGTTAAAAAAA	(SEQ ID NO.	4459)
7SD8_HP0631S623	3 CUACUACUAAATCCCTTACTCTTTGTTTTT	(SEQ ID NO.	4460)
7SD9_HP0632S624	4 CUACUACUTITITAGAAITITAGCGAAAI	(SEQ ID NO.	4461)
7SD10_HP0633S625	25 CUACUACUAACTCATTCTTTGGTATAACCA	(SEQ ID NO.	4462)
7SD11_HP0634S626	26 CUACUACUATTCAAAAACCCTTATAAGAAA	(SEQ ID NO.	4463)
7SD12_HP0635S627	27 CUACUACUAAGCCCTTATTCATAATCCAAA	(SEQ ID NO.	4464)
7SE1_HP0636S628	8 CUACUACUATCACCCTTCGGCGATATTGTT	(SEQ ID NO.	4465)
7SE2_HP0637S629	9 CUACUACUAATCAATAAAAGCGTAAGGGA	(SEQ ID NO.	4466)
7SE3_HP0638S630	O CUACUACUAGTITITAATGTITIGTITITAAA	(SEQ ID NO.	4467)
7SE4_HP0639S631	1 CUACUACUATTATTTTTTTAGCTTGAAA	(SEQ ID NO.	4468)
7SE5_HP0640S632	2 CUACUACUATTTTAATTTTCTGCCTAT		4469)
7SE6_HP0641S633	3 CUACUACUALTAATGTTCTCCTTTTTTCTAA	(SEQ ID NO.	4470)
7SE7_HP0642S634	4 CUACUACUATTATTCAATCACTTCATAAAT		4471)
7SE8_HP0643S635	5 CUACUACUATCATGCTTTGAGCCTTAAAAC		4472)
7SE9_HP0644S636	6 CUACUACUACGCATGATTTTCTTTAAAGGT		4473)
7SE10_HP0645S637		(SEQ ID NO.	4474)
7SE11_HP0646S638	38 CUACUACUAGATTTATAAGCGTTTTTTAT	(SEQ ID NO.	4475)
7SE12_HP0647S63	39 CUACUACUATCTATCCTTTTTTTTTTAT	(SEQ ID NO.	4476)
7SF1_HP0648S640	0 CUACUACUACAAATCTTGGATTATTTTTTT	(SEQ ID NO.	4477)

	7SF2_HP0649S641	CUACUACUACGTTCAGTCTTTATGCTTTTT	(SEQ ID NO.	4478)
	7SF3_HP0650S642	CUACUACUATTAAGATTGGTTAAGAAATTG	(SEQ ID NO.	4479)
	7SF4_HP0651S643	CUACUACUTACTTTTAACCCATCTC	(SEQ ID NO.	4480)
•	7SF5_HP0652S644	CUACUACUATTTTTAAATCAAAGGCTTGAT	(SEQ ID NO.	4481)
	7SF6_HP0653S645	CUACUACUAACCCAATACCCTAAAATTAAG	(SEQ ID NO.	4482)
	7SF7_HP0654S646	CUACUACUAGCTAAAATTATTAAAATTTC	(SEQ ID NO.	4483)
	7SF8_HP0655S647	CUACUACUAGCATTTTAAAACCTTGTTCCC	(SEQ ID NO.	4484)
	7SF9_HP0656S648	CUACUACUATITITICAIGTIATITIAIACC	(SEQ ID NO.	4485)
	7SF10_HP0657S649	CUACUACUAGCATCATTTGTCCTTCTTTT	(SEQ ID NO.	4486)
	7SF11_HP0658S650	CUACUACUATCATCAACCCAATTTCTCTTT	(SEQ ID NO.	4487)
	7SF12_HP0659S651	CUACUACUATCACTCTCAAATCATCACAAT	(SEQ ID NO.	4488)
	7SG1_HP0660S652	CUACUACUATICAATITCTIGCATICAAIC	(SEQ ID NO.	4489)
	7SG2_HP0661S653	CUACUACUATTCCCTTTAAGTGGTCGTTTT	(SEQ ID NO.	4490)
٠	7SG3_HP0662S654	CUACUACUATCATTTGGCTTCCTTCAGTTT	(SEQ ID NO.	4491)
	7SG4_HP0663S655	CUACUACUACCAATTTCGTTTAATTCTCAT	(SEQ ID NO.	4492)
	7SG5_HP0664S656	CUACUACUAAATCAATGGTTTGCATTAAAA	(SEQ ID NO.	4493)
	7SG6_HP0665S657	CUACUACUATTTCATTCATAGCGTTTTACT	(SEQ ID NO.	4494)
	7SG7_HP0666S658	CUACUACUAGGTTAAAAAGGCTTTTTATTC	(SEO ID NO.	4495)
	7SG8_HP0667S659	CUACUACUAGATGCTATTTTGATGGAATTT	(SEO ID NO.	4496)
	7SG9_HP0668S660	CUACUACUATTCATCGTTGTTGGTTGC	(SEQ ID NO.	4497)
	7SG10_HP0669S661	CUACUACUATAATCACTCAAACCTCTTTTC	(SEQ ID NO.	4498)
	7SG11_HP0670S662	CUACUACUAAAGGGGTTTTAGCGGTTTGGC	(SEQ ID NO.	4499)
	7SG12_HP0671S663	CUACUACUAAAATCAGAAATTGTAACGATA	(SEQ ID NO.	4500)
-	7SH1_HP0672S664	CUACUACUATCTTTTATCCCTTTGATTTG	(SEQ ID NO.	4501)
	7SH2_HP0673S665	CUACUACUACATCAGGAGTAATAAAACAAT	(SEQ ID NO.	4502)
	7SH3_HP0674S666	CUACUACUATTAGTCATCTATTAAGTGAAT	(SEQ ID NO.	4503)
	7SH4_HP0675S667	CUACUACUAGGGTGTTTTTAATTTTTCTTCC	(SEQ ID NO.	4504)
	7SH5_HP0676S668	CUACUACUACCCCATTTTTAAGAAATTAA	(SEQ ID NO.	4505)
	7SH6_HP0677S669	CUACUACUATCAATTAAAAAAAAGAGTTTGT	(SEQ ID NO.	4506)
	7SH7_HP0678S670	CUACUACUATGATGCCTTTATTGGTCTGTT	(SEQ ID NO.	4507)
	7SH8_HP0679S671	CUACUACUATTAAGCCAATTTGACAGACGC	(SEQ ID NO.	4508)
	7SH9_HP0680S672	CUACUACUTATATTATTGGCAATTAAA	(SEQ ID NO.	4509)

	_
4	
1	. ``
п	\sim

				1610)
	7SH10_HP0681S673	CUACUACUAAAATCACCACCCCCATTTAGC	(סבות וט ואס.	4010)
	7SH11_HP0682S674	CUACUACUATGACTCATTTAAGATCACCAA	(SEQ ID NO.	4511)
	7SH12 HP0683S675	CUACUACUATTAAGGTTTCTTAAAAAACTT	(SEQ ID NO.	4512)
	7RA1 HP0587R580	CAUCAUCAUATGACGACTAAAAGAGTGAAT	(SEQ ID NO.	4513)
	7RA2 HP0588R581	CAUCAUCAUGGAGAATGAATGGCTAAAATG	(SEQ ID NO.	4514)
	1RA3 HP0589R582	CAUCAUCAUATGCGTGAGATTATTTCTGAT	(SEQ ID NO.	4515)
	7RA4 HP0590R583	CAUCAUCAUAAATGGCGTTTTAATTATGATG	(SEQ ID NO.	4516)
•	7RAS HP0591R584	CAUCAUCAUTAATGGAAGCGCAATTACGAT	(SEQ ID NO.	4517)
٠.	7RA6 HP0592R585	CAUCAUCAUTIGGGTIGCGTTTTTACCAAT	(SEQ ID NO.	4518)
	7RA7 HP0593R586	CAUCAUCAUTGACATGCTTTTAAAGAATTT	(SEQ ID NO.	4519)
	7RA8 HP0594R587	CAUCAUCAUCATGGAGTTTTTGGGACTGAT	(SEQ ID NO.	4520)
	7RA9 HP0595R588	CAUCAUCAUGGGATGCATGGATAAAGAAAC	Q	4521)
	7RA10 HP0596R589	CAUCAUCAUGCGTGTTAGAAAAATCTTTTT	(SEQ ID NO.	4522)
	7RA11 HP0597R590	CAUCAUCAUATGCTAAAAAAAGATTTTTTAT	(SEQ ID NO.	4523)
	7RA12_HP0598R591	CAUCAUCAUAAGTGTTTTGATGTTTTCTAA	\Box	4524)
	7RB1 HP0599R592	CAUCAUCAUTGCCATAATGTTTGGGAATAA	(SEQ ID NO.	4525)
	7RB2 HP0600R593	CAUCAUCAUCATGCAAACACCAATGGATAC	(SEQ ID NO.	4526)
	7RB3 HP0601R594	CAUCAUCAUCAATGGCTTTTCAGGTCAATA	(SEQ ID NO.	4527)
	7RB4_HP0602R595	CAUCAUCAUTGTGTTGGATAGTTTTGAGAT	(SEQ ID NO.	4528)
	7RB5 HP0603R596	CAUCAUCAUTTTATTGGCCAAAAAGGATTG	(SEQ ID NO.	4529)
	7RB6_HP0604R597	CAUCAUCAUAGGATTTATGATGATTTTCAT	(SEQ ID NO.	4530)
	7RB7_HP0605R598	CAUCAUCAUGGGATTGATGAATACTATCAT	(SEQ ID NO.	4531)
	7RB8 HP0606R599	CAUCAUCAUGAAAATGATACGAAAAATTTT	(SEQ ID NO.	4532)
	7RB9 HP0607R600	CAUCAUCAUAGGATATTTTGATGTATAAAA	(SEQ ID NO.	4533)
	7RB10 HP0608R601	CAUCAUCAUATGGTGGGTTTAGCTCCTATT	(SEQ ID NO.	4534)
	7RB11 HP0609R602	CAUCAUCAUGGTTCAAAATATGACTTATAG	(SEQ ID NO.	4535)
	7RB12_HP0610R603	CAUCAUCAUACACCTTTTTTGTGCAATTCA	(SEQ ID NO.	4536)
	7RC1 HP0611R604	CAUCAUCAUACATGCTATCACCAGCAACTT	(SEQ ID NO.	4537.)
	7RC2 HP0612R605	CAUCAUCAUGTGGGAGCAATTCTATCTATC	(SEQ ID NO.	4538)
	7RC3 HP0613R606	CAUCAUCAUTTATGATTTCTAACATCAGCA	(SEQ ID NO.	4539)
	7RC4 HP0614R607	CAUCAUCAUTTTAAGGAGCAATGATGGAAC	(SEQ ID NO.	4540)
	7RC5 HP0615R608	CAUCAUCAUACATGATAAAAAGCCAAAAAG	(SEQ ID NO.	4541)

•	7RD9_HP0632R624 7RD10_HP0633R625 7RD11_HP0634R626 7RD12_HP0635R627 7RE1_HP0633R629 7RE2_HP0633R629	CAUCAUCAUCATGTCAAAAAATCGTAGT CAUCAUCAUCATGTCAAAAATCGTAGT CAUCAUCAUTGGGTCAAAAATCCTAATT CAUCAUCAUTTGAATTGGTTTTTGTTTTTC CAUCAUCAUCATGCGTATAGTTTTGTTTTTTC CAUCAUCAUCCATGCATCAAAAAATTT CAUCAUCAUCATGCATCAAAAAAACCACTTAACTA	(SEQ ID NO. (SEQ I	4557) 4558) 4559) 4560) 4561) 4562)
	7RE1_HP0636R628 7RE2_HP0639R629 7RE3_HP0639R630 7RE5_HP0640R632 7RE6_HP0641R633 7RE7_HP0642R634 7RE8_HP0644R636 7RE1_HP0644R636 7RE11_HP0646R638 7RE11_HP0646R639	CAUCAUCAUTAGATAGTAGAAATTT CAUCAUCAUCCATGCATAGTAGAAATTT CAUCAUCAUCCATGCATCAAAAACTCATACTA CAUCAUCAUCAUGTTTTGATGGACAAAAAT CAUCAUCAUCAUGAAAAATGGACTTAGTAGAAGGAACAA CAUCAUCAUCAUGAAAAATGGACTTATTTTTTTCGTTTTT CAUCAUCAUCATGATTTTTTTTTCCACTCTTA CAUCAUCAUCATGATTTTTTTTTCCACTCTTA CAUCAUCAUCATGATTTTTTTTTTAAAAAA CAUCAUCAUCAUGGACAAACCATGATTAAAAAA CAUCAUCAUCAUGGACAAATTTTTTAGAGATTTTA		4561) 4562) 4563) 4564) 4565) 4566) 4566) 4567) 4569) 4571)

,	0	•
ı	Ē	۹
	4	7

		CIN CI CHO
7RF2_HP0649R641	CAUCAUCAUATGCGTATTGAGCATGATTTC	SEC ID NO.
7RF3 HP0650R642	CAUCAUCAUTTTATATGGAGCGTCTTTTGG	
7RF4 HP0651R643	CAUCAUCAUAAAGGATAACCATGTTCCAAC	ם נ
7RF5_HP0652R644	CAUCAUCAUAGGGTATTGGGTGCAAAAACT	\Box
7RP6 HP0653R645	CAUCAUCAUATGTTATCAAAAGACATCATT	Ω
7RF7_HP0654R646	CAUCAUCAUCATGGACTTTTTAGAAAAAGT	Ω
7RF8_HP0655R647	CAUCAUCAUATTAAAAATTAATTCTATCC	₽
7RF9_HP0656R648	CAUCAUCAUGGCAATGGCAAGAAATGTAAA	Ω .
7RF10 HP0657R649		Ω
7RF11 HP0658R650		(SEQ ID NO.
7RF12_HP0659R651	CAUCAUCAUATGAGGAAAATTTTTTTTTAT	(SEQ ID NO.
7RG1 HP0660R652	CAUCAUCAUTAGATTGTGCAACACTTCAAT	(SEQ ID NO.
7RG2_HP0661R653	CAUCAUCAUGAATGCAAGAAATTGAAATTT	(SEQ ID NO.
7PG3_HP0662R654	CAUCAUCAUAGGGAAAAATGATGAAAAAAAA	(SEQ ID NO.
7RG4_HP0663R655	CAUCAUCAUAAGGAAGCCAAATGAACACTT	(SEQ ID NO.
7RG5_HP0664R656	CAUCAUCAUAAGTGGAAAAATTACCTAAAA	(SEQ ID NO.
7RG6 HP0665R657	CAUCAUCAUATGCAAACCATTGATTTTGAA	(SEQ ID NO.
7RG7_HP0666R658	CAUCAUCAUAGTAAAACGCTATGAATGAAA	(SEQ ID NO.
7RG8_HP0667R659	CAUCAUCAUATGAAAATGCAAGAAATCAG	(SEQ ID NO.
7RG9_HP0668R660	CAUCAUCAUGTGCAATGCAAATTCCATCAA	(SEQ ID NO.
7RG10 HP0669R661		(SEQ ID NO.
7RG11_HP0670R662		(SEQ ID NO.
7RG12_HP0671R663		(SEQ ID NO
7RH1 HP0672R664		(SEQ ID NO
7RH2 HP0673R665	CAUCAUCAUAAAATATGGCAGTAAGATTTG	(SEQ ID NO
	CAUCAUCAUGATCTAAATGCTAGCTTATTG	(SEQ ID NO
7RH4_HP0675R667	CAUCAUCAUAATGAAACACCCCCTAGAAGA	(SEQ ID NO
7RH5 HP0676R668	CAUCAUCAUATGGTTTTATACCACTACTAT	(SEC ID NO
7RH6 HP0677R669	CAUCAUCAUATGGATATTTATGCGTTATAT	(SEQ ID NO
7RH7 HP0678R670	CAUCAUCAUGGGGGTTTTGGTTTTGGATGACG	(SEQ ID NO
7RH8 HP0679R671	CAUCAUCAUATGCTTTTTGCGATGATTGGT	(SEQ ID NO
7RH9 HP0680R672	CAUCAUCAUTTGATTACAGTGGTTAAACGA	(SEQ ID NO

4574)
4575)
4576)
4577)
4578)
4580)
4581)
4582)
4583)
4586)
4588)
4589)
4589)
4589)
4589)
4590)

7RH10_HP0681R673	CAUCAUCAUTATGGATACTACGAAAGAGAA	(SEQ ID NO.	4606)	
7RH11_HP0682R674	CAUCAUCAUGTGTGCCAAACATGCCTTGAA	(SEQ ID NO.	4607)	
7RH12_HP0683R675		(SEQ ID NO.	4608)	
8SA1_HP0685S676	CUACUACUACGCTTGAATGCTTGTTAATAT	(SEQ ID NO.	4609)	
8SA2_HP0686S677	CUACUACUAGTITAAAACTCATAATTCAAA	(SEQ ID NO.	4610)	
8SA3_HP0687S678	CUACUACUATTTAAACCAAAATTTGAGTCG	(SEQ ID NO.	4611)	
8SA4_HP0688S679	CUACUACUACATTTAGATTCAACCCCTAAC	(SEQ ID NO.	4612)	
8SA5_HP0689S680	CUACUACUATITAAGCAAACICCCIAAICI	(SEQ ID NO.	4613)	
8SA6_HP0690S681	CUACUACUATTCTCCTTATTTTTGTTCAAC	(SEQ ID NO.	4614)	
8SA7_HP0691S682	CUACUACUACTCTCATTTCGTGCTCCTT	(SEQ ID NO.	4615)	
8SA8_HP0692S683	CUACUACUACTATAAGCGCACCTCAAATTC	(SEQ ID NO.	4616)	
8SA9_HP0693S684	CUACUACUAAAAAACTCACACTAAAAAAAA	(SEQ ID NO.	4617)	
8SA10_HP0694S685	_	(SEQ ID NO.	4618)	
8SA11_HP0695S686	_	(SEQ ID NO.	4619)	
8SA12_HP0696S687	CUACUACUATTTATTTCTCATCAACCAACA	(SEQ ID NO.	4620)	
8SB1_HP0697S688	CUACUACUACAATCTTAGCGTCTTTCTGGG	(SEQ ID NO.	4621)	
8SB2_HP0698S689	CUACUACUAAAGTATAGTAGAACTCAT	(SEQ ID NO.	4622)	
8SB3_HP0699S690	CUACUACUAATCACTCATGGCTTATTTTGT	(SEO ID NO.	4623)	
8SB4_HP0700S691	CUACUAĊUAGTGTCT¢CCTAAAATTTAATT	(SEQ ID NO.	4624)	
8SB5_HP0701S692	CUACUACUAGCATCACTCAAACAAATTTTG	(SEQ ID NO.	4625)	
8SB6_HP0702S693	CUACUACUACGATTTTCATTCTTCTTCCTT	(SEQ ID NO.	4626)	
8SB7_HP0703S694	CUACUACUATCCCTACCTTTCCAAAACAA	(SEQ ID NO.	4627)	
8SB8_HP0704S695	CUACUACUAGCTAGCGGCAACAATAACCAT	(SEQ ID NO.	4628)	
8SB9_HP0705S696	CUACUACUACTATTTCAATTCCAAAGCTAA	(SEQ ID NO.	4629)	
8SB10_HP0706S697	CUACUACUATTAAAAGTGTAGTTATACCC	(SEQ ID NO.	4630)	
8SB11_HP0707S698	CUACUACUATACTCATGGCTTGAATTGAAA	(SEQ ID NO.	4631)	
8SB12_HP0708S699	CUACUACUATTCACTTAAAACGCAATATCG	(SEQ ID NO.	4632)	
8SC1_HP0709S700	CUACUACUATTTACTTAGCGCACTTCTTTA	(SEQ ID NO.	4633)	
8SC2_HP0710S701	CUACUACUACTCAAAACACCCACCCATAAT	(SEQ ID NO.	4634)	
	CUACUACUACATTATTAAAATCCCTAAAC	(SEQ ID NO.	4635)	
8SC4_HP0712S703	CUACUACUATTATAGCCATAGGCACTTGAA	(SEQ ID NO.	4636)	
8SC5_HP0714S704	CUACUACUATTTCAAGCGCGCATCAAATAG	(SEO ID NO.	4637)	

90CS HD07158705	CHACHACHAAGATCGCCATGTCTATACCT	(SEQ ID NO.
LEO/155/02	CHACHACHACCTTTAAGCGATCTTTATTG	(SEQ ID NO.
8SC8_HP0717S707	CUACUACUACGCTCTCATAACAATTCCACG	(SEQ ID NO.
8SC9_HP0718S708	CUACUACUTTTTAGGTTTTGCTCAATA	₽
8SC10 HP0719S709	CUACUACUACACTTCTTCACGCATTTTTTT	(SEQ ID NO.
_HP0720S710	CUACUACUATAAATTAAATTTATCTCACTT	(SEQ ID NO.
8SC12_HP0721S711	CUACUACUATTTAGTGCTTATCGCTGTGAT	Ω
8SD1 HP0723S712	CUACUACUACTTTCAATACTCTTCAAACAT	₽
8SD2_HP0724S713	CUACUACUAGGTGATAAAATCTACAAAACT	Ω
8SD3_HP0726S714	CUACUACUATAATGAGAACGAATCCAAACT	\Box
8SD4_HP0727S715	CUACUACUATICAAACGCTTTTTTGATICA	₽
8SD5_HP0728S716	CUACUACUATTTTATAGATCCATTAAACTC	(SEQ ID NO.
8SD6_HP0729S717	CUACUACUATTATGAAGTTTCCTTGTGGGT	₽
HP0730S718	CUACUACUATCATGCCTTGCCTTACTTTAA	₽
8SD8 HP0731S719	CUACUACUATICAGTICAIGCCICTITICAG	Ω
8SD9_HP0732S720	CUACUACUATGTTCTAGCGTTTCATTCTTC	
SD10 HP0733S721	CUACUACUATCCAACTAATCCTGCAATAAT	
8SD11_HP0734S722	CUACUACUATTTTAAAAAGGGCTTAAAAACC	
8SD12_HP0735S723	CUACUACUAGTTAATGGCTTTTTAAGTTTT	(SEQ ID NO.
8SE1 HP0736S724	CUACUACUACCTTAAATTCCATAATATTGC	
HP0737S725	CUACUACUACTTAAAATTAAAGTTTAATGT	
_HP0738S726	CUACUACUACATTACTTATTCTTTTGGATT	
8SE4_HP0739S727	CUACUACUACTAAGACTTTGCATGATGATA	(SEQ ID
HP0740S728	CUACUACUACTAAATGTAATTAGGGGCGTC	(SEQ ID NO.
_ HP0741S729	CUACUACUATTCAACCAAGCTCCTTTTCTA	
8SE7_HP0742S730	CUACUACUATTTTTATTCCCTTTTTAAGTG	(SEQ ID NO.
HP0743S731	CUACUACUACGGTTATGAGCCGAGTGCTCT	
HP07455732	CUACUACUAAACCGCTAATACCACACTACT	(SEQ ID NO.
8SE10 HP0746S733	CUACUACUATTTAGCGCTCTAAAAAAAAAC	
8SE11_HP0747S734	CUACUACUAACACTCATCCAATTCCCTTTT	(SEQ ID NO.
8SE12 HP0748S735	CUACUACUATTAAGAGTATTCATAAACTTC	
8SF1_HP0749S736	CUACUACUATTATACATGCCTAGTCCTCCA	(SEQ ID NO.
ı		

4639)
4640)
4641)
4642)
4643)
4644)
4644)
4644)
4646)
4651)
4652)
4653)
4656)
4656)
4656)
4667)
4663)
4663)
4666)

c	.,
c	٦
V	7

	8SF2_HP0750S737	CUACUACUATTAATTGCGTGCGATGAGTTT	(SEO ID NO.	4670)
	8SF3_HP0751S738	CUACUACUATITAGCCTCTTTTATCAAAGA	(SEQ ID NO.	4671)
	8SF4_HP0752S739	CUACUACUATCATTTGCACGGAATTGAATT	(SEQ ID NO.	4672)
	8SF5_HP0753S740	CUACUACUAAAAATGTTAGGCGAGTTCATC	(SEQ ID NO.	4673)
	8SF6_HP0754S741	CUACUACUATTAAGACAAAAATTTTTGAAT	(SEQ ID NO.	4674)
	8SF7_HP0755S742	CUACUACUATCACTTCCTTTTATCGTTGAT	(SEQ ID NO.	4675)
	8SF8_HP0756S743	CUACUACUAATTTTTCACTCTTCTTCATAA	(SEQ ID NO.	4676)
	8SF9_HP0757S744	CUACUACUAATCAAATATAGCGTTTTAACA	(SEQ ID NO.	4677)
	8SF10_HP0758S745	CUACUACUATIGATAGATTAGCCTAATAGT	(SEQ ID NO.	4678)
	8SF11_HP0759S746	CUACUACUACAATAATCAAGCCTTTTTCCC	(SEQ ID NO.	4679)
	8SF12_HP0760S747	CUACUACUAGGGAAAAAGGCTTGATTATTG	(SEO ID NO.	4680)
	8SG1_HP0761S748	CUACUACUAGCCCTCTAGCGTAATAGATCT	(SEQ ID NO.	4681)
	8SG2_HP0762S749	CUACUACUATTAATCCTTTAAATTGGAAAT	(SEQ ID NO.	4682)
	8SG3_HP0763S750	CUACUACUATTAGAATTTATTGTCCCACAA	(SEQ ID NO.	4683)
	8SG4_HP0764S751	CUACUACUATTCTAAATTATTTCTTAAGAA	(SEO ID NO.	4684)
	8SG5_HP0765S752	CUACUACUATCCTTTAGATGTTTATGATAT	(SEQ ID NO.	4685)
	8SG6_HP0766S753	CUACUACUACTTTAAATTTTCTATTTTTCCA	(SEQ ID NO.	4686)
	8SG7_HP0767S754	CUACUACUAGGTTTAGGGTAGGCTTATAAA	(SEO ID NO.	4687)
	8SG8_HP0768S755	CUACUACUTACCCCCCTGTGTATAAA	(SEQ ID NO.	4688)
	8SG9_HP0769S756	CUACUACUACTTCAGCCATTGGCCCTCTTT	(SEQ ID NO.	4689)
	8SG10_HP0770S757	CUACUACUAAAAATCTTAAAGAGGTTTAAT	(SEQ ID NO.	4690)
	8SG11_HP0771S758	CUACUACUATATTTGAGCTTTAAATTTGAT	(SEQ ID NO.	4691)
	8SG12_HP0772S759	CUACUACUACTAATCATTCTTGCTGAAGAA	(SEO ID NO.	4692)
	8SH1_HP0773S760	CUACUACUACTACAAATTAACCCTCTGTAA	(SEQ ID NO.	4693)
	8SH2_HP0774S761	CUACUACUAGCTCTTTCCTTAATATTAGTT	(SEQ ID NO.	4694)
•	8SH3_HP0775S762	CUACUACUATTATGATTCATAAGCGTCATC	(SEQ ID NO.	4695)
	8SH4_HP0776S763	CUACUACUATTATCAATTTCGTTCATCTAT	(SEQ ID NO.	4696)
	8SH5_HP0777S764	CUACUACUATAAAGGGCTTATTTTACCATA	(SEQ ID NO.	4697)
	8SH6_HP0778S765	CUACUACUACTCAGCGAATCACTAAAAACG	(SEQ ID NO.	4698)
	8SH7_HP0779S766	CUACUACUAAAACTAGAGCCTGAAATTCTC	(SEQ ID NO.	4699)
	8SH8_HP0780S767	CUACUACUATATCCCCTAGCGCCAATTATA	(SEQ ID NO.	4700)
	85H9_HP0781S768	CUACUACUATCTGAATATTATTCTTTTTT	(SEQ ID NO.	4701)
		-		

8SH10_HP0782S769	CUACUACUAATAGGGTTTAAAAAAAAATT	(SEQ ID NO.	4702)
8	CUACUACUACTATCAATTAGGCTTGGTAGA	(SEQ ID NO.	4703)
S	CUACUACUATTAGCAAAAGTTAGCTAAAAT	(SEQ ID NO.	4704)
ð	CAUCAUCAUGGTGTTTTTCTTTTTAAGGAC	(SEQ ID NO.	4705)
Ð	CAUCAUCAUTGGTAAATGAAAAGAATTTTA	(SEQ ID NO.	4706)
ð	CAUCAUCAUAACCCAATGAAAGAAATCACT	(SEQ ID NO.	4707)
ð	CAUCAUCAUAATGTTGTGCGTGTTTGATAT	(SEQ ID NO.	4708)
Ð	CAUCAUCAUCTATGATGAATATTCCTGGTA	(SEQ ID NO.	4709)
Ð	CAUCAUCAUATGAATGAAGTGGTTGTAGTG	(SEQ ID NO.	4710)
g	CAUCAUCAUAGGAGAATGAGATGAATAAGG	(SEQ ID NO.	4711)
Ð	CAUCAUCAUAATGAGAGAGGCTATCATTAA	(SEQ ID NO.	4712)
ð	CAUCAUCAUATGTTTTTATTAAGGCATTTG	(SEQ ID NO.	4713)
S	CAUCAUCAUTTTTGTTTTCAAATTTATTT	(SEQ ID NO.	4714)
5	CAUCAUCAUCTAAATGAAAGACGCAAGAGT	(SEQ ID NO.	4715)
5	CAUCAUCAUTCAAAATGGCAAATTTATTGA	(SEQ ID NO.	4716)
CA	CAUCAUCAUGAATGGTCATGTCAAAATACA	(SEQ ID NO.	4717)
5	CAUCAUCAUAGGAAAAGCTATGAAAGTAAC	(SEQ ID NO.	4718)
S	CAUCAUCAUTTTTTGACTAAAAAATTCAT	(SEQ ID NO.	4719)
S	CAUCAUCAUGCCATGAGTGATTTCGAAGTC	(SEQ ID NO.	4720)
S	CAUCAUCAUACACATGCAAGATAATTCAGT	(SEQ ID NO.	4721)
S	CAUCAUCAUTGAGTGATGCGTTTCTTTTCA	(SEQ ID NO.	4722)
S	CAUCAUCAUATGAAAATCGCCATTGTAGAA	(SEQ ID NO.	4723)
ð	CAUCAUCAUAATGGTCTCTAACTCCCTTAA	(SEQ ID NO.	4724)
Ğ	CAUCAUCAUAAAACCATTATGGATAAGATC	(SEQ ID NO.	4725)
3	CAUCAUCAUATGGAATTTATGAAAAAGTTT	(SEQ ID NO.	4726)
E.	CAUCAUCAUGGGATTGTTTGCAAGAAATAG	(SEQ ID NO.	4727)
E. C.	CAUCAUCAUTGAGTAAGCCATGAATATCAA	(SEQ ID NO.	4728)
g	CAUCAUCAUAGGAAATAATACAGATGAGAA	(SEQ ID NO.	4729)
ES	CAUCAUCAUGAGATAACCATGAGAAAACTA	(SEQ ID NO.	4730)
Y.	CAUCAUCAUATGTATGCGGCTCATCCTATT	(SEQ ID NO.	4731)
S	CAUCAUCAUAATGAACTATAAAGAATTATT	(SEQ ID NO.	4732)
B	CAUCAUCAUGTATAGACATGGCGATCTTAC	(SEQ ID NO.	4733)

٠.	

4740) 4741)

4738) 4739)

4737

4744)

4745)

474Ġ) 4747) 4748)

4749) 4750) 4751) 4752) 4753) 4754) 4755)

4756) 4757)

4758) 4759) 4760)

4762) 4761)

4743)

4742

(SEQ ID NO.			(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEO ID NO.	(SEC) ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.
CAUCAUCAUGGGTCGTTTGAATGGATATTT	CAUCAUCAUTGTTATGAGAGCGAATTTAGA	CAUCAUCAUATGCAAGTTTTAGCGTTAAAA	CAUCAUCAUAAGATGTTTGTGGTTTTTATA	CAUCAUCAUATGGTAAAATGCCAAAATTTG	CAUCAUCAUCAAAAAATGCGTGAAGAAGT	CAUCAUCAUAATGAAAAAAGCGTTGAAAAT	CAUCAUCAUGGTTATGGCTCAAAATTTACC	CAUCAUCAUGGTTAATGGTTGATGCCTTTT	CAUCAUCAUCGTTATGGGTAGAATTGAAT	CAUCAUCAUGAGAATAAATGGACTTTAAAA	CAUCAUCAUAGIGCAAGATTTTAAAAACCCA	CAUCAUCAUATGAACCACCTTTTAATCCTC	CAUCAUCAUGATGTTTTCTAAAATTTGCTC	CAUCAUCAUATGAAGAATGAAACGCTAGAA	CAUCAUCAUAACGCTTGGAATCCTATGGGT	CAUCAUCAUATGAAAAACATTTATCTTGAT	CAUCAUCAUACATGCAAGTTAAAGAAAACA	CAUCAUCAUACAATGCATTATTCTTATGAA	CAUCAUCAUATTTTAATGTTGCTTTTCACT	CAUCAUCAUATTGGATAAATTTAGTCTTCG	CAUCAUCAUGTGGAGTTTTGCGTTTTATTT	CAUCAUCAUATGGCCAAACGCAGTATCGCT	CAUCAUCAUTCATCATGCAAAGTCTTAGTT	CAUCAUCAUGGAAATGAACATGCAACATTT	CAUCAUCAUCGATGAAAGCGCGTGGGTTTA	CAUCAUCAUAACGCATGGCCATTAGACAAAA	CAUCAUCAUTIGGATGCAAAAAGTTTTCAT	CAUCAUCAUTTAGATGAGGTCTTGGATGAA	CAUCAUCAUAGGGTTTTAATGCCCCATTTT	CAUCAUCAUAGGGAATTGGATGAGTGTGAT	CAUCAUCAUTATGAATACTCTTAAAAAGCA
BRC6_HP0715R705	8RC7_HP0716R706	BRCB_HP0717R707	8RC9_HP0718R708	8RC10_HP0719R709	9RC11_HP0720R710	8RC12_HP0721R711	8RD1_HP0723R712	8RD2_HP0724R713	8RD3_HP0726R714	8RD4_HP0727R715	8RD5_HP0728R716	8RD6_HP0729R717	8RD7_HP0730R718	8RD8_HP0731R719	8RD9_HP0732R720	8RD10_HP0733R721	8RD11_HP0734R722	8RD12_HP0735R723	8RE1_HP0736R724	8RE2_HP0737R725	8RE3_HP0738R726	8RE4_HP0739R727	8RE5_HP0740R728	8RE6_HP0741R729	8RE7_HP0742R730	8RE8_HP0743R731	8RE9_HP0745R732	8RE10_HP0746R733	8RE11_HP0747R734	8RE12_HP0748R735	8RF1_HP0749R736

ď	7
~	1
v	1

	1200720 rads	CANCANCAUATGTATAAATTAGGGGTGTTT	(SEQ
	BRFZ_DF0757	CALICATION TO CONTRATEGE CANTE	(SEQ I
	BRF3_HPU/51K/30	CAUCACCACTCOTTACATAGCAATAGGT	(SEQ
	BRF4 HFU / 52K / 35	CACCASICATION TO THE TROUBLE AT A CGCTAA	(SEQ
	BRF5_HP0753K/40	CAUCAUCACCACCACACACACACACATTTT	(SEQ
	BKF6_HPU/34K/41	CALICALICATINGGTIGITITAAAAACGATITI	(SEQ
	8KF/_HPU/35K/42	CAUCAUCAUGAGATGAAGATTACGAAGAC	(SEQ
	BDF9 HP0757R744	CAUCAUCAUGATTATGAAGAAGAGTGAAAA	(SEQ
	BRF10 HP0758R745	CAUCAUCAUATGCTAGAAAATAGCTCTATA	(SEQ
	8RF11 HP0759R746	CAUCAUCAUTTTTAGATGTGCTGGTGGTCG	(SEQ
	BRF12 HP0760R747	CAUCAUCAUAGAATGCAAATTGCAACAGCA	(SEQ
	RRG1 HP0761R748	CAUCAUCAUTTGGCTTGCAAGCTTTTGTTT	(SEO
	BRG2_HP0762R749	CAUCAUCAUTAATGAGAATTAAGGCTTATT	(SEQ
	8RG3 HP0763R750	CAUCAUCAUATGITITAATITITITCAAAAAA	(SEO
	8RG4_HP0764R751	CAUCAUCAUACATGCCATTGCCATTTATTA	(SEQ
	8RG5 HP0765R752	CAUCÁUCAUGAAATCATGGAAGAACAAAAG	(SEC)
	8RG6_HP0766R753	CAUCAUCAUAGAGGGGGTAATTCATGTTAG	(SEQ
	8RG7_HP0767R754	CAUCAUCAUAGITCCTTAIGGAAAAAGICC	SEQ.
	8RG8 HP0768R755	CAUCAUCAUAGGGAGTGTTAGTAGATAGTT	OES)
	8RG9_HP0769R756	CAUCAUCAUTIGAAAAACCCTATICATIGAT	(SEQ
	8PG10 HP0770R757		(SEO
	8RG11_HP0771R758		(SEQ
	8RG12 HP0772R759		(SEO
	9RH1 HP0773R760		(SEO
	8RH2_HP0774R761	CAUCAUCAUGAATGAACATGGAACAAAAAA	(SEQ
	RRH3_HP0775R762	CAUCAUCAUGATAGATGAACGAAATTGATA	(SEQ
	8RH4_HP0776R763	CAUCAUCAUACATTGGATAGAACTCAAAAT	SEC
	BRH5 HP0777R764	CAUCAUCAUGGATCATGCAAGCAAAGATAA	(SEC
	BRH6 HP0778R765	CAUCAUCAUAGTGCGTTTTGGTAAAATTGA	SEC.
	BRH7 HP0779R766	CAUCAUCAUAGAAATGATGAAAGATTTTTT	(SEC
•	8RH8 HP0780R767	CAUCAUCAUAGAGTGGCGGTGAAAAAAATC	ישר) המה
	8RH9_HP0781R768	CAUCAUCAUATGCCATACGCCTTAAGAAAA) 10)
	l	•	

4766) 4767) 4768) 4769) 4770)	4772) 4773) 4774) 4775)	4777) 4778) 4779) 4780) 4781)	4783) 4784) 4785) 4786) 4787)	4789) 4790) 4791) 4792) 4793) 4794) 4795) 4795)
ON OO N N N N N N N N N N N N N N N N N N	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		(SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO.	
				naahaahoa

	8RH10_HP0782R769	CAUCAUCAUGTGTTAAAATTTCAAAAATTA	(SEQ ID N
	8RH11_HP0783R770	CAUCAUCAUGTGGCGTTGCCCTTTTATTTT	(SEQ ID N
	8RH12_HP0784R771	CAUCAUCAUGTGTTGTTTACAGTTATTTT	(SEQ ID N
	9SA1_HP0785S772	CUACUACUATCATTGGCGCACAATATCAAT	(SEQ ID N
	9SA2_HP0786S773	CUACUACUAAAGGATCTATTTGGCAAATAA	(SEQ ID N
	9SA3_HP0787S774	CUACUACUATTATTCATTCCTTAACACGCT	(SEQ ID N
	9SA4_HP0788S775	CUACUACUAAGGGTTTAAAGCTTCCACACG	(SEQ ID N
	9SA5_HP0789S776	CUACUACUACTATTTTAGGGCTTGTTTTTC	(SEO ID N
	9SA6_HP0790S777	CUACUACUATTACGCAAGCTCTTTGCTATT	(SEQ ID N
	9SA7_HP0791S778	CUACUACUACAAGGCTTTAAGCTCTCATCG	(SEQ ID N
	9SA8_HP0792S779	CUACUACUAAATCCTTTTAAGAAATCTTTC	(SEC) ID N
	9SA9_HP0793S780	CUACUACUATGTTACTCGTGTTTTTTTTTTT	(SEQ ID N
	9SA10_HP0794S781	CUACUACUATCACTTCACGTTTTTCTGTAA	(SEQ ID N
	9SA11_HP0795S782	CUACUACUATTAACCCGCTTGAATTTTTTG	(SEQ ID N
	9SA12_HP0796S783	CUACUACUAAAACTAAAAGTCATAAGTTG	(SEQ ID N
	9SB1_HP0797S784	CUACUACUATGTCTTTATCGGTTTCTTTTG	(SEQ ID N
•	9SB2_HP0798S785	CUACUACUATTTTCTATTTTTAGCGTTAT	(SEO ID N
	9SB3_NP0799S786	CUACUACGGCATTTTTTATCCTATTGT	(SEO ID N
	9SB4_HP0800S787	CUACUACUAACTCCTTTTAAAGCTAAAAGC	(SEQ ID N
	9SB5_HP0801S788	CUACUACUAACCTAGCCCCCACAAACCGGT	(SEQ ID N
	9SB6_HP0802S789	CUACUACUAGCACTCATAATTTTCACAATA	(SEQ ID N
	9SB7_HP0803S790	CUACUACUAAGCTCTTAAAATTTGTAAGTC	(SEQ ID N
	9SB8_HP0804S791	CUACUACTTAAAGGCTAATCGTTTCTA	(SEO ID N
	9SB9_HP0805S792	CUACUACUATCTAATGTTTGCCAATTCTGA	(SEQ ID N
	9SB10_HP0806S793	CUACUACUATITAGGGTTGTAATGTTTTGA	(SEQ ID N
	9SB11_HP0807S794	CUACUACUAGCTCACATACGCTGTGATGCT	(SEQ ID N
	9SB12_HP0808S795	CUACUACUAATTTATTCATTTGACGAAGAA	(SEQ ID N
	9SC1_HP0809S796	CUACUACUATTATTGGATAATGAAATCAGT	(SEC) ID N
	9SC2_HP0810S797	CUACUACUAATTCCTATTGAAAATAAGTTA	(SEQ ID N
	9SC3_HP0811S798	CUACUACUATITITIACIGGCIGAIGATI	(SEQ ID N
	9SC4_HP0812S799	CUACUACUATTACATTTTTTTTTTTTCAC	(SEQ ID N
	9SC5_HP08135800	CUACUACUACAATTAAGCCATCCTTGAAAC	(SEQ ID N

									٠												٠.					٠.				٠.	٠
4/30.)	4799)	4800)	4801)	4802)	4803)	4804)	4805)	4806)	4807)	4808)	4809)	4810)	4811)	4812)	4813)	4814)	4815)	4816)	4817)	4818)	4819)	4820)	4821)	4822)	4823)	4824)	4825)	4826)	N	4828)	\sim
2	E D	000	EQ ID	EQD	(SEQ ID NO.	EQ ID	ш	<u>Б</u> О	0	EQ ID	EQ ID	E0 D	EQ D	EÒ D	EÓ ID	<u>G</u> 0∃	Q Q	0 0 E	Ω.	O O	<u>0</u>	O O	Ö	O O	Q. Ö.	O O	Ö	O.	O O	Q D	C C
					-			•		-																-					

537

$\overline{}$	_	∵	<u> </u>	<u> </u>		<u> </u>	_	<u> </u>	_	<u>-</u>	_	<u> </u>	<u> </u>	<u> </u>			_		_	_	_	_	_	<u>_</u>		<u> </u>	_		_	_	_
4830	4831	4832	4833	4834	4835	4836	4837	4838	4839	4840	4841	4842	4843	4844)	4845	4846	4847	4848	4849	4850	4851	4852	4853	4854	4855	4856	4857	4858	4859	4860	4861
(SEQ ID NO:	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.
CUACUACCCCTTAATCTAAATTTCATA	CUACUACUATTTAGCCCTCAAATTGAGATT	CUACUACUATCATTCTTGCTGTTTTGTGGGG	CUACUACUAGCAGGTTAAAACTGAAAGGTG	CUACUACUAATGCTTTATAACCCTAATCTT	CUACUACUATAAAATCACTGCTCTTGTTTA	CUACUACUACATTCCTCAAAAAACT	CUACUACUATGITITITCCITITAGATICGI	CUACUACUATCAATTTTCCAAACGAATCAT	CUACUACUAAAATCTAAAAAGTGATATTTT	CUACUACUAGCTATTAGCCTAAAAGTTTGT	CUACUACUAGATTTAATGGTGTTCTAAATA	CUACUACUAATTATACAAACTGCCAATATT	CUACUACUATGTTACTAAGACTTTTTAGGA	CUACUACUATTAATGCCCTTCATCGGTTAA	CUACUACUATTTCTTTTACAATTCACCCAT	CUACUACUTACTTAATCTTAAATCT	CUACUACUAGATAAAACGAGCTTATAAGA	CUACUACUAACCATTTTAAGATTTGATATT	CUACUACUAGCCTAGCTTTGGCATTCTAAA	CUACUACUAACGCATAAAAATTTAATTTT	CUACUACUAATTCACTTACCTTCTTCAACT	CUACUACUTGGCTAGAGCCAGGGCTTG	CUACUACUAATGATTATAGAGTAAGAGGGT	CUACUACUATTCATTGGAGCTCGCTGTCAG	CUACUACUATTACCAGCGATAGCCTAAAGA	CUACUACUATCATAATATTTCAACAAATC	CUACUACUAGCATTAAAGGGCGTTGTCTTT	CUACUACUACTACCCTATCGTGTCCAACAA	CUACUACUACTCACGCATTGTTTAAAAGTT	CUACUACUATCAAACAAGCTCTTTGATACT	CUACUACUATTTCACCACTCTTCCTTAATA
3SC6_HP0814S801_C		9SC8_HP0816S803 C	_	9SC10_HP0818S805 C	9SC11_HP0819S806 C	_	9SD1_HP0821S808 C	9SD2_HP0822S809_C	_	9SD4_HP08245811 C	9SD5_HP0825S812_C	_	9SD7_HP0827S814_C	_	9SD9_HP0829S816_C	9SD10_HP0830S817 C	9SD11_HP0831S818 C	_		9SE2_HP08345821 C	_	9SE4_HP0836S823_C	_	_	9SE7_HP0839S826 C	_	_	9SE10_HP0842S829 C	9SE11_HP0843S830 C	_	9SF1_HP0845S832 C

~	٠
≈	5
v	i

4862) 4863) 4864)	4865) 4866)	4867) 4868)	4869)	4871)	4872)	4874)	4875)	4877)	4878)	4879)	4880)	4881)	4882)	4883)	4884)	4885)	4886)	4887)	4888)	4889)	4890)	4891)	4892)	4893)
(SEQ ID NO. (SEQ ID NO. (SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	Ω	(SEQ ID NO.	0	(SEC) ID NO.	(SEQ ID NO.	(SEQ ID NO.			(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.
CUACUACUACTATTTTCATTAACCTCATC CUACUACUACCCTTTCTAGCTCTGCTTCGC CUACUACUAACTCATGTTATTCCTTGTTTT	CUACUACUATTTTCCTATTGTTCCAGTTCC CUACUACUATTGCTCTATTTTATGCATTTT	CUACUACUAAAAAGCCTTTATTGATTATAAG CUACUACUATTAAAAAGAAAGCGATGGGTT	CUACUACUATGCGGTTTCATTTTTTGCTCG		CUACUACUAAGCCCIAAIIIIGAAIIICII CUACUACUACTAATTTTTATGAGCGAAATG	CUACUACUATCAATCATTGCATGTCCTTTT	CUACUACUATTTTTTCATGCGCACTGTCCT	CUACUACUATTGTTAGTGTTCATGCGAATG	CUACUACUATCATTTGCATTCTAGTATCCC	CUACUACUAGCCTACTTCTTATTCATTTCT	CUACUACUAAATCAATGCGTTCCTTGAATG	CUACUACUTAATGCTCATGCCTTACTC	_	Ξ,	CUACUACUACGIGGGCATIATITGICTITC	CUACUACUACGGTTATTCCGCTAACATTTC	CUACUACUACTTATTGCTTAAGATTCAATA	CUACUACUAACTCGCTTTAGTGCAAAATCG	CUACUACUATTCCTAAGCTTTTTTGAGGAA	CUACUACUAATCATTTTTAGAAAAAATCA	CUACUACUATTAGACAATCGTATAGGACAC	CUACUACUATTACTTTTTCTTTTTGTGTG	CUACUACUAGCTCCATTAACTACCATTTGT	CUACUACUAAGTGGCTTACAAATGGTAGTT
9SF2_HP0846S833 9SF3_HP0847S834 9SF4_HP0848S835	9SF5_HP0849S836 9SF6_HP0850S837	9SF7_HP0851S838 9SF8_HP0852S839	9SF9_HP0853S840 9SF10_HP0854S841	9SF11_HP0855S842	9SG1_HP0857S844	9SG2_HP0858S845	9SG3_HP0859S846 9SG4_HP0860S847	9SG5_HP0861S848	9SG6_HP0862S849	9SG7_HP0863S850	9SG8_HP0864S851	9SG9_HP0865S852	9SG10_HP0866S853	9SG11_HP0867S854	9SG12_HP0868S855	9SH1_HP0869S856	9SH2_HP0870S857	9SH3_HP0871S858	9SH4_HP0872S859	9SH5_HP0873S860	9SH6_HP0874S861	9SH7_HP0875S862	9SH8_HP0876S863	9SH9_HP0877S864

4894) 4895) 4896) 4897)	4898) 4899) 4900)	4901) 4902) 4903) 4904)	4905) 4906) 4907)	4909) 4910) 4911)	4912) 4913) 4914) 4915)	4916) 4917) 4918) 4919)	4920) 4921) 4922) 4923) 4924)
(SEQ ID NO. (SEQ I		(SEQ ID NO. (SEQ ID NO. (SEQ ID NO.	(SEQ ID NO. (SEQ ID NO. (SEQ ID NO.		(SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO.	(SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO.	(SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO.
,	CAUCAUCAUATGATAAAAGCAATCATTGGA CAUCAUCAUTTTGCCAAATAGATCCTTAAT CAUCAUCAUATGAACTATAAAGTTGCATCT	CAUCAUCAUAGGCATAACATGAATTACGAA CAUCAUCAUGGGGCAAAATGCATAAAATAG CAUCAUCAUATGCAAGAATACCACATTCAT CAUCAUCAUCGAGTAACAACCATGATTAAC	CAUCAUCAUGCATGGCGTTATTAGAGATTA CAUCAUCAUGAGAGATGATGGGATACATTC CAUCAUCAUAAAAATGAATCTTGAAGTGAA	CAUCAUCAUAGAACGCTTGAACAAACTGCT CAUCAUCAUTAGAACGATGAAAGCAAATAA CAUCAUCAUATGCCGCTCACTCATTTGAAT CAUCAUCAUAAATGCAAACGATTCATATAG	CAUCAUCAUGGTGTTAAAAATCATTCAAGG CAUCAUCAUAATGATGGTAGAAGTGCGATT CAUCAUCAUAGTATCCTTGAAACGATTAGA CAUCAUCAUCCTGATGAGAGTAATAGA	CAUCAUCAUTAGAATGATCTTAAAACGAGT CAUCAUCAUAUATGCGTGTTTTTTTTTTTCAT CAUCAUCAUATGTTAGATGATATTCCTATT CAUCAUCAUATGAATGGTTATTTGAGAGTA	CAUCAUCAUATGATTGGCATAGATATTGTC CAUCAUCAUCATGGCAGAAGAACAAGAAAA CAUCAUCAUCAUGGGTTTTTGAAAATTTTTCT CAUCAUCAUGAAAATCGTGCGATCGTTTGG CAUCAUCAUGAAAATTTTTGGAAATTTTTTGG
9SH10_HP0878S865 9SH11_HP0879S866 9SH12_HP0880S867	9RA2_HP0786R773 9RA3_HP0787R774 9RA4_HP0788R775	9RA5_HP0789R776 9RA6_HP0790R777 9RA7_HP0791R778 9RA8_HP0792R779	9RA9_HP0793R780 9RA10_HP0794R781 9RA11_HP0795R782	9RA12_HP0796R783 9RB1_HP0797R784 9RB2_HP0798R785 9RB3_HP0799R786	9RB4_HP0800R787 9RB5_HP0801R788 9RB6_HP0802R789	9RB9_HP0804R791 9RB9_HP0805R792 9RB10_HP0806R793	9RB12_HP0808R795 9RC1_HP0809R796 9RC2_HP0810R797 9RC4_HP0812R799

١
١
8

4957)	(SEQ ID NO.	CAUCAUCAUCGCCGTTTAATGGATTTTTGT	9RF1_HP0845R832
4955)	(SEQ ID NO.	CAUCAUCAUTIGITITGAIGCGGAAIIGITITG CAUCAUCAUGGAAGAGHGGHGAAAAIITIAC	9RE11_HP0843R830 9RE12_HP0844R831
4954)	(SEQ ID NO.	CAUCAUCAUCCCTTTAATGCTAGAAGCCCT	9RE10_HP0842R829
4953)	(SEQ ID NO.	CAUCAUCAUTATTATGAATTTTTAGAAGA	9RE9_HP0841R828
4952)	(SEQ ID NO.	CAUCAUCAUACATGCCAAATCATCAAAACA	9RE8_HP0840R827
4951.)	(SEQ ID NO.	CAUCAUCAUATGAAAAACTTTTCCCCCACTT	9RE7_HP0839R826
4950)	(SEQ ID NO.	CAUCAUCAUCTCTATAATCATGCGGTATTT	9RE6_HP0838R825
4949)	(SEQ ID NO.	CAUCAUCAUCCTAATAATGTCATTGAATTG	9RES_HP0837R824
4948)	(SEQ ID NO.	CAUCAUCAUAATGCCCATGCGTTTGCACAC	9RE4_HP0836R823
4947.)	(SEQ ID NO.	CAUCAUCAUCATGAACAAAGCGGAATTTAT	9RE3_HP0835R822
4946	(SEQ ID NO.	CAUCAUCAUAGATGAATACAAGCCATAAAA	9RE2_HP0834R821
4945	(SEQ ID NO.	CAUCAUCAUCGTTGTTTTTAGTCAAAAAA	9REL_HP0833R820
4944	(SEQ ID NO.	CAUCAUCAUTTATGTGGATCACCCAAGAAA	9RD12_HP0832R819
4943	(SEQ ID NO.	CAUCAUCAUGACAATATCAAATCTTAAAAT	9RD11_HP0831R818
4942	(SEQ ID NO.	CAUCAUCAUGCTAAAAACATGATCACTTTA	9RD10_HP0830R817
4941	(SEQ ID NO.	CAUCAUCAUAAGGATAGAAAATGAGAATTT	9RD9_HP0829R816
4940	(SEQ ID NO.	CAUCAUCAUATGGAACACAGAGTATTTACT	9RD8_HP0828R815
4939	(SEQ ID NO.	CAUCAUCAUGAATTTTATCTTGAGAAACAT	9RD7_HP0827R814
4938	(SEO ID NO.	CAUCAUCAUTITGCGTGTTTTTGCCATTTC	9RD6_HP0826R813
4937	(SEQ ID NO.	CAUCAUCAUATGATAGATTGCGCGATTATT	9RD5_HP0825R812
4936	(SEQ ID NO.	CAUCAUCAUTAATGAGTCACTATATTGAAT	9RD4_HP0824R811
4935	(SEQ ID NO.	CAUCAUCAUTGAATGCGCTTTTTGAACAAC	9RD3_HP0823R810
4934	(SEQ ID NO.	CAUCAUCAUCATGAAAAAAAGATTGAATAT	9RD2_HP0822R809
4933	(SEQ ID NO.	CAUCAUCAUTGAATGGCTGATTTATTGTCC	9RD1_HP0821R808
4932	(SEQ ID NO.	CAUCAUCAUATGGAACAAAATATTTTCTCC	9RC12_HP0820R807
4931	(SEQ ID NO.	CAUCAUCAUATGAAAGAAATCGTTACAATA	9RC11_HP0819R806
4930	(SEQ ID NO.	CAUCAUCAUAGTTTGGTTATAATGCTAGGC	9RC10_HP0818R805
4929	(SEQ ID NO.	CAUCAUCAUGAATGAATCGCATGAATAAAA	9RC9_HP0817R804
4928	(SEQ ID NO.	CAUCAUCAUAAGATGGCTAAGAAAAACAAA	9RC8_HP0816R803
4927	(SEQ ID NO.	CAUCAUCAUGITITIGGAITITATCAACCATA	9RC7_HP0815R802
4926	(SEQ ID NO.	CAUCAUCAUAATTGTTAAGCCGGCTAGAAA	9RC6_HP0814R801

	ななりしなりしたなどもなべんしいませつしてはない。その	(SEQ ID NO.	4
9RF2_HP0846R833	CAUCAUCAUGCC TIGCAAGIGATICCACCAA		4
9RF3_HP0847R834	CAUCAUCAUGGAATAACATGAGTTACGAAA		r . 7
9RF4_HP0848R835	CAUCAUCAUATGTTTTGCTTTTGAAAATTTTG	(SECTION O.	7
9RF5_HP0849R836	CAUCAUCAUGGGGGCAAAATGCATAAAATA	(SEQ ID NO.	प '
9RF6_HP0850R837	CAUCAUCAUCATGGAAAACAACCAAACAA	(SEQ ID NO.	4
9RF7 HP0851R838	CAUCAUCAUTIGAATGGTATTTGACAGAAC	(SEQ ID NO.	4
GREE HP0852R839	CAUCAUCAUAATGAAACCGCAAGACATTGA	Ω	٧.
орго ировезкв40	CAUCAUCAUAGATGCTACAAACCATCAACT	(SEQ ID NO.	7
ODETO HPOR54R841	CAUCAUCAUCATGTCATTGAAAGTGTTTGA	(SEQ ID NO.	7
90F11 HP0855R842	CAUCAUCAUAATGCTAGCTTCCATCATCTC		7
9RF12 HP0856R843	CAUCAUCAUATGGAATTTTATAAAAAAAAA	(SEQ ID NO.	7
9RG1 HP0857R844	CAUCAUCAUGACATGCAATGATTGATAATT		•
9RG2_HP0858R845	CAUCAUCGCATGAAAAAATCTTAGTC	Ω	-
9RG3 HP0859R846	CAUCAUCAUAGAATGCGTTATATTTGATGAT	\Box	•
9RG4 HP0860R847	CAUCAUCATTCGCATGAACACTAACAA		-
9RG5_HP0861R848	CAUCAUCAUGAATGCAAATGATGCACAATT	0	-
9RG6_HP0862R849	CAUCAUCAUATGCCAGCTAGGCAATCTTTT	<u> </u>	-
9RG7_HP0863R850	CAUCAUCAUATGAATAAACCATTTTTAATC		-
9RG8 HP0864R851	CAUCAUCAUGGCATGAGCATTAAGGAAAAT	Ω	
9RG9_HP0865R852	CAUCAUCAUATGAAATTAAAATCCAAAAA	Ω	
9RG10 HP0866R853	CAUCAUCAUATGAATAAAGAACCTATGAGT		
9RG11_HP0867R854	CAUCAUCAUATGCCCACGATTTTAGTGAGC	₽ :	
9RG12_HP0868R855	CAUCAUCAUACCGATGCAAGAAGAATTGAA	₽	
9RH1 HP0869R856	CAUCAUCAUGITIAGIATGCATGAATACIC	Ω !	
9RH2 HP0870R857	CAUCAUCAUCATGCTTAGGTCTTTATGGTC	Ω :	
9RH3_HP0871R858	CAUCAUCAUCAAGGAGCAAAAAAAGATGAAA	₽	
	CAUCAUCATGCAAGATTTACCCCCATG		
9RHS HP0873R860	CAUCAUCAUTTGTCTTTATGCGAGAATTTT	(SEQ ID NO.	
9RH6 HP0874R861	CAUCAUCAUTATGAAACGAAGGGATTTTAT	(SEQ ID NO.	
9RH7 HP0875R862	CAUCAUCAVAAGATGGTTAATAAAGATGTG	(SEQ ID NO.	
9RH8_HP0876R863	CAUCAUCAUGITGITGGAIGITTTTAAGAG	(SEQ ID NO.	
9RH9 HP0877R864	CAUCAUCAUATGCGTATTTTAGGAATAGAT	(SEQ ID NO.	
1			

4972) 4974) 4975) 4975) 4977) 4978) 4978)

4965) 4966) 4967) 4968) 4969) 4970)

4963) 4964)

4962)

4981)

4982) 4983)

4984)

4985) 4986)

CAUCAUCAUAATGAAAGCAAACACAATCAT CAUCAUCAUGGATGATGAATGGGATCAGTC CAUCAUCAUGAAAGATAAATGAAAAAAAAAAAAAAAAAAA
CUACCACCACACACACACACACACACACACACACACACA
CUACUACUATTTAAGAGCGCAGTTGTTGT
CUACUACUATTTCTTGTTCTAGCCTTTTAT
CUACUACUAAAACATTTAAAAACCTTGAAA
CUACUACUAGGAGGTGTTTAAAAAAACTTC
CUACUACUATATTTAGAAACTATACCTCAT
CUACUACUACCTCTACAACGCATACACCAC
CUACUACUATCACACCCCCTAGTTCTAAA
CUACUACUATTAAGCATCACGCTTCCTTTT
CUACUACUATTTAAACACCCTCGTGTTTCC
CUACUACUAGGTGTGGGCGGTTCAAAACAG
CUACUACUAITATAAGTITICACAAIGCIT
CUACUACUAAAGGGGTGTGGGTGGATTAAA
CUACUACUATTTTAAGATTGAGCTTCAAC
CUACUACUATTAGTAAGCGAACACATAATT
CUACUACUAATGGTCAGCTCTCAAGGGGGC
CUACUACUAGGGGCTTAGAGCAATTTTCAA
CUACUACUATATTATTGCGTTTCGTTCATT
CUACUACUATTAAAACGAATGCGTGGACTG
CUACUACUACCGCCTATCCTACCTTATCAT
CUACUACUATTTTCCTTATTTTTTACTTAA
CUACUACUAGCTTTCAAAATCCTTTCATCT
CUACUACUAGCTTAAAATCACGCATAAAGA
CUACUACUAGTGTCGTTCATGCTGTCTCCT
CUACUACUACCTTTTATTTTTCAAGCTAA
CUACUACUATTATTCAAAAAATTCTCCAAA
CUACUACUATTTATCCTAGATTTAAAAAGT
CUACUACUAACCAATTTTATTTTGAATCGG
CUACUACTTAGAATGAATACCCATAAG

	ATTACT TO THE PROPERTY OF THE	(SEQ ID NO.	5022)
	CHOCKERSTERNINGSANACTTCAGCGTGAGGTT	(SEQ ID NO.	5023)
10SC7_HP0914SB98	COACOACOALCERENTATAAAAACTTATAG	(SEQ ID NO.	5024)
10SC8_HP0915S899	CHACORCORTORINGTITIECTOG	(SEQ ID NO.	5025)
10SC9_HP0916S900	CITACITACIDATCAAGCGATAATCTCTTGAAA	(SEQ ID NO.	5026)
10SC10_HF091/S901	CONCOUNTERTITITION OF THE TRAINING OF THE TRAIN	(SEQ ID NO.	5027)
10SC11_HP0918S902	CINCURCECCATCANATIACTICANAT	(SEQ ID NO.	5028)
10SC12_HP09198903	CINCURCINETIFICATION	(SEQ ID NO.	5029)
105D1_HF092035	CUACUACUAAAATGACTTAATAATGATACA	(SEQ ID NO.	2030)
10SDZ_HF09ZZS906	CUACUACUAATGATACCATTAAAAAGCATA	Ω	5031)
10SD3_HF03ZS300	CHACHACUACCCCCTAAAAACTATAAACGT	(SEQ ID NO.	5032)
10SD4_HF09Z3S307	CHACHACHATTTAGTTTTTTGCCTCAAAT	(SEQ ID NO.	5033)
10SD5_HF09Z4S908	CHACUACUATCATGCTTTGATCCTTGAATT	(SEQ ID NO.	5034)
10SD6_HF03253505	CHACHACHATCAAAATTCGTCATTATTTTC	(SEQ ID NO.	5032)
10SD7_HF09Z6S910	CHIPCHIADADADATTTTCCATTTADATC	(SEQ ID NO.	5036)
10SD8_HP0927S911	CITACITACITATIATIAN CCTAAGATTTTA	(SEQ ID NO.	5037)
	CONCOMPANIATION OF THE CONTINUATION OF THE CONT	(SEQ ID NO.	5038)
10SD10_HF0929353	CHECHACHAGETTTTACTCACTTTAACAT	(SEQ ID NO.	5039)
10SD11_HP0930S914	CONCOLOCIONALITADA A TITIGCT CGCTA	(SEQ ID NO.	5040)
	CONCONCINATIONALIBOCCIATAACA	(SEQ ID NO.	5041)
10SEI_HP0932S916	CHACHACHACATTTTAAGGGATCTGGTGT	(SEQ ID NO.	5042)
10SE2_HP0933S91/	CURCOLOGICATION	(SEQ ID NO.	5043)
10SE3_HP0934S918	CONCORCOLLINATED TO THE TRANSPORT OF THE	(SEQ ID NO.	5044)
•	CHACHACHACGCATCCTTCATGCTGTGGGC	(SEQ ID NO.	5045)
10SE5_HP09368320	CIACITACIDATATIATICITIGAGCCATATC	(SEQ ID NO.	5046)
10SE6_HF093/S9Z1	CITACITACUTAGCGAGGTTAAACGCTGTTGGC	(SEQ ID NO.	5047)
10SE7_HP0938S922	CHACHACHACCAACTTAATTTAAGATTTTT	(SEQ ID NO.	5048)
10SE8_HF09398983	CHACHIACHIAATTAGGGCTGGCTGACATCTT	(SEQ ID NO.	5049)
10SE9_HP0940S924	CITACITACITATICCATGGTTTGATTTAAAT	(SEQ ID NO.	5020)
10SE10_HP0941S925	CINCIPCTITITIANCATGCCATTITAC	(SEQ ID NO.	5051)
10SE11_HP09425926	CUACUACUTAATCCCTAAAAATGCAG	(SEQ ID NO.	5052)
IOSEIL INFOLATORIO	CUACUACUATTACTTAATGGCTATCGCTTC	(SEQ ID NO.	5053)
10SF1_nF03445346			·

٦	۰	į	
•	ς	ı	•
t	ı	_	١

																						٠									
5054)	5055)	5056)	5057)	5058)	5059)	5060)	5061)	5062)	5063)	5064)	5065)	5066)	5067)	5068)	5069)	5070)	5071)	5072)	5073)	5074)	5075)	5076)	5077.)	5078)	5079)	5080)	5081)	5082)	5083)	5084)	5085)
(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NÓ.	(SEQ ID NO.	(SEQ ID NO.	(SEC) ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.
CUACUACUAATTCAAGAGGATTTAAGATTG	CUACUACUATTCAAGTTTTTAGATTTTCAC	CUACUACUATTAAAAACGCACCACCATAGT	CUACUACCTACAAAAACGCTTCTAACT	CUACUACUAGCACCTCCTATTTATGGTATG	CUACUACUACTTTAAAAAATCTTTGAAGTC	CUACUACUAACCITICAAAACCCIAAAITC	CUACUACUAGITIGGGGTAAGGIAGITI	CUACUACUAACTACCTTAACGCACAAACG	CUACUACUATAATCACAACCAAGTAATCGC	CUACUACUAAATTTCATTGATTTTCCTTTA	CUACUACUAAATCCTTAAATTTCAAATTCT	CUACUACUATGTTTATCCTTTTAATGTTT	CUACUACUAAACTTAAACAATCAAACTAAT	CUACUACUACGCTTTCCTTTAAATGATTTG	CUACUACUACTTAACTAACGCCATTTTCAG	CUACUACUACCTTTTAAGCGCGTCTGATCA	CUACUACUAGCGTTAAATTAGTTGTTTCT	CUACUACUATTCTTCAATCATCGTCCTCTT	CUACUACUATAACGCTCATTGAATCCCCTT	CUACUACUATTAAGAATAATAAGCTTTCTT	CUACUACUAGTTCATTGTTGATCCTTTAAA	CUACUACUACAATTTCATAAAACAATCTTG	CUACUACUATCAAAGCCTTTTTCAAACGAA	CUACUACUAACTCAAACGATTTTAATCTTT	CUACUACUAATCATTCCTCCCCTAAATTGT	CUACUACUATCAATGCAATTCTCCTAATCT	CUACUACUACTAAATCGCAATTTCTTTAAT	CUACUACUATTTAGGACTTTTTAAAGCTCT	ĊUAĊUACUATTAAAATAGGGGTTCGTCCAT	CUACUACUACTATTCAATGATCTTGGGCAC	CUACUACUATTCAGCCTTTTTTTTAACTCAT
10SF2_HP0945S929	10SF3_HP0946S930	10SF4_HP0947S931	10SF5_HP0948S932	10SF6_HP0949S933	10SF7_HP0950S934	10SF8_HP0951S935	10SF9_HP0952S936	10SF10_HP0953S937	10SF11_HP0954S938	10SF12_HP0955S939	10SG1_HP0956S940	10SG2_HP0957S941	10SG3_HP0958S942	10SG4_HP0959S943	10SG5_HP0960S944	10SG6_HP0961S945	10SG7_HP0962S946	10SGB_HP0963S947	10SG9_HP0964S948	10SG10_HP0965S949	10SG11_HP0966S950	10SG12_HP0967S951	10SH1_HP0968S952	10SH2_HP0969S953	10SH3_HP0970S954	10SH4_HP0971S955	10SH5_HP0972S956	10SH6_HP0973S957	10SH7_HP0974S958	10SH8_HP0975S959	10SH9_HP0976S960

	はかしんかけかけんけいけん かいかかんけんけんけん はっぱん よっぱん	OR OI OBS	5086)	
10SH10_HF09//S961	CUACUACUALITATIGAATGIATITAGIA		2000	
10SH11_HP0978S962	CUACUACUATCTTAAAAGAATTTAGAAATC	(SEC) ID NO.	2087)	
10SH12 HP0979S963	CUACUACUATCAGTCTTGCTGGATTCTCAT	(SEQ ID NO.	5088)	
10RA1 HP0881R868	CAUCAUCAUTGTGGGTATAATGCAAAAAGT	(SEQ ID NO.	2083)	
10RA2 HP0883R869	CAUCAUCAUAATGATAGTGGGTTTTGATAGG	(SEQ ID NO.	2030)	
10RA3 HP0884R870	CAUCAUCAUAAAAATIGAGCTTGGAGCGTT	(SEQ ID NO.	5091)	
10RA4 HP0885R871	CAUCAUCAUTITGATGATGGCTAATATTCT	(SEQ ID NO.	5092)	
10RA5 HP0886R872	CAUCAUCAUAGGTTTTTAAATGTTTATTTA	(SEQ ID NO.	5093)	
10RA6 HP0887R873	CAUCAUCAUAGAAAGGAAAAAAAATGGAAAT	(SEQ ID NO.	5094)	
10RA7 HP0888R874	CAUCAUCAUGGGTGTGATGGTTTTAGAAGT	(SEQ ID NO.	5095)	
10RA8 HP0889R875	CAUCAUCAUGCGTGATGCTTAAAACCTATC	(SEQ ID NO.	2096)	
10RA9 HP0890R876	CAUCAUCAUATGCTGTTAGATCAAGGGTAT	(SEQ ID NO.	2097)	
10RA10 HP0891R877	CAUCAUCAUAATGCCTCAAATACAATCATC	(SEQ ID NO.	5098)	
10RA11 HP0892R878	CAUCAUCAUAAAAATGCTGACGATTGAAAC	(SEQ ID NO.	2033)	
10RA12 HP0893R879	CAUCAUCAUAACATGCCAAACACCACCAAC	(SEQ ID NO.	5100)	
10RB1 HP0894R880	CAUCAUCAUGGTGTTGAAGCTCAATCTTAA	(SEQ ID NO.	5101)	
10RB2 HP0895R881	CAUCAUCAUTIGGTATITITAAAAAAGGAA	(SEQ ID NO.	5102)	
10RB3 HP0896R882	CAUCAUCAUAAAACATGAAAAAAAACCCTTT	(SEQ ID NO.	5103)	
10RB4 HP0897R883	CAUCAUCAUGGAATGCCAGGACCAAAACCT	(SEQ ID NO.	5104)	
10RB5 HP0898R884	CAUCAUCAUACAATGAGCGTTGATCACCTC	(SEQ ID NO.	5105)	
10RB6 HP0899R885	CAUCAUCAUATGTGTTTAGCGATCCCCTCT	(SEQ ID NO.	5106)	
10RB7 HP0900R886	CAUCAUCAUGAACAACATGAGCGAACAACG	(SEQ ID NO.	5107)	
10RB8 HP0901R887	CAUCAUCAUAAATGATGAAAGCCGTTTTTA	(SEQ ID NO.	5108)	
10RB9 HP0902R888	CAUCAUCAUTITGATGGAAGTGGTTCATIT		5109)	
10RB10 HP0905R889	CAUCAUCAUGCATGCAAGGTTTATGGATTT		5110)	
10RB11_HP0906R890	CAUCAUCAUAAGGATAACCATGCCATCTCC	(SEQ ID NO.	5111)	
10RB12 HP0907R891	CAUCAUCAUATGGCTATTGATTTAGCAGAA		5112)	
10RC1 HP0908R892	CAUCAUCAUCATGAACGACACCTTATTAAA		5113)	
10RC2 HP0909R893	CAUCAUCAUTAATGATACCCACACACAGCTTA		5114)	
10RC3_HP0910R894	CAUCAUCAUTITGAATAATITAGACATTAA	(SEQ ID NO.	5115)	
10RC4_HP0911R895	CAUCAUCAUCTTGTTAGAAACTTTGCAATT		5116)	
10RC5 HP0912R896	CAUCAUCAUAAATCATGATAAAGAAAATA	(SEQ ID NO.	5117)	
l	•			

10RC6_HP0913R897	CAUCAUCAUGAGACAAACATGAAACAAAAT	(SEO ID NO	5118)
10RC7_HP0914R898	CAUCAUCAUGAGAGTTTAGTGAGGCAAGAA	(SEQ ID NO.	
10RC8_HP0915R899	CAUCAUCAUATGGCTAAGATCAATGGTTAT	(SEQ ID NO.	5120)
10RC9_HP0916R900	CAUCAUCAUATGAATGACAAGCGTTTTAGA	(SEQ ID NO.	5121)
10RC10_HP0917R901	CAUCAUCAUCGATAATGTCCCCCTTAACCC	(SEQ ID NO.	5122)
10RC11_HP0918R902	CAUCAUCAUTGATGGCGTTAGTGTATCTCG	(SEQ ID NO.	5123)
10RC12_HP0919R903	CAUCAUCAUACATICTTITAAGGATIA	(SEQ ID NO.	5124)
10RD1_HP0920R904	CAUCAUCAUGAGTAAAACATGGCATTGTAT	(SEC) ID NO.	5125)
10RD2_HP0921R905	CAUCAUCAUCGATGAAAATTTTTATCAATG	(SEQ ID NO.	5126)
10RD3_HP0922R906	CAUCAUCAUAATGGCGTTTAAAAAGGCCAG	(SEQ ID NO.	5127)
10RD4_HP0923R907	CAUCAUCACCCATGCAATTTCAAAAG	(SEQ ID NO.	5128)
10RDS_HP0924R908	CAUCAUCAUATGCCGTTTATCAATATCAAA	(SEQ ID NO.	5129)
10RD6_HP0925R909	CAUCAUCAUAACAGAATGAATACTTATAAA	(SEQ ID NO.	5130)
10RD7_HP0926R910	CAUCAUCAUATCAAAGCATGAATTTAAATT	(SEQ ID NO.	5131)
10RD8_HP0927R911	CAUCAUCAUATGCGAGCGCGTTGCTCAAAG	(SEQ ID NO.	5132)
10RD9_HP0928R912	CAUCAUCAUATGGAAAATTTTTTCAACCAG	(SEQ ID NO.	5133)
10RD10_HP0929R913	CAUCAUCAUAGCATGAGTAGCCCTAATTTA	(SEQ ID NO.	5134)
10RD11_HP0930R914	CAUCAUCAUCATGAAAAAAGATTTTACTCAC	(SEQ ID NO.	5135)
10RD12_HP0931R915	CAUCAUCAUGGGAATGTTAAAGTGAGTAAA	(SEQ ID NO.	5136)
10RE1_HP0932R916	CAUCAUCAUATAAGCCTTGTTATTTTCTTG	(SEQ ID NO.	5137)
10RE2_HP0933R917	CAUCAUCAUATGGTTATCAGGCGATTGTAT	(SEQ ID NO.	5138)
10RE3_HP0934R918	CAUCAUCAUTAAAAATGAAACTCCCGGTCG	(SEQ ID NO.	5139)
10RE4_HP0935R919	CAUCAUCAUATGACCATCAAAGTTTTTTCG	(SEC) ID NO.	5140)
10RES_HP0936R920	CAUCAUCAUATAGTGATGGCCCACTTTGGG	(SEQ ID NO.	5141)
10RE6_HP0937R921	CAUCAUCAUTIGAGCIATICIGATITIATIA	(SEQ ID NO.	5142)
10RE7_HP0938R922	CAUCAUCAUATGGGTGTGTTTTTGGATAAG	(SEQ ID NO.	5143)
10RE8_HP0939R923	CAUCAUCAUATGTCAGCCAGCCCTAATCTG	(SEQ ID NO.	5144)
10RE9_HP0940R924	CAUCAUCAUTAAAATGAAAAAAGTTTTATT	(SEQ ID NO.	5145)
10RE10_HP0941R925	CAUCAUCAUAGTAAAATGGCATGTTAAAAA	(SEQ ID NO.	5146)
10RE11_HP0942R926	CAUCAUCAUTATGGAAACGATTGATTCGGT	(SEÓ ID NO.	5147)
10RE12_HP0943R927	CAUCAUCAUAGCATGAAAAAAGAGGTCGTG	(SEQ ID NO.	5148)
10RF1_HP0944R928	CAUCAUCAUCATGAAAGAAGTCATCCATTC	(SEO ID NO.	5149)

-													٠					,												
5150)	5152)	5155)	5154)	5155)	5156)	5157)	5158)	5159)	5160)	5161)	5162)	5163)	5164)	5165)	5166)	5167)	5168)	5169)	5170)	5171)	5172)	5173)	5174)	5175)	5176)	5177)	5178)	5179)	5180)	5181)
(SEQ ID NO.	(SEQ ID NO.	(SECTIONO.	(SEO ID NO.	(SEQ ID NO.	(SEQ ID NO.		(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEÒ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	Ω	Ω	(SEQ ID NO.	Ω	\mathbf{Q}	(SEQ ID NO.	(SEQ ID NO.	Ω	\Box	₽	Ω	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.
CAUCAUCAUGTGGTGTATTTGCCAACATA CAUCAUCAUGGTGGGATTGTCAGCATCAAG	CAUCAUCAUTITIGITAAGCGITITIGAGIG	CAUCAUCAUATGCGTTTTTACATTATCTTT	CAUCAUCAUATGCGTTGCGTGGTGTATTCT	CAUCAUCAUAACATGGGATTTGCAGATTTC	CAUCAUCAUGIGAIGCAAGGGITITCIIITA	CAUCAUCAUAATGAAATTTAAATTTTTGAA	CAUCAUCAUTITGITTAAAAGAATGGITTT	CAUCAUCAUATCAATGAAATTTTTGGATCA	CAUCAUCAUGATCATGAACGCTTGGAATAC	CAUCAUCAUACATGGAAAAAGCTTATAAAA	CAUCAUCAUTTGTTTAAGTTTTTCTACCTT	CAUCAUCAUGAAAGCGATGAACACCCACCT	CAUCAUCAUCTGAAAATGGCGTTAGTTAAG	CAUCAUCAUATGCAAGATTTTTCAAGTTTA	CAUCAUCAUATGGAAATTGCAGTATTTGGT	CAUCAUCAUAGGACGATGATTGAAGAAAAC	CAUCAUCAUATGAGCGTTAATTTTTAAG	CAUCAUCAUAGAGTGTTACAATGCATGGCG	CAUCAUCAUACAATGAACGAGCAAGAACTC	CAUCAUCAUTAAAGGATTGATGATGGTTTT	CAUCAUCAUAACCAATAAAGGAGTTAAAAT	CAUCAUCAUATGCTCGCTTTAGAAATTTAT	CAUCAUCAUAATGATGCTCGCTTCCATTAT	CAUCAUCAUGATTAGGAGAATTGCATTGAA	CAUCAUCAUCTTTTTAATGAGCATGTTTA	CAUCAUCAUTTGCATTCAGATGAATTGTTA	CAUCAUCAUTTIGAAACAITTAACCCCACT	CAUCAUCAUAAATGGCGCAAAAAACTCTTT	CAUCAUCAUAAGGAAAAGAATGCAAATTGA	CAUCAUCAUTAACATGAATTTTCAAGAAAA
10RF2_HP0945R929 10RF3_HP0946R930	10RF4_HP0947R931	10RF5_HP0948R932	10RF6_HP0949R933	10RF7 HP0950R934	10RF8 HP0951R935	10RF9 HP0952R936	10RF10 HP0953R937	108F11 HP0954R938	10RF12 HP0955R939	10RG1 HP0956R940	10RG2 HP0957R941	10RG3 HP0958R942	10RG4 HP0959R943	10RG5 HP0960R944	10RG6 HP0961R945	10RG7 HP0962R946	10RG8 HP0963R947	10RG9 HP0964R948	10RG10 HP0965R949	10RG11 HP0966R950	10RG12 HP0967R951	10RH1 HP0968R952	10RH2 HP0969R953	10RH3 HP0970R954	10RH4 HP0971R955	10RH5 HP0972R956	10RH6 HP0973R957	10RH7 HP0974R958	10RH8 HP0975R959	10RH9_HP0976R960

												•							•		٠										
5182)	5183)	5184)	5185)	5186)	5187)	5188)	5189)	5190)	5191)	5192)	5193)	5194)	5195)	5196)	5197)	5198)	5199)	5200)	5201)	5202)	5203)	5204)	5205)	5206)	5207)	5208)	5209)	5210)	5211)	5212)	5213)
(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	Ω	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.
CAUCAUCAUGAGTTCTTATGATTGAATGGA	CAUCAUCAUAGGGGAAATCATGGAACATAA	CAUCAUCAUTGIGGCIAIGGIICAICAAIC	CUACUACUAGGTTCTAGCCAAATAGTATCC	CUACUACUAATCAGCGATGAAGAGCTTGAC	CUACUACUAACTAATAATTTTGTAAGACTAA	CUACUACUACACACCAATCATTTAGGAGAG	CUACUACUATCTAAAGCCCATAATTGATGT	CUACUACUACTAAACAAGAGCAAGAGAAAC	CUACUACUATTATCAACGCCTAGAGTTATT	CUACUACUATACTCATAGGGTTTTTATAGT	CUACUACUACTTCATAGCTCCATAACTAGC	CUACUACUAACCCTTAATCCCATATACTAA	CUACUACUAGGGTTTAGTGATGAGAGATAG	CUACUACUACTATATTACTTGCGGAAATTC	CUACUACUACTTTTCATTGATAGGGATTGA	CUACUACUATTTATCGTCTACGCTTAGGTG	CUACUACUACACCTTACTTCTTGTCCTCTA	CUACUACUAGCATTATCTATTACGCCCTTT	CUACUACUATTAATAAACTTTGAGTTAGG	CUACUACUAAACTCACATCCCCATGTCATA	CUACUACUACATCATTTTTTGATCCTTAAA	CUACUACUATCACAACTTGCTCGCCTTATC	CUACUACUACTTTACTTAGCGTATTTTTA	CUACUACUATTAAAAATCCATTCCATAGTT	CUACUACUACTATTTGAGAAGTTGCACTAC	CUACUACUAGITCIGACITITAAGCATTAT	CUACUACUATAATCCATCAAAACACTTCTT	CUACUACUAGCTAATTTAATGCGGTGTTTC	CUACUACUAGCGCTAGTGGGATAAAAGATT	CUACUACUATTTGAACGATAACCCTTAAAA	CUACUACUATGTTTCATCTTAAATCCGCTC
10RH10_HP0977R961	10RH11_HP0978R962	10RH12_HP0979R963	11SA1_HP0980S964	11SA2_HP0981S965	11SA3_HP0982S966	11SA4_HP0983S967	11SA5_HP0984S968	11SA6_HP0985S969	11SA7_HP0986S970	11SA8_HP0987S971	11SA9_HP0989S973	11SA10_HP0990S974	11SA11_HP0991S975	11SA12_HP0992S976	11SB1_HP0993S977	11SB2_HP0994S978	11SB3_HP0995S979	11SB4_HP0996S980	11SB5_HP0997S981	11SB6_HP0999S983	11SB7_HP1000S984	11SB8_HP1001S985	11SB9_HP1002S986	11SB10_HP1003S987	11SB11_HP1004S988	11SB12_HP1005S989	11SC1_HP1006S990	11SC2_HP1008S991	11SC3_HP1009S992	11SC4_HP1010S993	11SC5_NP1011S994

NO. 5214)	NO. 5215)	NO. 5216)	NO. 5217)	NO. 5218)	_	NO. 5220)	NO. 5221)	NO. 5222)	NO. 5223)	NO. 5224)	NO. 5225)	NO. 5226)	NO. 5227)	NO. 5228)	NO. 5229)	VO. 5230)	JO. 5231)	10. 5232)	(0. 5233)	(10. 5234)	10. 5235)	10. 5236)	10. 5237)	10. 5238)	IO. 5239.)	IO. 5240)	10. 5241)	10. 5242)	NO. 5243)	10. 5244)
(SEQ ID NO	(SEQ ID NO	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID N	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID N	(SEQ ID NO
CUACUACUAAGGCTCTTTTAAGGTTTTCAAA	CUACUACUATCATGCAATTACCTCATATTG	CUACUACUAAAGAAATATCTTTATTAAAA	CUACUACUATCATGCTTTCAAAAAGACTTG	CUACUACUATTAAGATTTAAATATTTAAT	CUACUACUAGAAAAGATTATATCAAATCTT	CUACUACUATTAATAGAATCGTGGTAAGAA	CUACUACUACGACCCACCCTATCATTTCA	CUACUACUACCTTTTATCACATTTAAAGTT	CUACUACUAGTTATTTGCGCGGTAAGTTAT	CUACUACUATIGITITAAGAAATICTITIA	CUACUACUATTAAAACAAAAACTTCCCAAA	CUACUACUATCCTTACAATTCTTTTTCTAA	CUACUACUAGCTCATTTTTAAATAAAATC	CUACUACUAAGATCAATTTCTTATCTTATC	CUACUACUAATCTTTAACATTCACTCTCT	CUACUACUAGCITAGATAGGGCTATCTITA	CUACUACUACCAATCTCATAATTTTAATTT	CUACUACUAAGATTTAATGTTTCAATTGTT	CUACUACUATCTCACTCTTCTTCTTTTC	CUACUACUATCAGCCATGATCCACTCCTAA	CUACUACUAATCAGATAGCGGGCCTTTTGG	CUACUACUATICAAGCCIACCCCAAAIACI	CUACUACUAATTGTTCATGCTTGTTCCTTA	CUACUACUAATTTCACCACTCCCCTTTTTT	CUACUACUACATCACAAAAGCTCAGACCTA	CUACUACUACCCTTTTATTTTTGATTGTTA	CUACUACUATGCTAAAAAGCACTTTTATCT	CUACUACUATTATCTGTCTTTAATGCCTAA	CUACUACUATTCTCCTTTTTTATCAATTAT	CUACUACUATTAGTTTTAAGCGTTGTTGAA
11SC6_HP1012S995	11SC7_HP1013S996	11SC8_HP1014S997	11SC9_HP1015S998	11SC10_HP1016S999	11SC11_HP1017S1000	11SC12_HP1018S1001	11SD1_HP1019S1002	11SD2_HP1020S1003	11SD3_HP1021S1004	11SD4_HP1022S1005	11SD5_HP1023S1006	11SD6_HP1024S1007	11SD7_HP1025S1008	11SD8_HP1026S1009	11SD9_HP1027S1010	11SD10_HP1028S1011	11SD11_HP1029S1012	11SD12_HP1030S1013	11SE1_HP1031S1014	11SE2_HP1032S1015	11SE3_HP1033S1016	11SE4_HP1034S1017	11SE5_HP1035S1018	11SE6_HP1036S1019	11SE7_HP1037S1020	11SE8_HP1038S1021	11SE9_HP1039S1022	11SB10_HP1040S1023	11SE11_HP1041S1024	11SE12_HP1042S1025

							٠.			-	•		٠			•	•					٠							•		
5246)	5247)	5248)	5249)	5250)	5251)	5252)	5253)	5254)	5255)	5256)	5257)	5258)	5259)	5260)	5261)	5262)	5263)	5264)	5265)	5266)	5267)	5268)	5269)	5270)	5271)	5272)	5273)	5274)	5275)	5276)	5277)
(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NÓ.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEC) ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.
CUACUACUATTAACTAAGCTTGATTTTTAG	CUACUACUATTTTAGATTTTACTCCTCCAT	CUACUACUATTCGCATTATTTCACCATTCA	CUACUACUACTICTATTTTTAGTCATTA	CUACUACUAGTTCATTAGAGAGTTCTTTTT	CUACUACUATCATGCTATGCTTCTCTCTT	CUACUACUATTTTAATTTCAGTCTTTCTCA	CUACUACUACTAAATAGGAGGCAAAATGTA	CUACUACUATTCAGGATTAAGCGAAAGCCA	CUACUACUATCATAATACTTCCTTTATGTC	CUACUACUATTAACATGACTATCCTTTCAT	CUACUACUATTAAAAATAAACGCATAATT	CUACUACUACCTTTACAATAAATAGTTGTA	CUACUACUATTATTTTTAGAACACATAT	CUACUACUACATTAATGATAACTTTCTAAT	CUACUACUATTTCTAAACAAGATTAAAATA	CUACUACUATCTTCAAACATTCTCTTTTTC	CUACUACUATCTAAATCAAATTCTTTCAAC	CUACUACUAGTICATAAAATCAGCATCCCA	CUACUACUACTTAACATAAACTTTCCTTTG	CUACUACUAGCATATTTACCTCTTATCCTT	CUACUACUATTATTTTAAAAGGAGTGAATC	CUACUACUACTCTCTCCGCCATTTAAAAAT	CUACUACUATACATTGGCTTTAACACTCAA	CUACUACUATCCTTAATTTATTGGTTGTTT	CUACUACUACTCTTAACTCGCTTGCTCTTC	CUACUACUAGGTTAATAGGCATTAGAGACT	CUACUACUATCATGCGCTTTTATTTTTATT	CUACUACUATTTCAATGATCCTTAAT	CUACUACUATACTTCTATATCACACCTT	CUACUACUATTTTCGCTTTAAACGAATAG	CUACUACUTACACAAATTTCACTAAGA
 11SF2_HP1044S1027	11SF3_HP1045S1028	11SF4_HP1046S1029	11SF5_HP1047S1030	11SF6_HP1048S1031	11SF7_HP1049S1032	11SF8_HP1050S1033	11SF9_HP1051S1034	11SF10_HP1052S1035	11SF11_HP1053S1036	11SF12_HP1054S1037	11SG1_HP1055S1038	11SG2_HP1056S1039	11SG3_HP1057S1040	11SG4_HP1058S1041	11SG5_HP1059S1042	11SG6_HP1060S1043	11SG7_HP1061S1044	11SG8_HP1062S1045	11SG9_HP1063S1046	11SG10_HP1064S1047	11SG11_HP1065\$1048	11SG12_HP1066S1049	11SH1_HP1067S1050	11SH2_HP1068S1051	11SH3_HP1069S1052	11SH4_HP1070S1053	11SH5_HP1071S1054	11SH6_HP1072S1055	11SH7_HP1073S1056	11SH8_HP1074S1057	11SH9_HP1075S1058

-	
u	_
u	_
-	

O DO LO DE LATE O LITTO L'E	CH KHH K K K CHOOD K KHOHH K KIIO KIIO KIIO		10203
SCOTS9/OTAH OTHETT	CUACUACUAAIICIAAGCCCICAAAIIAIC	(SECTIONO.	9770
11SH11_HP1077S1060	CUACUACUATAGAATTCAGCTCTCTAGTTT	(SEQ ID NO.	5279)
11SH12_HP1078S1061	CUACUACUATTAGAAAATTTTAGGATTTGT	(SEQ ID NO.	5280)
11RA1_HP0980R964	CAUCAUCAUGIGGAGCATGATGTICACTGT	(SEQ ID NO.	5281)
11RA2_HP0981R965	CAUCAUCAUAAAGAAGAAAATGAAGAAAAT	(SEQ ID NO.	5282)
11RA3_HP0982R966	CAUCAUCAUCTTGCTACCCCAAAATTCAGG	(SEQ ID NO.	5283)
11RA4_HP0983R967	CAUCAUCAUAAAAGGAAAAATTTATGGATG	(SEQ ID NO.	5284)
11RA5_HP0984R968	CAUCAUCAUATGGAAAAATATAACGATAAA	(SEQ ID NO.	5285)
11RA6_HP0985R969	CAUCAUCAUATGGGGCGTTGGTTCCTTGGA	(SEQ ID NO.	5286)
11RA7_HP0986R970	CAUCAUCAUCCCATTAAAGATGTGGAAACT	(SEQ ID NO.	5287)
11RA8_HP0987R971	CAUCAUCAUATGCTAGATAGGGCTATATTA	(SEQ ID NO.	5288)
11RA9_HP0989R973	CAUCAUCAUTTATTTTTGCTTAACGCTATC	(SEQ ID NO.	5289)
11RA10_HP0990R974	CAUCAUCAUAGAAATGTTGTGTAAAATGGT	(SEQ ID NO.	5290)
11RA11_HP0991R975	CAUCAUCAUAATTTATGGCTTTTGAAATGA	(SEQ ID NO.	5291)
11RA12_HP0992R976	CAUCAUCAUAATAGAAAAATGATTAAATTA	(SEQ ID NO.	5292)
11RB1_HP0993R977	CAUCAUCAUATGICATITGCCCCTAIGITA	(SEQ ID NO.	5293)
11RB2_HP0994R978	CAUCAUCAUATGTCCTTTCTATCAATCCCT	(SEQ ID NO.	5294)
11RB3_HP0995R979	CAUCAUCAUGGAGCAATATGCCACATAACA	(SEQ ID NO.	5295)
11RB4_HP0996R980	CAUCAUCAUAATGAAACGCTCCCACTTAGA	(SEQ ID NO.	5296)
11RB5_HP0997R981	CAUCAUCAUTTATTTTGCTTAACGCTATC	(SEQ ID NO.	5297)
11RB6_HP0999R983	CAUCAUCAUAAATGAGCAAAGACAGAGATT	(SEQ ID NO.	5298)
11RB7_HP1000R984	CAUCAUCAUGGAATAAGCGATGATAATCAC	(SEQ ID NO.	5299)
11RB8_HP1001R985	CAUCAUCAUATGGAATTTAAAAACACCAAA	(SEQ ID NO.	5300)
11RB9_HP1002R986	CAUCAUCAUTAAATGAAAGAAACAAGACTT	(SEQ ID NO.	5301)
11RB10_HP1003R987	CAUCAUCAUGITITIGGGTAGTGCAACTICT	(SEQ ID NO.	5302)
11RB11_HP1004R988	CAUCAUCAUAAATGGCGTTAGAAAAAGTT	(SEQ ID NO.	5303)
11RB12_HP1005R989	CAUCAUCAUTATGTCAAATATTATTACAGA	(SEQ ID NO.	5304)
11RC1_HP1006R990	CAUCAUCAUGTGGTTTCACTGAAAGAGAGT	(SEQ ID NO.	5305)
11RC2_HP1008R991	CAUCAUCAUCTATGAAAAAAATTGATGATA	(SEQ ID NO.	5306)
11RC3_HP1009R992	CAUCAUCAUGTGTATTGTTTTTATTCTTTG	(SEQ ID NO.	5307)
11RC4_HP1010R993	CAUCAUCAUATTGAATCGTTTCTTTAACCG	(SEQ ID NO.	5308)
11RC5 HP1011R994	CAUCAUCAUATGCTTTATTCATTAGTAAAA	(SEQ ID NO.	5309)

٠.																-						٠			,						
5310)	5311)	5312)	5313)	5314)	5315)	5316)	5317)	5318)	5319)	5320)	5321)	5322)	5323)	5324)	5325)	5326)	5327)	5328)	5329)	5330)	5331)	5332)	5333)	5334)	5335)	5336)	5337)	5338)	5339)	5340)	5341)
(SEO ID NO	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ IĎ NÓ.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	ON CHORS
CAUCAUCAUGCGGATTTAAGATGAAACATT	CAUCAUCAUAGCCTTATAACATGCAATTTC	CAUCAUCAUATTGCATGAATGGTTCCAATC	CAUCAUCAUCTGTTAGTGCTTTTTATTGTT	CAUCAUCAUCTGTGGTTTTTAATGTGTGTGG	CAUCAUCAUAAATGCTTTTGATCGTTTTTT	CAUCAUCAUCATGATGAAAAAAACCCTTTT	CAUCAUCAUAGAGCGAGTGAGTGTCCCCTC	CAUCAUCAUATGTCTTTGATTAGAGTGAAT	CAUCAUCAUAAAAGGAAGAATTGATGAAAA	CAUCAUCAUGATTCATGCATTCAAGAACTC	CAUCAUCAUTITAATGCAATATAAGAAAAA	CAUCAUCAUTCCATGAGTAAGAGTTTATAC	CAUCAUCAUGTGTGCGATTATGATGAACCG	CAUCAUCAUAAAAATGAGCCTGACTTCGC	CAUCAUCAUTATCAGCATGAAAAGATTAGA	CAUCAUCAUTATGAGATTGGTGAGTCTTGT	CAUCAUCAUATGGCTATTTTTGGGGAATTA	CAUCAUCAUAGTGAGAAATGCAAGATTTTA	CAUCAUCAUAGTGGATCATGGCTGATATTT	CAUCAUCAUTTATGATTTTTGATGATGAAA	CAUCAUCAUACTTCTAATGTATTCTAAAAT	CAUCAUCAUAATAAGGAACAAGCATGAACA	CAUCAUCAUGGGGAGTGGTGAAATTCTATA	CAUCAUCAUGTGATGCGAGAGATCCTTACT	CAUCAUCAUCCCATGAAAGGATTAGAAAGA	CAUCAUCAUATGAAAATTTTAGTGATTCAA	CAUCAUCAUGGTGTGCGAGTTTGTGTTGA	CAUCAUCAUATGGCTTTGAATCTGGAGAAA	CAUCAUCAUATTTAGATTATGGCAAACGA	CAUCAUCAUATGATGCAAGTTTACCACCTT	かけるなけらなけられていないなかなからなけるしになってなって
11RC6 HP1012R995	11RC7_HP1013R996	11RC8_HP1014R997	11RC9_HP1015R998	11RC10_HP1016R999	11RC11_HP1017R1000	11RC12_HP1018R1001	11RD1_HP1019R1002	11RD2_HP1020R1003	11RD3_HP1021R1004	11RD4_HP1022R1005	11RD5_HP1023R1006	11RD6_HP1024R1007	11RD7_HP1025R1008	11RD8_HP1026R1009	11RD9_HP1027R1010	11RD10_HP1028R1011	11RD11_HP1029R1012	11RD12_HP1030R1013	11RE1_HP1031R1014	11RE2_HP1032R1015	11RE3_HP1033R1016	11RE4_HP1034R1017	11RES_HP1035R1018	11RE6_HP1036R1019	11RE7_HP1037R1020	11RE8_HP1038R1021	11RE9_HP1039R1022	11RE10_HP1040R1023	11RE11_HP1041R1024	11RE12_HP1042R1025	11RF1 HP1043R1026

																٠.																
5342)	5343)	5344)	5345)	5346)	5347)	5348)	5349)	5350)	5351)	5352)	5353)	5354)	5355)	5356)	5357)	5358)	5329)	5360)	5361)	5362)	5363)	5364)	5365)	5366)	5367)	5368)	5369)	5370)	5371)	5372)	5373)	
(SEO ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	Ω	(SEQ ID NO.	\bigcirc	Δ.	(SEQ ID NO.	Ω	Ω	(SEQ ID NO.	Ω	(SEQ ID NO.	₽	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEO ID NO.	(SEO ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	
CAUCAUCAUAAGGGTGATATGCTGATCTCC	CAUCAUCAUGGAGATGCGATGCAATTAGAC	CAUCAUCAUATGACTAAAAAAATAGAAGAG	CAUCAUCAUCTAATGAACGCTCATAAAGAA	CAUCAUCAUGAAGCATAGCATGAGTGGTAT	CAUCAUCAUGATAATGATGGGGTTCTTATT	CAUCAUCAUTIGGIAGIGAGIGIICCIGCA	CAUCAUCAUGGTGTATCAAAACAATTTTTT	CAUCAUCAUTTATGAAACAAACAACCATTA	CAUCAUCAUCTTAATGAGCAATGGATAAAA	CAUCAUCAUTATTTGATTTTTAACGCTTTA	CAUCAUCAUAATGTTGAAATTTAAATATGG	CAUCAUCAUTIGGGTATCAATATGTGTTCT	CAUCAUCAUCGATTTTGGGTCTTAAAAAAT	CAUCAUCAUCACTTAGGATTTTAATGAGC	CAUCAUCAUATGAAAGAACGGATAGTCAAT	CAUCAUCAUTTATGTTTGGCATGGGCTTTT	CAUCAUCAUAGAGAATGTTTGAAGATTTAA	CAUCAUCAUGITGAAAGAATTTGAITTAGA	CAUCAUCAUCTGATTTTATGAACCCCTTAT	CAUCAUCAUACTGAATGCTTTATGCATCAA	CAUCAUCAUTGAAGGATAAGAGGTAAATAT	CAUCAUCAUGTGCATTATTTAAGAATTTTA	CAUCAUCAUTTGAAACTACTGGTAGTAGAT	CAUCAUCAUGTGTTAAAGCCAATGTATTAT	CAUCAUCAUTAATGAAACCAACGAACGAAC	CAUCAUCAUGAGTGCTAGCTTACAAACAGA	CAUCAUCAUATGCCTATTAACCCTCTCTAT	CAUCAUCAUCGCATGAAAGAATCTTTTAC	CAUCAUCAUATGAAAGCAACTTTTCAAGTG	CAUCAUCAUATAAGCATGGGCATCAAAGAA	CAUCAUCAUAGAGAGATGGGATGAAAAAA	
11RF2 HP1044R1027	11RF3 HP1045R1028	11RF4 HP1046R1029	11RF5 HP1047R1030	11RF6 HP1048R1031	11RF7 HP1049R1032	11RF8 HP1050R1033	11RF9 HP1051R1034	11RF10 HP1052R1035	11RF11 HP1053R1036	11RF12 HP1054R1037	11RG1 HP1055R1038	11RG2 HP1056R1039	11RG3 HP1057R1040	11RG4 HP1058R1041	11RG5 HP1059R1042	11RG6 HP1060R1043	11RG7 HP1061R1044	11RG8 HP1062R1045	11RG9 HP1063R1046	11RG10 HP1064R1047	11RG11 HP1065R1048	11RG12 HP1066R1049	11RH1 HP1067R1050	11RH2 HP1068R1051	11RH3 HP1069R1052	11RH4 HP1070R1053	11RHS HP1071R1054	11RH6 HP1072R1055	11RH7 HP1073R1056	11RH8 HP1074R1057	11RH9 HP1075R1058	l

5374) 5375) 5376) 5377) 5378)	5380) 5381) 5382) 5383) 5384)	5385) 5386) 5387) 5388) 5389) 5390)	5392) 5393) 5394) 5395) 5396) 5397)	5399) 5400) 5401) 5402) 5403) 5404)
(SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO.	(SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO.			(SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO.
CAUCAUCAUTTTATGGATATTTTAAAAACT CAUCAUCAUTGTGAAATTGTGGTTTCCTTA CAUCAUCAUAUATGGCAGATAAAGAAATACTG CUACUACUATGCTTTAACCAAAAAGATTCT CUACUACUAGGTTCATCTCTTTTCGTTCAA CUACUACUACCTTAAAGCCACTCTGCATTT	CUACUACUATAAAACCCTTAGCATTCTGTC CUACUACUAGTTAGAATTTAGCGCTAAGAG CUACUACUACUACAATCTAATAGCAAAAA CUACUACUACCATTAAAATTGAGGTAGGG	CUACUACUAAGTCATTTTAACACAAATTAT CUACUACUATCATGGGTTGAGTAATCTTTT CUACUACUATCATGGGTTGCACATGTCTTT CUACUACUAGCCTAAAAGTTTTGCAAAT CUACUACUATCATTCCAAATAGGTTTTTTT CUACUACUATTAAGCTTTTGCAGGGGTTTT CUACUACUATTAAGCTTTTGTGGGTAGGA	CUACUACUAGAGCTATGAAGCAAGAAAAG CUACUACUACUACTAAAGCGATTGGGCTTT CUACUACUATTAACCTTGATTTTCTATAT CUACUACUATCATATCTTAAGGGGATAGG CUACUACUACCAAAACTTTTGATCTTAAGGCGATAGG CUACUACUATGCCATGATCTTTTTTTTTTTC CUACUACUATTTATACCTTTATACCAAAAC	CUACUACUACCCTTTATTGATAGAGTGGTT CUACUACUATCTTGGGTAAGTTTCAGTTTT CUACUACUATTAATCTTATCATGCAGTAA CUACUACUATTTTGGCTCTTAGCTTTTTTTT CUACUACUATTTTGGCTCTTAGGTTTTTTT CUACUACUAGGTTATTTAGAGGTTTTTTTT CUACUACUAAAACCTCTAAATAACCATATC
11RH10_HP1076R1059 11RH11_HP1077R1060 11RH12_HP1078R1061 12SA1_HP1079S1062 12SA2_HP1080S1063 12SA3_HP1081S1064	12SA4_HP1082S1065 12SA5_HP1083S1066 12SA6_HP1084S1067 12SA7_HP1085S1068 12SA8_HP1086S1069	12SA9_HP1087S1070 12SA10_HP1088S1071 12SA11_HP1089S1072 12SA12_HP1090S1073 12SB1_HP1091S1074 12SB2_HP1092S1075 12SB3_HP1093S1076	12SB4_HP1094\$1077 12SB5_HP1095\$1078 12SB6_HP1096\$1079 12SB7_HP1097\$1080 12SB8_HP1098\$1081 12SB9_HP1099\$1082	12SB11_HP1101S1084 12SB12_HP1102S1085 12SC1_HP1103S1086 12SC2_HP1104S1087 12SC3_HP1105S1088 12SC4_HP1106S1089 12SC5_HP1107S1090

9	2 6) (8)	(60	(0	1)	12)	13)	(4)	. (2)	(9)	(7)	(8)	(6)	(0:	<u>.</u>	22)	23)	24)	25)	(9:	. (23	(8;	(6;	00	31	(2)	33)	4	35)	(9)	1
5406			5409	, 5410	. 5411	5412	, 5413)	, 5414	, 5415)	, 5416)	, 5417	5418	5419	, 5420)	5421	, 5422	, 5423)	, 5424	, 5425)	, 5426)	, 5427	, 5428)	. 5429)	. 5430)	, 5431	. 5432	, 5433	, 5434		. 5436	1
ON CI CES	(SEO ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEO ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO.	(SEQ ID NO	(SEQ ID NO.	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(: · · · · · · · · · · · · · · · · · ·
かん みかん シー・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・	CHACHACHATTATGATTTTTTTTTTTTTTTTTTTTTTTTT	CUACUACUACCTTTTTAAAAAAAGCTCATT	CUACUACUATTATACTTTAGCTTCTTCT	CUACUACUATTATTCAAACACCCTTTTAAA	CUACUACUAGCTTAAAAAATATAAGTGTAG	CUACUACUACGTTTAAAGCGTTCTTAATTG	CUACUACUATCAATGTTTTGATAATGATTG	CUACUACUATTAATTTTTTGTGGTAGGATT	CUACUACUAGITATCGGCTTGAAGTGTTC	CUACUACUAACAAAGAATTAAAATTCTTTC	CUACUACUATGGGTAGAAAACTTATTGTTT	CUACUACUATTACGCCTGCACTCTTAAAAA	CUACUACUAATTAAATCGCCTTTAACATTT	CUACUACUACTAGCTTATCCCCAATAAATC	CUACUACUACTTACTACCCATGCGAACATG	CUACUACUATCATGGTTTTTGCATGGTGGTG	CUACUACUAATTACTTCATTAATTTGACAT	CUACUACUATTACCAATCAAAGGCTTGTAT	CUACUACUACCTCATTGTTCTTCCTTAGTG	CUACUACUACCTTATCAGTTGGCATTTTT	CUACUACUACCCTGCTTTTTAAGGACTTGT	CUACUACUACTTTTTTTTTAGAAGACAAA	CUACUACUACCCCTTAAAGAGACTCAATCT	CUACUACUACCCTTAGGAATTTTTCATGTT	CUACUACUATITITATITIAGGGCTTCTACG	CUACUACUACTCCTACTCGCTATAAGTGAG	CUACUACUATGATTAAATAGATTGAATAAC	CUACUACUATGCATTTAAAGCCTTTGTTTC	CUACUACUACATTCATCAACTCCCTAAACC	CUACUACUAAAGCGTTAAGACATCATTTTT	
tootsoottan spect	12509-1110931093	12SC8 HP1110S1093	12SC9_HP1111S1094	12SC10 HP1112S1095	12SC11_HP1113S1096	12SC12_HP1114S1097	12SD1 HP1115S1098	12SD2_HP1116S1099	12SD3_HP1117S1100	12SD4_HP1118S1101	12SD5_HP1119S1102	12SD6_HP1120S1103	12SD7 HP1121S1104	12SD8_HP1122S1105	12SD9_HP1123S1106	12SD10_HP1124S1107	12SD11_HP1125S1108	12SD12 HP1126S1109	12SE1_HP1127S1110	12SE2_HP1128S1111	12SE3_HP1129S1112	12SE4_HP1130S1113	12SE5_HP1131S1114	12SE6 HP1132S1115	12SE7_HP1133S1116	12SE8 HP1134S1117	12SE9_HP1135S1118	12SE10 HP1136S1119	12SE11_HP1137S1120	12SE12 HP1138S1121	I

12SF2_HP1140S1123	CUACUACUAACTCACATCCTATCATAAATC	(SEQ ID NO.	5438)	
12SF3_HP1141S1124	CUACUACUATTGTCTCATGCCAAAATACCG	(SEQ ID NO.	5439)	
12SF4_HP1142S1125	CUACUACUATTACTTCATTCTCATCAT	(SEQ ID NO.	5440)	
12SF5_HP1143S1126	CUACUACUACTAATCTTCTAAATCCTCCCC	(SEQ ID NO.	5441)	
12SF6_HP1144S1127	CUACUACUACTAGGCGCATGCCGAATAATG	(SEQ ID NO.	5442)	
12SF7_HP1145S1128	CUACUACUATGTGGGGATCGTGTTAGTTCT	(SEQ ID NO.	5443)	
12SF8_HP1146S1129	CUACUACUACGGCTTCTAGATCAAGACTTC	(SEQ ID NO.	5444)	
12SF9_HP1147S1130	CUACUACUACAGAGATTAATGGCGGACTTC	(SEQ ID NO.	5445)	
12SF10_HP1148S1131	CUACUACUATCATGATTTGTGCTGTTTGAA	(SEQ ID NO.	5446)	
12SF11_HP1149S1132	CUACUACUATTTCACTCAACTATTCTCTAA	(SEQ ID NO.	5447)	
12SF12_HP1150S1133	CUACUACCCCACTAAAAGCATAGAAAC	(SEQ ID NO.	5448)	
12SG1_HP1151S1134	CUACUACUACCTTAGGCTTTTTGAGAAGT	(SEQ ID NO.	5449)	
12SG2_HP1152S1135	CUACUACUAAAAAGTTAGCGCATTTTAGGG	(SEQ ID NO.	5450)	
12SG3_HP1153S1136	CUACUACUACTATCCTTTTATTATGGTTGT	(SEQ ID NO.	5451)	
12SG4_HP1154S1137	CUACUACUATTAAGCTCGTTCTCTTTT	(SEQ ID NO.	5452)	
12SG5_HP1155S1138	CUACUACUAATTTTAGGCGCTCAAAATCGT	(SEQ ID NO.	5453)	
12SG6_HP1156S1139	CUACUACUAGITIAAICAAAAGCCIAIGIT	(SEQ ID NO.	5454)	
12SG7_HP1157S1140	CUACUACUATTAAAACCCCATGATGTAATT	(SEQ ID NO.	5455)	
12SG8_HP1158S1141	CUACUACUATTTTAGAGGCGCATTTTTT	(SEQ ID NO.	5456)	
12SG9_HP1159S1142	CUACUACUAAATTTTTCAAAGCCCTTCATA	(SEÓ ID NO.	5457)	
12SG10_HP1160S1143	CUACUACUACCTAATCCTGTGTGCGTTCAA	(SEQ ID NO.	5458)	
12SG11_HP1161S1144	CUACUACUATAAAAATTAAGCGAAAGAAC	(SEQ ID NO.	5459)	
12SG12_HP1162S1145	CUACUACUACATCTTGCTTAAAAACCCCATT	(SEQ ID NO.	5460)	•
12SH1_HP1163S1146	CUACUACUATTAATTCTTTTGGCGTTTTTC	(SEQ ID NO.	5461)	
12SH2_HP1164S1147	CUACUACUAGAGTGAGCGGCTTTAAGAGTG	(SEQ ID NO.	5462)	
12SH3_HP1165S1148	CUACUACUAGCCGCTCACTCATCAAACGGC	(SEQ ID NO.	5463)	
12SH4_HP1166S1149	CUACUACUACTATTGGTTGTAATTTTTATA	(SEQ ID NO.	5464)	
12SH5_HP1167S1150	CUACUACUACATCAAAAAGATGCTACTAGA	(SEQ ID NO.	5465)	•
12SH6_HP1168S1151	CUACUACUATTCAAGAGGCTTTGATGTAGG	(SEQ ID NO.	5466)	
12SH7_HP1169S1152	CUACUACCATTTTAAGCCACTTTCTTT	(SEÓ ID NÓ.	5467)	
12SH8_HP1170S1153	CUACUACUATTTTACCCTCTAATGTGTTGG	(SEQ ID NO.	5468)	
12SH9_HP1171\$1154	CUACUACUATATTTAACAGCTCCCTAAAAA	(SEQ ID NO.	5469)	

																							,							
5470)	5471)	5473)	5474)	5475)	5476)	5477)	5478)	5479)	5480)	5481)	5482)	5483)	5484)	5485)	5486)	5487)	5488)	5489)	5490)	5491)	5492)	5493)	5494)	5495)	5496)	5497)	5498)	5499)	5500)	5501)
(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	₽	Ω	₽	(SEO ID NO.	(SEQ ID NO.	_	(SEQ ID NO.	(SEQ ID NO.	Ω	Δ.	(SEQ ID NO.	(SEQ ID NO.
CUACUACUATCATTCAAAAATAATTTCTTC	CUACUACUAPATGAAGCGAAGAATAAAGAC CUACUACUATTTAGGAGTTTTCTTCTTGCT	CAUCAUGGATTTAATGATTCAGTCTGT	CAUCAUCAUATGAAAAAGATTGCATTTTTT	CAUCAUCAUCGTTTGACAGAATGCTAAGGG	CAUCAUCAUAGGTTAAGCATTTGAAACTCT	CAUCAUCAUAAAAGGAAAAAAATGAAAAAT	CAUCAUCAUATGCCAAAAAAATGCCGACAC	CAUCAUCAUGGAATGGGCTTGAAAAATCTC	CAUCAUCAUTTTAATGCGCTTAGATTACGC	CAUCAUCAUGGGAATGTTGAATTTTTTATC	CAUCAUCAUGGAAAAATTTGATGCGATTGA	CAUCAUCAUAACGCATGAACTTAGAAAAAC	CAUCAUCAUGTGCAACCGATGAAATCTAAA	CAUCAUCAUCAAGGATAGCCATGAACCCCC	CAUCAUCAUCATGCAAAATGGGTATTATGC	CAUCAUCAUATGGAACACTCTTTAATCATT	CAUCAUCAUGGTGTGTGAGCGAAAACTTTT	CAUCAUCAUTITGCTTAACGCTATCAAGTT	CAUCAUCAUGGATAGAGGAATGAGGAAAAA	CAUCAUCAUTTGATCAAATGGCTTTAAAAA	CAUCAUCAUATGTTAGAAAATGTCAAAAAG	CAUCAUCAUAAATGCAAGATAAAATAG	CAUCAUCAUTICATGCCTAAGCATTCTTTA	CAUCAUCAUTTGATGTTAGATTTTGATTTG	CAUCAUCATGGGTTATCAATTGTTTGA	CAUCAUCAUTATGCCAAAAACTGAAACTTA	CAUCAUCAUTTAATGAGAGTTCAATCTAAA	CAUCAUCAUTITITIATGACTTCAGCTTCA	CAUCAUCAUGGCTGTGTTTTAGTTTGATTT	CAUCAUTGTGGGGCAGGATAACATAAG
12SH10_HP1172S1155	12SH11_HP1173S1156	12RA1 HP1079R1062	12RA2 HP1080R1063	12RA3 HP1081R1064		12RA5 HP1083R1066	12RA6 HP1084R1067	12RA7 HP1085R1068	12RA8_HP1086R1069	12RA9 HP1087R1070	12RA10 HP1088R1071	12RA11 HP1089R1072	12RA12_HP1090R1073	12RB1_HP1091R1074	12RB2 HP1092R1075	12RB3_HP1093R1076	12RB4 HP1094R1077	12RB5_HP1095R1078	12RB6 HP1096R1079	12RB7 HP1097R1080	12RB8 HP1098R1081	12RB9 HP1099R1082	12RB10 HP1100R1083	12RB11 HP1101R1084	12RB12 HP1102R1085	12RC1 HP1103R1086	12RC2 HP1104R1087	12RC3_HP1105R1088	12RC4_HP1106R1089	12RC5_HP1107R1090

							•									•									:			
5502) 5503)	5505)	5507)	5508)	2200)	5510)	5511)	5512)	5513)	5514)	5515)	5516)	5517)	5518)	5519)	5520)	5521)	5522)	5523)	5524)	5525)	5526)	5527)	5528)	5529)	5530)	5531)	5532)	5533)
(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEC ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEĞ IÖ NO.	(SEQ ID NO.	(SEQ ID NO.
CAUCAUCAUTATTACCATGTTTCAAATTAG CAUCAUCAUATGAAAGATTGGAACGAATTT CAUCAUCAUAAAAATATGGCAAAAAGTATT	CAUCAUCAUTATCATGGTAAAAGAAGTCAA	CAUCAUCAUTIGAAACGAGCGTTATACTTA	CAUCAUCAUAAAACAIGCCCTTATTIGATT	CAUCAUCAUATGATCAATTACCCTAATCTA	CAUCAUCAUAGGAGTGAAGTTACCCAAAGC	CAUCAUCAUAGTAACAATGGGATACGCAAG	CAUCAUCAUGATGAGACGGAGTTTTTGAA	CAUCAUCAUAAAATGGGCGGAATCTTATCT	CAUCAUCAUATGGTCGTTTTTACATTCTCAT	CAUCAUCAUACTTTTATGGATTTTTGCTCT	CAUCAUCAUATGGAATGAATATCAAATTAA	CAUCAUCAUCATGCAAAACCATGATTTAGA	CAUCAUCAUGGATGAAAAGGCTTTTTTTA	CAUCAUCAUATGAAGAGATCTTCTGTATTT	CAUCAUCAUAGGAAGAACAATGAGGTATTT	CAUCAUCAUAAAATGCCAACTGATAAGGAG	CAUCAUCAUGCTAATTTGCATGAGTAAGAG	CAUCAUCAUGGTTTTTATGAATTACGATAA	CAUCAUCAUATGTTAGATTCAATCGTTTAT	CAUCAUCAUGTGATGGCTTTGTTGAAAATT	CAUCAUCAUATGAAAGCGATGGAAGGTAAA	CAUCAUCAUATGGCGAATTTAAGAGACATT	CAUCAUCAUGAGATAAATAATGTCCCAACT	CAUCAUCAUATGCAAGATTTAAAAGTGATC	CAUCAUCAUTGATGAATGTTTGTAGTTAAA	CAUCAUCAUATAGGTTATGAATATATCGGT	CAUCAUCAUGGTAGTGATGGCAAAAAATAA	CAUCAUCAUGATGTGAGTATGATGAGTGAA
								٠.													-		•	÷				
12RC6_HP1108R1091 12RC7_HP1109R1092 12RC8 HP1110R1093	12RC9_HP1111R1094	12RC11_HP1113R1096	12RC12_HP1114R1097	12RD1_HP1115R1098	12RD2_HP1116R1099	12RD3_HP1117R1100	12RD4_HP1118R1101	12RD5_HP1119R1102	12RD6_HP1120R1103	12RD7_HP1121R1104	12RD8_HP1122R1105	12RD9_HP1123R1106	12RD10_HP1124R1107	12RD11_HP1125R1108	12RD12_HP1126R1109	12RE1_HP1127R1110	12RE2_HP1128R1111	12RE3_HP1129R1112	12RE4_HP1130R1113	12RES_HP1131R1114	12RE6_HP1132R1115	12RE7_HP1133R1116	12RE8_HP1134R1117	12RE9_HP1135R1118	12RE10_HP1136R1119	12RE11_HP1137R1120	12RE12_HP1138R1121	12RF1_HP1139R1122

12RH10_HP1172R1155	CAUCAUATGAAAACAAACGGGCTTTTTT	(SEQ ID NO.	5566)
12RH11_HP1173R1156	CAUCAUCAUAGGATTTGTTGATGAGTTATT	(SEQ ID NO.	5567)
12RH12_HP1174R1157	CAUCAUCAUGGTATGCAAAAAACTTCTAAC	(SEQ ID NO.	5568)
13SA1_HP1175S1158	CUACUACTTAACGAAAGATAAATACAG	(SEQ ID NO.	5569)
13SA2_HP1176S1159	CUACUACUAGCGTTTTTTAAATTTTGAAAAG	(SEQ ID NO.	5570)
13SA3_HP1177S1160	CUACUAGUATTAATAGGCAAACACATAATT	(SEQ ID NO.	5571)
13SA4_HP1178S1161	CUACUACUAAGGCTAACTCATCATCTCCAA	(SEQ ID NO.	5572)
13SA5_HP1179S1162	CUACUACUAGGGGTCATGGTTGTCCTTTAA	(SEQ ID NO.	5573)
13SA6_HP1180S1163	CUACUACUACTTTTAATGAGCGTTTAGCCC	(SEQ ID NO.	5574)
13SA7_HP1181S1164	CUACUACUATAATTGTTŢTATTTTCTAAAG	(SEQ ID NO.	5575)
13SA8_HP1182S1165	CUACUACUAAGCTTAAGCGTCTAAATATTT	(SEQ ID NO.	5576)
13SA9_HP1183S1166	CUACUACUATCAAGCTTTTTTTGTTGAGTAT	(SEQ ID NO.	5577)
13SA10_HP1184S1167	CUACUACUATTATTTATTGGTTAAGTTTTC	(SEQ ID NO.	5578)
13SA11_HP1185S1168	CUACUACUACTCTTTATGTTTTTTAAACT	(SEQ ID NO.	5579)
13SA12_HP1186S1169	CUACUACUAGGCTCTTCTAATCACAAACCA	(SEQ ID NO.	5580)
13SB1_HP1187S1170	CUACUACUAAACGATTTTATGGTGTTTTTCT	(SEQ ID NO.	5581)
13SB2_HP1189S1172	CUACUACUATCAAGCGTTCTTAATGTAATG	(SEQ ID NO.	5582)
13SB3_HP1190S1173	CUACUACUAAGCGACATTATAAGTCTTCAT	(SEQ ID NO.	5583)
13SB4_HP1191S1174	CUACUACUATTAAGGCTCTTCTAAAAGAGT	(SEQ ID NO.	5584)
13SB5_HP1192S1175	CUACUACUACATTAGACCACTGAGTTTTTA	(SEQ ID NO.	5585)
13SB6_HP1193S1176	CUACUACUACTTTTATTGATTCACCATTTC	(SEQ ID NO.	5586)
13SB7_HP1194S1177	CUACUACUACGITITITAAGAITGAATACA	(SEQ ID NO.	5587)
13SB8_HP1195S1178	CUACUACUAAATAAGAGAGCGTTATAATTA	(SEQ ID NO.	5588)
13SB9_HP1196S1179	CUACUACUATAACTCCAATTACCAGCGGTA	(SEQ ID NO.	5589)
13SB10_HP1197S1180	CUACUACUATTICCICTIATTITITICTIGI	(SEQ ID NO.	5590)
13SB11_HP1198S1181	CUACUACUATATCAAAATTTAGAGTTATCC	(SEQ ID NO.	5591)
13\$B12_HP1199S1182	CUACUACUAGÍCITACITGACITCAACCIT	(SEQ ID NO.	5592)
13SC1_HP1200S1183	CUACUACUACCATCACAGGCTCTTAGTTTT	(SEQ ID NO.	5593)
13SC2_HP1201S1184	CUACUACUATAACGCTATTTAATATCCATC	(SEQ ID NO.	5594)
13SC3_HP1202S1185	CUACUACCAATCAATCCACACACTTCTA	(SEQ ID NO.	5595)
13SC4_HP1203S1186	CUACUACUACATGTTTTCTCCTTAAAAGT	(SEQ ID NO.	5596)
13SC5_HP1204S1187	CUACUACUACTAGCTCTTCAATTTGATTTC	(SEQ ID NO:	5597)

5598) 5599) 5600) 5601) 5602)	5604) 5605) 5606) 5607) 5608) 5609)	5611) 5612) 5613) 5614) 5615) 5615) 5617) 5618) 5619)	5623) 5624) 5625) 5626) 5627) 5628)
		(SEQ ID NO. (SEQ I	(SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO.
CUACUACUATTATTCAATAATATTGCTCAC CUACUACUATTAGCCGAGATTGTCTTTGTG CUACUACUACTTTACTTTTTTATAAAGTTT CUACUACUAGCAACCGCTATAAAGTATT CUACUACUAGCAACCGCTTGTTTAAAAGTATT	CUACUACUATTGITIAITITIAAAITITITAG CUACUACUATTTAAAATTTTAAGCTACT CUACUACUATTTTAATGITCCTTTTTTAA CUACUACUATCTCACTTACGCTGIAAAGAG CUACUACUAAAAACCCGCCTTTAAATAATC CUACUACUAAAAACCCGCCTTTAAATAATC	CUACUACUATTAAGAATATTCTTTCAAATC CUACUACUAAGTCAGTCTTCTTTTATA CUACUACUACUATTATTTCAACCTTTCTTTATA CUACUACUACUATTAAAGCGTGCAAGCATCCCGAA CUACUACUACTTAAAGCGTGCAAGCATCCAC CUACUACUATTTAAAGCTTCTTTTTTTTTTT CUACUACUATTTTAATGAATGCCTACAAA CUACUACUAACAATCATAAAAGAGGTGGGGAAG CUACUACUACUATTATTTAATGAATGCCTACAAA CUACUACUACUATTATTTAAATACCCTACAAAG CUACUACUACUATTATTTAAATGAATGATAAA CUACUACUACUATTATTTAAATACCCTCTTTTTTTTTT	CUACUACUATTCACAGAGTAACCTTATTGA CUACUACUAGGTTCAATCCGTTTCTTCCAA CUACUACUATTAAAGAATCACATCCATGGT CUACUACUACATCGCTTAAATTTTTTTTAA CUACUACUAAATTTAATGGCGCACCAAACT CUACUACUAGAGACCATTATAAAAAAACCT
13SC6_HP1205S1188 13SC7_HP1206S1189 13SC8_HP1207S1190 13SC9_HP1208S1191 13SC10_HP1209S1192	13SD1_HP1212S1194 13SD2_HP1212S1195 13SD3_HP1214S1197 13SD4_HP1215S1198 13SD5_HP1215S1199	13SD/_HP121851201 13SDB_HP1219S1202 13SD9_HP1220S1203 13SD10_HP1221S1204 13SD11_HP1222S1205 13SD12_HP1224S1206 13SE1_HP1224S1207 13SE2_HP1225S1208 13SE3_HP1226S1209 13SE4_HP1227S1210 13SE5_HP1227S1210	13SE7_HP1230S1213 13SE8_HP1231S1214 13SE9_HP1232S1215 13SE10_HP1233S1216 13SE11_HP1234S1217 13SE12_HP1235S1218

13572_HP123751220 CUACUACUACCCCTAAAAAATCCTTTAACAA 13574_HP123851221 CUACUACUACUACCAAGGTTAGGGATTATT 13574_HP123851222 CUACUACUACCAAGCTTAATAATGAAGGGGATTATT 13575_HP12451223 CUACUACUACCAACATTAATAATGAATGAAGGAATTT 13571_HP124531226 CUACUACUACUACCAACATTAATAATGAATTTTAAGATTTT 13571_HP124531226 CUACUACUACUACAACATTTAAGTAAGGGGATTATTT 13571_HP124531230 CUACUACUACUACATAACACTTTAAGAATTTTTAAGAATTTTTTAAGATTTTTTTAAGATTTTTT
--

_	
	যু
•	c
ι	^

(SEQ ID NO. 5695)	(SEQ ID NO. 5696)	(SEQ ID NO. 5697)	(SEQ ID NO. 5698)	(SEQ ID NO. 5699)	(SEQ ID NO. 5700)	(SEQ ID NO. 5701)	(SEQ ID NO. 5702)	(SEQ ID NO. 5703)	(SEQ ID NO. 5704)	(SEQ ID NO. 5705)	(SEQ ID NO. 5706)	(SEQ ID NO. 5707)	(SEQ ID NO. 5708)	(SEQ ID NO. 5709)	(SEQ ID NO. 5710)	D NO	D NO.	D NO.	(SEQ ID NO. 5714)	(SEQ ID NO. 5715)	(SEQ ID NO. 5716)		(SEQ ID NO. 5718)	(SEQ ID NO. 5719)	(SEQ ID NO. 5720)	D NO	(SEQ ID NO. 5722)	(SEQ ID NO. 5723)		(SEQ ID NO. 5725)
CAUCAUCAUCACTTAAATTATGGCAAAAAA (CAUCAUCAUAATCATGGCGCTTGAAGTGGT (CAUCAUCAUCAATGAACTACATCGGTTCTA (CAUCAUCAUTTTAATTTGGAGTTTGATAAA (CAUCAUCAUATGCTGGATTTGTCTTATAGC (CAUCAUCAUGATTGAAAAAAGATTACTATTA (CAUCAUCAUATGAAATTTTTAGCGTTATTT (CAUCAUCAUATATGGATTTTATCACCATCA (CAUCAUCAUGIGAGAAAAGGAAIGCAITIG (CAUCAUCAUCATGAGCGCGGATGTGGGTTA (CAUCAUCAUTAATCATGATTTATTGGTTGT (CAUCAUCAUGAATGCACTCTCCAAATTTAG (CAUCAUCAUATGAAAGATAACAATAACTAT (CAUCAUCAUAAATGCCATCACACAAAAACC (CAUCAUCAUTAAAATGCTAGTAGAAATAGA (CAUCAUCAUGGCATTGGACAACACTCTCAA (CAUCAUCAUGTGCGTGTGGAAGAAAATTAT (CAUCAUCAUGATAAACATGCTTGAAGATTA (CAUCAUCAUATGAGGGAGATTGTATGGGTG (CAUCAUCAUGCATGAATTTTGTCTTTTAT (CAUCAUCAUTGAAGTGAAAATGAGAGAAAT (CAUCAUCAUACAAACGATGAAAAAGGTTAT (CAUCAUCAUAAGACCTAIGCIACAIAAAAA (CAUCAUCAUTAGGGTGTTAATCGTTCAAAA (CAUCAUCAUCAATGAAAATTTCTACGATT (CAUCAUCAUACTCTGTGAAAAACTCCAACC (CAUCAUCAUATGATTGTAAAACGCCTTAAC (CAUCAUCAUATGGCTGTTTCTTCTATCAAT (CAUCAUCAUATGCGTAATACCATTTTATTT (CAUCAUCAUATGCAACTAAGCCCCTTACAA (CAUCAUCAUAAAATCATGAGACTCAAACTA (
13KC/_HP1Z06K1189	13RC8_HP1207R1190	13RC9_HP1208R1191	13RC10_HP1209R1192	13RC11_HP1210R1193	13RC12_HP1211R1194	13RD1_HP1212R1195	13RD2_HP1213R1196	13RD3_HP1214R1197	13RD4_HP1215R1198	13RD5_HP1216R1199	13RD6_HP1217R1200	13RD7_HP1218R1201	13RD8_HP1219R1202	13RD9_HP1220R1203	13RD10_HP1221R1204	13RD11_HP1222R1205	13RD12_HP1223R1206	13RE1_HP1224R1207	13RE2_HP1225R1208	13RE3_HP1226R1209	13RE4_HP1227R1210	13RES_HP1228R1211	13RE6_HP1229R1212	13RE7_HP1230R1213	13RE8_HP123_R1214	13RE9_HP1232R1215	13RE10_HP1233R1216	13RE11_HP1234R1217	13RE12_HP1235R1218	13RF1_HP1236R1219

5758) 5759)	5760)	5761)	5762)	5763)	5764)	5765)	2266)	5767)	5768)	2,6979	(0775	5771)	5772)	5773)	5774)	5775)	5776)	5777)	5778)	5779)	5780)	5781)	5782)	5783)	5784)	5785)	5786)	5787)	5788)	2789)
(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.
CAUCAUCAUATGTTTGAAACCATTGCCTTT CAUCAUCAUGAATCTCTATGATAGGGTTAA	CAUCAUCAUATGCAATATTCTTCTTTGCTG	CUACUACUAGACTATCTATTAACATAAGAG	CUACUACUATTTTGACTTAAGCCACAAATT	CUACUACUATTATGACTCCTTGTTTTTGAA	CUACUACUACTCTATTTTAAAGTTTTTCTA	CUACUACUATGTTTAGTCCTTTTCGTCTTC	CUACUACUATTAAAAAATCATTCCTCCTAT	CUACUACUAACCICATITIAAACCICCITI	CUACUACUATCATCTTAATACTCTCTTAAA	CUACUACUATCTCTTTCATAATAACCCTTC	CUACUACUATTCATAAGCTTGTTTTCCTGA	CUACUACUATCAAACTCGTTCAAAATAGGT	CUACUACUACTACATCTTGCGGTAATTGAT	CUACUACUAGTTCTTATGCGATGGATAAAT	CUACUACUATTATTGGGCGTAAGCTTCTAG	CUACUACUATCAACTTTGATACGCCATATC	CUACUACUACCCAAAGCTACCTGTCATACA	CUACUACUATTAAATCACCACCCTAATTTA	CUACUACUATCACTGCTTGCATGACTTATT	CUACUACUAACCCGCTTATAAGAATTTTTG	CUACUACUATTTCATACAAATTCAATGGTG	CUACUACUATCAGTCGTTACCTCCTTTATC	CUACUACUATTACTTAGAATACAATTCTAC	CUACUACUACCTCCTTACACTCTTCTTCTT	CUACUACUAATCTCCTTATTCGCTACTTGC	CUACUACUAATGCTTTATCCTTGTCTTTGT	CUACUACUAAATTCATTTATATCTAAAAGT	CUACUACUACCATTAACGCTCCGTAAGAAT	CUACUACUAGAÍTGCCATTAAAAGCCTACC	CUACUACUATTACITCIGCCCCCCCTTGITIT
13RH10_HP1269R1252 13RH11_HP1270R1253	13RH12_HP1271R1254	14SA1_HP1272S1255	14SA2_HP1273S1256	14SA3_HP1274S1257	14SA4_HP1275S1258	14SA5_HP1276S1259	14SA6_HP1277S1260	14SA7_HP1278S1261		14SA9_HP1281S1263	14SA10_HP1282S1264	14SA11_HP1283S1265	14SA12_HP1284S1266	14SB1_HP1285S1267	14SB2_HP1286S1268	14SB3_HP1287S1269	14SB4_HP1288S1270	14SB5_HP1289S1271		14SB7_HP1291S1273	14SB8_HP1292S1274	14SB9_HP1293S1275	14SB10_HP1294S1276	14SB11_HP1295S1277	14SB12_HP1296S1278		14SC2_HP1298S1280	14SC3_HP1299S1281	14SC4_HP1300S1282	14SC5_HP1301S1283

PAACTACGCCTTGATTT (SEO ID NO 5790)	(SEQ ID NO.		CITIACCAAAIGCIACA (SEQ ID NO. 5793)	CCAACTGGCTTTTCTCA (SEQ ID NO. 5794)	ACCCCTTATCTCACTTT (SEQ ID NO. 5795)	TTAGGCTTTCTTCACA (SEQ ID NO. 5796)	CATTATACAACCTCCG (SEQ ID NO. 5797)	ATACTCCCACTACTAAA (SEQ ID NO. 5798)	CCAACGCTAGAAGAATA (SEQ ID NO. 5799)	PATCTTTCAATTCAGTA (SEQ ID NO. 5800)	recetecetetete (SEQ ID NO. 5801)	TACCTTCTGCTTGATT (SEQ ID NO. 5802)	TRACTIGCCAATCTITT (SEQ ID NO. 5803)	ACCITIATITATGITTC (SEQID NO. 5804)	CTTAAGCACCAAGGGC (SEQ ID NO. 5805)	PACTCCTCTGTCTTATC (SEQID NO. 5806)	ACCECTCTAATGCGTCC (SEQ ID NO. 5807)	TACTTCGTTTCCATAG (SEQ ID NO. 5808)	PACCAAAATAGATTGAA (SEQ ID NO. 5809)	TAGAGGTGGAACAACG (SEQ ID NO. 5810)	TRAATAAGGCGTTGTT (SEO ID NO. 5811)	ACTCACATGTTTCATG (SEQ ID NO. 5812)	CCTTAGGCCCGATCAT (SEO ID NO. 5813)	TABARTCCAGGCTTGTT (SEO ID NO. 5814)	CTAATCCTTTAAGGTT (SEQ ID NO. 5815)	CAATAATCCCCATTGT (SEQ ID NO. 5816)	TTTGATTGCTTTTAAT (SEQ ID NO. 5817)	GATTAAAAAAGCCTT (SEQ ID NO. 5818)	CATTCTAACTGCTTCC (SEQ ID NO. 5819)	TGAACCAGTCTTTAAT (SEQ ID NO. 5820)	
CUACUACUATTTTAACTACGCCTTGATTT	CUACUACUAGTCATAGAGCGATCCCGTTCT	CUACUACUATTATTTTTAGCTGTTTTTACC	CUACUACUAAATCCTTTACCAAATGCTACA	CUACUACUACTTACCAACTGGCTTTTCTCA	CUACUACUAATTAACCCCTTATCTCACTTT	CUACUACUAACTCCTTAGGCTTTCTTCACA	CUACUACUTTTCATTATACAACCTCCG	CUACUACUAGCITATACTCCCACTACTAAA	CUACUACUATTACTCAACGCTAGAAGAATA	CUACUACUACTTTTATCTTTCAATTCAGTA	CUACUACUAATTATTGCCTCCCTCTTCTGC	CUACUACUACTACTTACCTTCTGCTTGATT	CUACUACUACCCCTTACTTGCCAATCTTTT	CUACUACUATTTAACCTTTATTTATGTTTC	CUACUACUACCTTTCTTAAGCACCAAGGGC	CUACUACUATTTTACTCCTCTGTCTTATC	CUACUACUATTATACCGCTCTAATGCGTCC	CUACUACUAAGGACTACTTCGTTTCCATAG	CUACUACUAATTATACCAAAATAGATTGAA	CUACUACUAACTCTTAGAGGTGGAACAACG	CUACUACUACCTTTTAAATAAGGCGTTGTT	CUACUACUATCCCTACTCACATGTTTCATG	CUACUACUATCAAGCCTTAGGCCCGATCAT	CUACUACUATCTTATAAATCCAGGCTTGTT	CUACUACUATCATTCTAATCCTTTAAGGTT	CUACUACUATCATTCAATAATCCCCATTGT	CUACUACUATCATGTTTGATTGCTTTTAAT	CUACUACUATTAGGGATTAAAAAAAGCCTT	CUACUACUAATCAACATTCTAACTGCTTCC	CUACUACUATTATTTGAACCAGTCTTTAAT	
14SC6 HP1302S1284	14SC7_HP1303S1285	14SC8_HP1304S1286	14SC9_HP1305S1287	14SC10_HP1306S1288	14SC11_HP1307S1289	14SC12_HP1308S1290	14SD1_HP1309S1291	14SD2_HP1310S1292	14SD3_HP1311S1293	14SD4_HP1312S1294	14SD5_HP1313S1295	14SD6_HP1314S1296	14SD7_HP1315S1297	14SD8_HP1316S1298	14SD9_HP1317S1299	14SD10_HP1318S1300	14SD11_HP1319S1301	14SD12_HP1320S1302	14SE1_HP1321S1303	14SE2_HP1322S1304	14SE3_HP1323S1305	14SE4_HP1324S1306	14SE5_HP1325S1307	14SE6_HP1326S1308	14SE7_HP1327S1309	14SE8_HP1328S1310	14SE9_HP1329S1311	14SE10_HP1330S1312	14SE11_HP1331S1313	14SE12_HP1332S1314	j

5822) 5823) 5824) 5825) 5825) 5827)	5829) 5830) 5831) 5832) 5833)	5834) 5835) 5836) 5837)	5839) 5839) 5840) 5841) 5842)	5844) 5845) 5845) 5846) 5847)	5849) 5850) 5851) 5852) 5853)
(SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO.		(SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO.	(SEQ ID NO. (SEQ I	(SEQ ID NO. (SEQ I	(SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO. (SEQ ID NO.
CUACUACUATTATTGTTGTTTAAATTGTGG CUACUACUACUATTAGTTTTTAAACA CUACUACUAGGTTTAGGCGTGTTTTTTAAT CUACUACUAGGCTAAACCTAAACTAGCC CUACUACUATAAGACGCTATTCATTGTATT CUACUACUATTTCATTTTTTTCATGATCCTG	CUACUACUAAATCAGTCTTCTTTCAAGCTA CUACUACUATTAGTAAGCAAACACATAATT CUACUACUATTTTTTAACTTTTTTCATTTT CUACUACUACTACAACCAGCCTTTCTTTTT CUACUACUAAGAGTTAATGGCGTTTGTCAT CUACUACUAAGAGTTAATGGCGTTTGTCCA	CUACUACUATCTTTTAATTTTGTGCTATAT CUACUACUACATCAATCATAAACTAAAATC CUACUACUAAGTCAAAAAGCTTCATTGTTC CUACUACUACGATTGGACTTTTTTATTTGAC	CUACUACUAACCCCATGAGTTTTTATTTCT CUACUACUACTCTATCGCAAAGACAATAAC CUACUACUATTAAGAGTCTTTTAGGAGAT CUACUACUATGAGGTGTTTTAGGGTTTTGTGG CUACUACUAGTCTTTAAGCCATTTTCATGT CUACUACUACUACATTAAGATAACTCCATCAT	CUACUACUACGTTATCAGTTGGCATGAAAT CUACUACUACUACTACCATTTTAAGCCTTTTCT CUACUACUAAACTCATGCATGCTTAAACCC CUACUACUAAACTCATGCATGCTTAAACCC	CUACUACUATCAAGTTGTAACTATATCATA CUACUACUATTATCCTTTTATAATTGTTTG CUACUACUATTATCCTTGAAATTGAACGCA CUACUACUATTTTATCAGCCGTTTTTAGA CUACUACUATTTTATCAGCCGTTTTTAGA
14SF2_HP1334S1316 14SF3_HP1335S1317 14SF4_HP1336S1318 14SF5_HP1337S1319 14SF6_HP1338S1320 14SF6_HP1339S1321	14SF9_HP1341S1323 14SF10_HP1342S1324 14SF11_HP1343S1325 14SF12_HP1344S1326 14SG1_HP1345S1327 14SG2_HP1346S1328	14SG3_HP1347S1329 14SG4_HP1348S1330 14SG5_HP1349S1331	14SG6_HP1350S1332 14SG7_HP1351S1333 14SG8_HP1352S1334 14SG9_HP1354S1335 14SG10_HP1355S1336	14SG12_HP1357S1338 14SH1_HP1358S1339 14SH2_HP1359S1340 14SH3_HP1360S1341 14SH4_HP1361S1342	14SH6_HP1362S1343 14SH6_HP1363S1344 14SH7_HP1364S1345 14SH8_HP1366S1347 14SH9_HP1367S1348

HP1368S1349 CUACUACUAATAAATCTTATTCAAAATCAA HP1370S1349 CUACUACUACUAATAAATCAAAATCAAAAATCAAAAAAAA
CUACUACUATAAAATTAGGCTAATTGTTTT
CAUCAUCAUAGATAAGAAATGCAGTTTTTA
CAUCAUCAUTCTCTTATGTTAATAGATAGT
CAUCAUCAUTITGIGGCTIAAGICAAAAI
CAUCAUCAUATAACATGGACATTAGCATTT
CAUCAUCAUATGGATAAAAAGGACAAAAT
CAUCAUCAUAAGGAGGTTTTAAAATGAGGTA
CAUCAUCAUAAGAGAGTATTAAGATGAATA
CAUCAUCAUCATGCCTAGCGTGTTAGAAA
CAUCAUCAUAGCTTATGAAAATCTTTTTA
CAUCAUCAUTGATGATCAGTCTCATAGAAA
CAUCAUCAUCTGTTTTTGAAATCTTTACTC
CAUCAUCAUATGGATTTTATAGGGTTTTGAA
CAUCAUCAUATGAGTGTTTTAAATGCCAAA
CAUCAUCAUAATGAAAAAAGCGTTAATATC
CAUCAUCAUAAATGCAAGTTTCACAATATC
CAUCAUCAUGTGTGCCAAACATGCCTTGAA
CAUCAUCAUGGAGAGAGCATGAATGTCAAA
CAUCAUCAUGCATGTTAATAACCACCCAAC
CAUCAUCAUGTCATGCAAGCAGTGATTTTA
CAUCAUCAUATGAGACACAAACACGGATAC
CAUCAUCAUGGGTTAGAGCATGAAAGTTAT
CAUCAUCAUATGGCAAGATATAGAGGTGCA
CAUCAUCAUTAATGGCTAAGAGAAATGTAA
CAUCAUCAUATAAAGCATGGCAAGGATTGC
CAUCAUCAUATGAAAGTCAGGCCATCAGTG
CAUCAUCAUTTAATGGCAAGAGATGATGTT
CAUCAUCAUTTAATGGCAATCTCTATTAAA
CAUCAUCAUATGAATAAAGCTATTGCTAGT
CAUCAUCAUATGATAATGGGATTAGAAAAT

	. 5887)	. 5888)	. 5889)	2890)	5891)	5892)	5893)	5894)	5895)	2896)	5897)	5898)	2899)	2800)	5901)	5902)	5903)	5904)	2902)	2906)	2807)	5908)	2909)	5910)	5911)	5912)	5913)	5914)	5915)	5916)	5917)	
(טבע ובי ואס	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEC) ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NÓ.	(SEQ ID NO.	\mathbf{Q}	(SEC) ID NO.	(SEQ ID NO.	(SEQ ID NO.	
CAUCAUCAUTATGACAGAAAGGTAT	CAUCAUCAUGTGATGAACGCGAAAGCATTG	CAUCAUCAUATGTCAAGAATCGGGAAAAGA	CAUCAUCAUGGATAAGATATGGTAAATGAT	CAUCAUCAUAAAAGTGAGATAAGGGGTTAA	CAUCAUCAUCATGTTTGGTTTGAAACAATT	CAUCAUCAUATGAAAAGCGAAATCAAAAAA	CAUCAUCAUATGATACAGAGTTTTACAAGA	CAUCAUCAUAGGGTAAGCAATGAATACAAA	CAUCAUCAUATGAAATATACTGAATTGAAA	CAUCAUCAUAATCATGTTAATGCCAAAAAG	CAUCAUCAUGGCATGGGACAAAAAGTTAAT	CAUCAUCAUATGAGTAAAGCGTTATTAAGA	CAUCAUCAUAATGTCTAGGTCAATTAAAAA	CAUCAUCAUATGGCGATTAAAACTTATAAG	CAUCAUCAUATGGCAGACATCATGGATATA	CAUCAUCAUATGAGTAAGGCCATCGTTTTA	CAUCAUCAUGGTTAGATATGGAATTTTTAG	CAUCAUCAUTTAGGAGAGTTTATGGAAAAA	CAUCAUCAUTAAAAATGCGCTACGATTAT	CAUCAUCAUGGTGTTTTTAATGATTTTTA	CAUCAUCAUTIGGGTTGCGTATCAATGACT	CAUCAUCAUATGAATCCTGAAAAAGCCACT	CAUCAUCAUATGCAATTTAGAATTGAACAT	CAUCAUCAUCAAAACGATGAAAAAGTTAGC	CAUCAUCAUGAGCATGCTATCTTTTATAAG	CAUCAUCAUGAATGAAACGGATTTTATGGT	CAUCAUGGGATTATTGAATGATAGAAA	CAUCAUCAUTAGAATGTTGATGCATTCTAT	CAUCAUCAUTGTTGATGCATGAGTTTCTAA	CAUCAUCAUTCGTGGAATTGAGTTATTATG	CAUCAUCAUATGAGATTTTTTGCTTTTTC	
77777	14RC7_HP1303R1285	14RC8_HP1304R1286	14RC9_HP1305R1287	14RC10_HP1306R1288	14RC11_HP1307R1289		14RD1_HP1309R1291	14RD2_HP1310R1292	14RD3_HP1311R1293	14RD4_HP1312R1294	14RD5_HP1313R1295	14RD6_HP1314R1296	14RD7_HP1315R1297	14RD8_HP1316R1298	14RD9_HP1317R1299	14RD10_HP1318R1300	14RD11_HP1319R1301	14RD12_HP1320R1302	14RE1_HP1321R1303	14RE2_HP1322R1304	14RE3_HP1323R1305	14RE4_HP1324RT306	14RE5_HP1325R1307	14RE6_HP1326R1308	14RE7_HP1327R1309	14RE8_HP1328R1310	14RE9_HP1329R1311	14RE10_HP1330R1312	14RE11_HP1331R1313	14kE12_HP1332R1314	14RF1_HP1333R1315	

Areray cetan cadyl	A STATE OF THE PARTY OF THE PAR		200
AFE DELIGIBLE	CAUCAUCAUAIGICAAAAAAAGIAGCIAIA	(SEC ID NO.	29.10
14RF3_HP1335R1317	CAUCAUCAUTGGTTAAAAAAAGGTGGTTAT	(SEQ ID NO.	5919)
14RF4_HP1336R1318	CAUCAUCAUGTAATGGCCAAAATTGAATTG	(SEQ ID NO.	5920)
14RF5_HP1337R1319	CAUCAUCAUGCGTCTAGCTTTGAATACAAT	(SEQ ID NO.	5921)
14RF6_HP1338R1320	CAUCAUCAUAATGGATACACCCCAATAAAGA	(SEQ ID NO.	5922)
14RF7_HP1339R1321	CAUCAUCAUATGTCTGTATCGCATGTTGCT	(SEQ ID NO.	5923)
14RF8_HP1340R1322	CAUCAUCAUAAATGAAAAGCATCAGAAGAG	(SEQ ID NO.	5924)
14RF9_HP1341R1323	CAUCAUCAUATGAAAATTTCTCCATCTCCA	(SEQ ID NO.	5925)
14RF10_HP1342R1324	CAUCAUCAUAACATGAAAAAATCCCTCTTA	(SEQ ID NO.	5926)
14RF11_HP1343R1325	CAUCAUCAUTCATGGAATTTTTATCCTCAC	(SEQ ID NO.	5927)
14RF12_HP1344R1326	CAUCAUCAUAAGGATCGCTTATGGTGAACG	(SEQ ID NO.	5928)
14RG1_HP1345R1327	CAUCAUCAUTTCATGTTAGCTAAAATGTCG	(SEQ ID NO.	5929)
14RG2_HP1346R1328	CAUCAUCAUAAAGGGAAAACATGCCAATTA	(SEQ ID NO.	5930)
14RG3_HP1347R1329	CAUCAUCAUGAACAATGAAGCTTTTTGACT	(SEQ ID NO.	5931)
14RG4_HP1348R1330	CAUCAUCAUATGAAGTCAAATAAAAAGTCC	(SEQ ID NO.	5932)
14RG5_HP1349R1331	CAUCAUCAUTAAAAACTCATGGGGTTTTTA	(SEQ ID NO.	5933)
14RG6_HP1350R1332	CAUCAUCAUGGGTGGTGTTATTAACAATGA	(SEQ ID NO.	5934)
14RG7_HP1351R1333	CAUCAUCAUAGGACTCTTAATGGACTATCA	(SEQ ID NO.	5935)
14RG8_HP1352R1334	CAUCAUCAUATGGATTTTTAAAAGAAAAC	(SEQ ID NO.	5936)
14RG9_HP1354R1335	CAUCAUCAUACATGCTAAAAGAATATTTAG	(SEQ ID NO.	5937)
14RG10_HP1355R1336	CAUCAUCAUATGGAGATTAGAACCTTTTTA	(SEQ ID NO.	5938)
14RG11_HP1356R1337	CAUCAUCAUGAATTTCATGCCAACTGATAA	(SEQ ID NO.	5939)
14RG12_HP1357R1338	CAUCAUCAUATGGCAGGGTTAAAATGGTAG	(SEQ ID NO.	5940)
14RH1_HP1358R1339	CAUCAUCAUATGTTATCTTCTAGTGATTTG	(SEQ ID NO.	5941)
14RH2_HP1359R1340	CAUCAUCAUATGGCTATTTGGGGGTGGTGT	(SEQ ID NO.	5942)
14RH3_HP1360R1341	CAUCAUCAUCAAATCATTGCTTAAAAAAT	(SEQ ID NO.	5943)
14RH4_HP1361R1342	CAUCAUCAUGGTGTGTGGGGTGTTTTTAAG	(SEQ ID NO.	5944)
14RH5_HP1362R1343	CAUCAUCAUAATGGATCATTTAAAGCATTT	(SEQ ID NO.	5945)
14RH6_HP1363R1344	CAUCAUCAUAAAGATGCTTTCAGTGTATGA	(SEQ ID NO.	5946)
14RH7_HP1364R1345	CAUCAUCAUGITGGCTATCGCTTTAACCCA	(SEQ ID NO.	5947.)
14RH8_HP1366R1347	CAUCAUCAUGATATTTGACATGCCAAAATT	(SEQ ID NO.	5948)
14RH9_HP1367R1348	CAUCAUCAUTGTTTGATTTTGAATAAGATT	(SEQ ID NO.	5949)

								-								-															
5982)	5983)	5984)	5985)	5986)	2987)	2988)	2989)	2880)	5991)	5992)	5993)	5994)	5995)	2996)	5997)	2998)	2999)	(0009	6001)	6002)	6003)	6004)	6005)	(9009)	(2009	6008)	(6009	601Ö)	6011)	6012)	6013)
(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ.ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.
CUACUACUACATTTAAGAACGCTCCAAATA	CUACUACUATTAATGATACTCGTCTATGTG	CUACUACUATCACCCCATTAACCCCAAATC	CUACUACUATCAAAGAATGGCACAATCTCC	CUACUACUATCACAAACCACTTAAATTTTC	CUACUACUAAAAAGTTCTCTCATTAATGA	CUACUACUACTITITCATCAAGITITCTITI	CUACUACUATGGGGCTTATCGAATCAAATT	CUACUACUATTTAATCATTCTAGATCAAAA	CUACUACTACCTCATGCCCGCCAGCTTG	CUACUACUATGTTGGGGTGTGAATTTTATT	CUACUACUAGGGGGGGGTTTATTCTACATT	CUACUACUACGITATTTCGCATTCAAAAGG	CUACUACUATTAGGCGTTTTGATAAGGAAG	CUACUACUAGTTTTGTGTATCCATTAGAT	CUACUACUATGICCTITAAGAGAGIITGA	CUACUACUACCCTATCTCAAAATCTTCACT	CUACUACUATTTCTAGCCGATGATTTTGGG	CUACUACUATTCCATGATATTCCTTTTATC	CUACUACUAGCATTTAAAGCTCTTTAGTCC	CUACUACUAATCCTTTTATCATCGCTCTTT	CUACUACUAGICITITATICITITITAG	CUACUACUACACTTCATGCTTTATTGTTCC	CUACUACUATTAAAAACGATAAACATAATC	CUACUACUACTATAAAATAACCGATGAAAA	CUACUACUATCAAATTTGCTGAGAGAGTTT	CUACUACUATCATGCTTTAAGCCCTAATTC	CUACUACUATCAAAAAGAATGGGCATGACA	CUACUACUACATTAGCCTTTTAAAAGGTAA	CUACUACUACCACAAACGCCCCAATCAATA	CUACUACUAAAAAATCACTCCCTTAAAAAC	CUACUACUATCAAAACACCACCGTTTTATT
15SC6 HP1401S1381	15SC7_HP1402S1382	15SC8 HP1403S1383	15SC9 HP1404S1384	15SC10 HP1405S1385	15SC11 HP1406S1386	15SC12 HP1407S1387	15SD1 HP1408S1388	15SD2 HP1409S1389	15SD3_HP1410S1390	15SD4 HP1411S1391	15SD5_HP1412S1392	15SD6 HP1413S1393	15SD7 HP1414S1394	15SD8 HP1415S1395	15SD9 HP1416S1396	15SD10 HP1418S1397	15SD11 HP1419S1398	15SD12 HP1420S1399	15SE1 HP1421S1400	15SB2 HP1422S1401	15SE3_HP1423S1402	15SE4 HP1424S1403	15SE5 HP1425S1404	15SE6 HP1426S1405	15SE7 HP1428S1407	15SE8 HP1429S1408	15SE9 HP1430S1409	15SE10 HP1431S1410	15SE11 HP1432S1411	15SE12_HP1433S1412	15SF1 HP1434S1413

CUACUACUATTAGAGAATGTTTGGGAAAAT CUACUACUATTATAGAGAAAGAGGAAGAGCTAAAAAT
CUACUACUAATGCGTCAAGGCTTAATGACC CUACUACUATGAGTTTCATTCGCCCCCTTT CUACUACUACTACCATTTCTTTCATTATTA CUACUACUATTAGGCTTTTGCTTAATAATCTTC
CUACUACUACTAAAACTAATTTTTTGATT CUACUACUAAGGGTTTTAGACGGAAAGCTTT CUACUACUATTATTGTTTCGCATAGGTATG
CUACUACUATGTGATTAAACCTTAATGATG CUACUACUATTTGCATCAATGTTCCTTTTT CUACUACUATCATTCATTGTTAAAGTCGTT CUACUACUATTCATTTGCTAAGCAAAATT
CUACUACUATTAGAAATCCACCCGTAATT CUACUACUAATTCCTCTTATAACCCCGTAT CUACUACUATTTCATTATTAATCCTTACTC CUACUACUACCTACTTTTTAACCATGCCCA
CUACUACUATAATTTAAAACATACGCTTA CUACUACUAGATACCCCTTACAATAACGCT CUACUACUAAAGCTAATCCCCTTTAACATT CUACUACUACTCAAGCTAAATCCCTCCACT
CUACUACUATAAATCAAAAAGGGGTTTAG CUACUACUACUAACTCAAGGGGTTTTAA CUACUACUATTTTATTTTTTAACGGGCT CUACUACUATTTTTCCTTTCTCCAAAATT CUACUACUACCGCGGCGATTAAAGGTGTAATTT
CUACUACUAGTTAGTAGCGTTCATTATATG

15SH10 HP1467S1446	CUACUACUAAAAAGGTTAAAAATTTATAGCT	(SEQ ID NO.	6046)
15SH11_HP1468S1447	CUACUACUATTAGCCAACTTCAAAATCCA	(SEQ ID NO.	6047)
15SH12_HP1469S1448	CUACUACUAGGTTAAAAATCCCTCAAGTAA	(SEQ ID NO.	6048)
15RA1_HP1372R1352	CAUCAUCAUGCATGCGTTTTTATTTTAAAT	(SEQ ID NO.	6049)
15RA2_HP1373R1353	CAUCAUCAUGGCATGATTTTTAGCAAATTG	(SEQ ID NO.	6050)
15RA3_HP1374R1354	CAUCAUCAUAGAGGAATAACATGAACGAAA	(SEQ ID NO.	6051)
15RA4_HP1375R1355	CAUCAUCAUAGAGAGAGATTAAAAAATGAG	(SEQ ID NO.	6052)
15RAS_HP1376R1356	CAUCAUCAUATGGAACAAAGCCATCAAAAC	(SEQ ID NO.	6053)
15RA6_HP1377R1357	CAUCAUCAUATGTCTTTAAGGAGAAGATTT	(SEQ ID NO.	6054)
15RA7_HP1378R1358	CAUCAUCAUATGCGTTTAAAACATTTTAAA	(SEO ID NO.	6055)
15RA8_HP1379R1359	CAUCAUCAUAAATGACTGAAGATTTTCCTA	(SEQ ID NO.	(9209
15RA9_HP1380R1360	CAUCAUCAUGGCTTATGGGGGGGGAGTTTAG	(SEQ ID NO.	(209
15RA10_HP1381R1361	CAUCAUCAUTTTAGGGGTGCGAGGAGCGAA	(SEQ ID NO.	6058)
15RA11_HP1382R1362	CAUCAUCAUATGACCAATATCACCCCTGAA	(SEQ ID NO.	6029)
15RA12_HP1383R1363	CAUCAUCAUGTGTTTTTGGCTTCAGGGGTG	(SEQ ID NO.	(0909
15RB1_HP1384R1364	CAUCAUCAUAGGGAGAATGATGCAAAATAG	(SEQ ID NO.	6061)
15RB2_HP1385R1365	CAUCAUCAUAGGGTTTTTATGGATTACAAA	(SEQ ID NO.	6062)
15RB3_HP1386R1366	CAUCAUCAUAGTATTTTGAAAGTAGCTCCG	(SEQ ID NO.	6063)
15RB4_HP1387R1367	CAUCAUCAUGGGGGCGTGAATGATAAAAT	(SEQ ID NO.	6064)
15RB5_HP1388R1368	CAUCAUCAUCACATGAATAATATTTGGTTT	(SEQ ID NO.	(2909
15RB6_HP1389R1369	CAUCAUCAUTATGATGACAGAAGAAACCTA	(SEQ ID NO.	(9909
15RB7_HP1390R1370	CAUCAUCAUACCAATGAGCGAACCATTAGA	(SEQ ID NO.	(2909
15RB8_HP1391R1371	CAUCAUCAUGGTTAGCATGGGTGTTTCCGC	(SEQ ID NO.	(8909
15RB9_HP1392R1372	CAUCAUCAUATGAAATTTTTTTTTAAAG	(SEQ ID NO.	(6909)
15RB10_HP1393R1373	CAUCAUCAUAACATGCGAGATTTCAATAAC	(SEQ ID NO.	(0209)
15RB11_HP1394R1374	CAUCAUCAUATGAAAGATTCACTTCAAACT	(SEQ ID NO.	6071)
15RB12_HP1395R1375	CAUCAUCAUCACATGAAAAAAATTTTTTTT	(SEQ ID NO.	6072)
15RC1_HP1396R1376	CAUCAUCAUAATGGAAAAAGAGCTCGTTAC	(SEQ ID NO.	6073)
15RC2_HP1397R1377	CAUCAUCAUGGGTTTTTATGGCAAAATTG	(SEQ ID NO.	6074)
15RC3_HP1398R1378	CAUCAUCAUCATGACTATTGGGCTAGTTAA	(SEQ ID NO.	6075)
15RC4_HP1399R1379	CAUCAUCAUATAAAATGATTTTAGTAGGAT	(SEQ ID NO.	(920)
15RC5_HP1400R1380	CAUCAUCAUAGGAGTTTGTGTTGCATAAAA	(SEQ ID NO.	(// 09

V	>
۲	-
Y	3

					• .														•												
(8/09	(6209	(0809	6081)	6082)	6083)	6084)	(2809	(9809	(2809	(8809	(6809	(0609	6091)	6092)	6093)	6094)	6095)	(9609	(2609	(8609	(6609	6100)	6101)	6102)	6103)	6104)	6105)	6106)	6107)	6108)	6109)
(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	Ω		Ω	(SEQ ID NO.	(SEQ ID NO.
CAUCAUCAUAATGAACGCTTATTGTTTGAC	CAUCAUCAUTATGATGAAAACAGAAAAAAA	CAUCAUCAUGTTAAAATGGCGATCAAAAAA	CAUCAUCAUGGGTTAATGGGGTGACAGAAC	CAUCAUCAUAAAAATGCCTATGAATATAAG	CAUCAUCAUATTATGCAAGAGATTTTTTA	CAUCAUCAUGCTGTCATTAATGAGAACT	CAUCAUCAUATACCCCATGTCATCTTTTT	CAUCAUCAUATGATGGCAAAAATAGATGTA	CAUCAUCAUATGCCTAAAAAAAGAGCTATTA	CAUCAUCAUATGTTATTGGATTATGATTTT	CAUCAUCAUATGGGTTTTCAAAATGAAAT	CAUCAUCAUATGACCCCTGAACTAAACCTC	CAUCAUCAUCATGAACCAACGCATAGAAAC	CAUCAUCTTTGAGTATTTATAAAGACA	CAUCAUCAUCTAATGGATACACAAAACTTA	CAUCAUCAUAATGCTAGAAACCACCATTGA	CAUCAUCAUGGAATATCATGGAATCACAAC	CAUCAUCAUATGCCCCTAAAATCCTTAAAA	CAUCAUCAUAGGGCTTTTGAAAACTTTACA	CAUCAUCAUTCAGTGGAAGAATACAAAGAC	CAUCAUCAUCATGCGAATAGACAAATTTTT	CAUCAUCAUATTTGTTTGAAGTTTCAAATT	CAUCAUCAUGTAATATGTTAGCGCAATTAG	CAUCAUCAUTCTATGCTAGGGTTTTAATCTT	CAUCAUCAUTAAAGCATGAAAGCTAGTATT	CAUCAUCAUATGCCCATTCTTTTTGATTGT	CAUCAUCAUTATGACGGATAACAACCAAAA	CAUCAUCAUTTATGGTAGTAGCTAAAAAGT	CAUCAUCAUGAGCTAGAATTTAAATTTCAA	CAUCAUCAUATGCTAAGCTATAAGCATTCT	CAUCAUTGAGATAAAGATGTTAGAATT
15RC6_HP1401R1381	15RC7_HP1402R1382	15RC8_HP1403R1383	15RC9_HP1404R1384	15RC10_HP1405R1385	15RC11_HP1406R1386	15RC12_HP1407R1387	15RD1_HP1408R1388	15RD2_HP1409R1389	15RD3_HP1410R1390	15RD4_HP1411R1391	15RD5_HP1412R1392	15RD6_HP1413R1393	15RD7_HP1414R1394	15RD8_HP1415R1395	15RD9_HP1416R1396	15RD10_HP1418R1397	15RD11_HP1419R1398	15RD12_HP1420R1399	15RE1_HP1421R1400	15RE2_HP1422R1401	15RE3_HP1423R1402	15RE4_HP1424R1403	15RE5_HP1425R1404	15RE6_HP1426R1405	15RE7_HP1428R1407	15RE8_HP1429R1408	15RE9_HP1430R1409	15RE10_HP1431R1410	15RE11_HP1432R1411	15RE12_HP1433R1412	15RF1 HP1434R1413

1	٠,	
i		
i	,	٠
•	•	3

 \mathbb{I}

6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	(27) 28)	· (9)	24) 25)	33)	22)	21)	19) 20)	6118).	6117)	6115) 6116)	6114).	6113)	6112)	6111)	
NO. 6134) NO. 6135) NO. 6136) NO. 6137) NO. 6139) NO. 6140)			10. 6127 (10)10. 6128 (10)		(10. 6124) (10. 6125)		(O. 6122)		VO. 6119 VO. 6120					٠.			
	(SEQ ID NO (SEQ ID NO (SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEC ID NO	100
CAUCAUCAUAGTGGAGGATTTAGCTTGAG CAUCAUCAUGTTAGACAATGAAAGAGAATA CAUCAUCAUCAUTCATGAAAAAAATCCATTT CAUCAUCAUCAUAATGTTTGATAAAAAACTTTC CAUCAUCAUCAUAATAATGATGAGAGCTACGG CAUCAUCAUTTGGAAAGGCATGTGAATTAC CAUCAUCAUTTAATGAAGGCATGTGAATTAC CAUCAUCAUTTAATGAAGACAGAGAAACA	CAUCAUCAUAACAATGAAAAATCAAGTTAA CAUCAUCAUCATTATTGAAAACAAA CAUCAUCAUATGTCAGAAATGATTAACGGG	CAUCAUCAUGAGTAAGGATTAATAATGAAA CAUCAUCAUGATAAGCAAATTGTGGATAAA	CAUCAUCAUATGAAAAATACATGGTCATCA CAUCAUCAUGACCATTAAAGGAGATTTTATG	CAUCAUCAUTGATGCAAAATTTTATTGAAA	CAUCAUCAUTACCTATGCGAAACAATAAAA CAUCAUCAUATGGATAAAAAACAACAATAAT	CAUCAUCAUTAATGCCAGACGAGCTAAGGG	CAUCAUCAUTTTTAAATGAAACGCACTTAC	CAUCAUCAUGAGCGGTGAAAAAAGTAGAAT	CAUCAUCAUAAAAAGGGGGGCGAATGAACT	CAUCAUCATGACGCATGTTTTGAAGT	CAUCAUCAUTAAGAGATTAAACATGCTCAT	CAUCAUCAUALGGCGI I I I I GGCAI AAAAGA CAUCAUCAUTTTATGATGGATCCAATTAAA	CAUCAUCAUATGGACAATAGCACAGACAGA	CAUCAUCAUGCATGITITITAAAACTIAIC	CAUCAUCAUATGAGTGAAAACATTAAAGGA))))) ++++11111+>+>>>>++>++>	CAUCAUCAUATGGCGTGTAAATTTTGCCCC
15RH2_HP1459R1438 15RH3_HP1460R1439 15RH4_HP1461R1440 15RH5_HP1462R1441 15RH6_HP1463R1442 15RH7_HP1464R1443 15RH9_HP1465R1444	15RG11_HP1456R1435 15RG12_HP1457R1436 15RH1_HP1458R1437	15RG9_HP1454R1433 15RG10_HP1455R1434	15RG7_HP1452R1431 15RG8_HP1453R1432	15RG6_HP1451R1430	15RG5_HP1450R1428	15RG3_HP1448R1427	15RG2_HP1447R1426	15RG1_HP1446R1425	15RF11_HP1444R1423 15RF12_HP1445R1424	15RF10_HP1443R1422	15RF9_HP1442R1421	15RF8_HP1441R1420	15RF6_HP1439R1418	15RF5_HP1438R1417	15RF4_HP1437R1416		15RF3_HP1436R1415

15RH10_HP1467R1446	:	(SEQ ID NO.	6142)	
15KH11_HP1468K1447	_	(SEQ ID NO.	6143)	
15RH12_HP1469R1448	_	(SEQ ID NO.	6144)	
16SA1_HP1470S1449	CUACUACUACTAACCTTTTAATTCATTCCA (S	(SEQ ID NO.	6145)	
16SA2_HP1471S1450	CUACUACCAACCCCTTTTAAAATAACGAGT (S	(SEQ ID NO.	6146)	
16SA3_HP1472S1451	CUACUACUATATCGCTTTGGGGGCATTTGG (S	SEQ ID NO.	6147)	
16SA4_HP1473S1452	CUACUACUAAAAATAAAATTATAACTCATT (S	SEQ ID NO.	6148)	
16SA5_HP1474S1453	CUACUACUAGGTTAAACAGCGCATTTTATA (S	(SEQ ID NO.	6149)	
16SA6_HP1475S1454	CUACUACUACCITCTAACACCACATACAIT (S	(SEQ ID NO.	6150)	
16SA7_HP1476S1455	CUACUACUATCAGITCAITCCCCAICGIGG (S	(SEQ ID NO.	6151)	
16SA8_HP1477S1456	CUACUACUATITCAIGAAIGICCITIAIAA (S	(SEQ ID NO.	6152)	
16SA9_HP1478S1457	CUACUACUATCAAAACCCGTTATCCACTTT (S	(SEQ ID NO.	6153)	
16SA10_HP1479S1458	CUACUACUATCAAAATCCATCATTCTAAAA (S	(SEQ ID NO.	6154)	
16SA11_HP1480S1459	CUACUACUAGCCTTAAAGGTATTTTTTAA (S	(SEQ ID NO.	6155)	
16SA12_HP1481S1460	CUACUACUATCAACCCTCTTTAATCGTTCT (S	(SEQ ID NO.	6156)	٠.
16SB1_HP1482S1461	CUACUACUACTTTAAGCCTTTTGGTCTGGC (S	(SEQ ID NO.	6157)	
16SB2_HP1483S1462	CUACUACUAACATTCCTTTAGTTTTTTTA (S	(SEQ ID NO.	6158)	
16SB3_HP1484S1463	CUACUACUATTAAAAAGGCTTGACAACCAC (S	(SEQ ID NO.	6159)	
16SB4_HP1485S1464	CUACUACUATCCCTAATTTATCTTATTTG (S	(SEQ ID NO.	6160)	
16SB5_HP1486S1465	CUACUACUATGAGATTTTTAAGCGTTTTCA (S)	(SEQ ID NO.	6161)	•
16SB6_HP1487S1466	CUACUACUAAAAAAATTCATGCACTAGCC (S	(SEQ ID NO.	6162)	
16SB7_HP1488S1467	CUACUACUATTTTAAGGTTTAATGGTAACT (SI	(SEQ ID NO.	6163)	
16SBB_HP1489S1468	CUACUACUACCTTAATAAACAAATTCATAA (SI	(SEQ ID NO.	6164)	
16SB9_HP1490S1469	CUACUACUATCATGCTTCATTTTCTCCCTG (SI	(SEQ ID NO.	6165)	•
16SB10_HP1491S1470	CUACUACUAAAACCCTAGAAATACTTTTCT (SI	(SEQ ID NO.	6166)	
16SB11_HP1492S1471	CUACUACUTAAAGCTTATCAAACTCC (SI	(SEQ ID NO.	6167)	
16SB12_HP1493S1472	CUACUACUATCATTCTTTAAGCCTTATTGG (S	(SEQ ID NO.	6168)	
16SC1_HP1494S1473	CUACUACUATGTTTTATCCTTGTTTTAAAT (SE	(SEQ ID NO.	6169)	
16SC2_HP1495S1474	CUACUACUAAAACCCTTAAAAATCAAAAAC (SE	(SEQ ID NÖ.	6170)	
16SC3_HP1496S1475	CUACUACUATCACTTCGCTTTAATCACACC (SE	(SEQ ID NO.	6171)	
16SC4_HP1497S1476	CUACUACUATTTGATAGAGTGCATTTAAC (SE	(SEQ ID NO.	6172)	
16SC5 HP1498S1477	CUACUACUAATAAATCCTACAACCTCTTAT (SE	(SEC) ID NO.	6173)	

16SC6 HP1499S1478	CUACUACUATTAGCACATGGTGGTTGAGTT	(SEO ID NO.	6174)
16SC7_HP1500S1479	CUACUACUACAATCAAAATAAAGAATTGAA	(SEQ ID NO.	6175)
16SC8_HP1501S1480	CUACUACTACCAAACTTAAAAAGTATA	(SEQ ID NO.	6176)
16SC9_HP1502S1481	CUACUACUATGAAACGCTCTTAAACAAACC	(SEQ ID NO.	6177)
16SC10_HP1503S1482	CUACUACUAGGTTTGTTTAAGAGCGTTTCA	(SEQ ID NO.	6178)
16SC11_HP1504S1483	CUACUACUAAAGGGCGCTAGTTTAGAAGCG	(SEQ ID NO.	6179)
16SC12_HP1505S1484	CUACUACUATCTTAAGAGTTTTCTATCCAT	(SEQ ID NO.	6180)
16SD1_HP1506S1485	CUACUACUAAGTCTCATGATGGGAAAAAG	(SEQ ID NO.	6181)
16SD2_HP1507S1486	CUACUACUACTAGCGTTCAATCACTTCATA	(SEQ ID NO.	6182)
16SD3_HP1508S1487	CUACUACUAGCTTCAATCCTCACTTGGTGC	(SEQ ID NO.	6183)
16SD4_HP1509S1488	CUACUACUATCATAAGACTTTCTTTTCCTT	(SEQ ID NO.	6184)
16SD5_HP1510S1489	CUACUACUAGGCTAAAGATTGCTTTCATAG	(SEQ ID NO.	6185)
16SD6_HP1511S1490	CUACUACUATTACTGAGCGGCTGAATCAAG	(SEQ ID NO.	6186)
16SD7_HP1512S1491	CUACUACUATICATITIAGAACIGATAGGA	(SEQ ID NO.	6187)
16SD8_HP1513S1492	CUACUACUACGAATTTTTAAGCTTTTAATTAA	(SEQ ID NO.	6188)
16SD9_HP1514S1493	CUACUACUATTAATTCTTAAACAAAGACTC	(SEQ ID NO.	6189)
16SD10_HP1515S1494	CUACUACUACTTGAAAAACTATCGTTTGAT	(SEQ ID NO.	6190)
16SD11_HP1516S1495	CUACUACUATTATTTGTTCTGTTGCCAATA	(SEQ ID NO.	6191)
16SD12_HP1517S1496	CUACUACUAATTCACTGCCCCTCTTCAATG	(SEQ ID NO.	6192)
16SE1_HP1518S1497	CUACUACUATTAATTCCTTACATCGCTTAA	(SEQ ID NO.	6193)
16SE2_HP1519S1498	CUACUACUATTAAATTTTGACTTTCTCCAA	(SEQ ID NO.	6194)
16SE3_HP1520S1499	CUACUACUATCAAACAAGATTTGTAAGATA	(SEQ ID NO.	6195)
16SE4_HP1521S1500	CUACUACUACTCTAATCTTTACGATTTAAA	(SEQ ID NO.	6196)
16SE5_HP1523S1501	CUACUACUATITICAATITICAAATGITICCC	(SEQ ID NO.	6197)
16SE6_HP1524S1502	CUACUACUAACACTTTAATACTTCCTGTTG	(SEQ ID NO.	6198)
16SE7_HP1525S1503	CUACUACUAGGTTGGAATTAGTTTAAAGGT	(SEQ ID NO.	6199)
16SE8_HP1526S1504	CUACUACUATTAAACTAATTCCAACCCTAC	(SEQ ID NO.	6200)
16SE9_HP1527S1505	CUACUACUACCACCATCTTAAACTTCGTTG	(SEQ ID NO.	6201)
16SE10_HP1528S1506	CUACUACUACTATAACCTATTTATGACTTT		6202)
16SE11_HP1529S1507	CUACUACUACCTTTTTTCATTCACTTGAAT	(SEQ ID NO.	6203)
16SE12_HP1530S1508	CUACUACUATTAAATTATAAACTATCAAT	(SEQ ID NO.	6204)
16SF1_HP1531S1509	CUACUACUACACACATTTAAAACACCAATA	(SEQ ID NO.	6205)

16SH10_HP1567S1544	CUACUACUAGCGGCTTATAATGGGTTAGTG (S	(SEQ ID NO.	6238)
16SH11_HP1568S1545	CUACUACUATCATGGTTTTTCGCCTTTCTT (S	(SEQ ID NO.	6239)
16SH12_HP1569S1546	CUACUACUACGCATTAAAAACCTCCTTTGA (S	SEQ ID NO.	6240)
i6RA1_HP1470R1449	CAUCAUCAUAAGAGGGTTGAATGATGGAGC (S	(SEQ ID NO.	6241)
16RA2_HP1471R1450	CAUCAUCAUGTGTTGTCAAGTAAGAAATT (S	(SEQ ID NO.	6242)
16RA3_HP1472R1451	CAUCAUCAUATGAATAAAGTTCAATCTATT (S	(SEQ ID NO.	6243)
16RA4_HP1473R1452	CAUCAUCAUAATGCGCTGTTTAACCTGTTT (S	(SEQ ID NO.	6244)
16RA5_HP1474R1453	CAUCAUCAUCTTAAAATGTATGTGGTGTTA (S	(SEQ ID NO.	6245)
16RA6_HP1475R1454	CAUCAUCAUGATGCAAAAAATCGGCATTTA (S	(SEQ ID NO.	6246)
16RA7_HP1476R1455	CAUCAUCAUCGCAAATCTTATAAAGGACAT (S	SEQ ID NO.	6247)
16RA8_HP1477R1456	CAUCAUCAUTITIGAAAAITITIAAICCITIT (S	(SEQ ID NO.	6248)
16RA9_HP1478R1457	CAUCAUCAUAGITITIAGAATGATGGATTT (S	(SEQ ID NO.	6249)
16RA10_HP1479R1458	CAUCAUCAUGGCTAGTTTGTGCTGAATGAA (S	(SEQ ID NO.	6250)
16RA11_HP1480R1459	CAUCAUCAUAGGGTTGAATGATTGATAGAA (S	(SEQ ID NO.	6251)
16RA12_HP1481R1460	CAUCAUCAUCTTAAAGCATGCGAGTGTTTG (S	(SEQ ID NO.	6252)
16RB1_HP1482R1461	CAUCAUCAUAATGTTATGCAAGATGAATTA (S	(SEQ ID NO.	6253)
16RB2_HP1483R1462	CAUCAUCAUATGAAAAAAAAAAAGCATCTC (S	(SEQ ID NO.	6254)
16RB3_HP1484R1463	CAUCAUCAUTGGTATGGGATTTTTGAATGG (S	SEQ ID NO.	6255)
16RB4_HP1485R1464	CAUCAUCAUGTGAAAACGCTTAAAAATCTC (S	(SEQ ID NO.	6256)
16RB5_HP1486R1465	CAUCAUCAUGGCTAGTGCATGAATTTTTT (S	(SEQ ID NO.	6257)
16RB6_HP1487R1466	CAUCAUCAUGGATTGTTTTGTTCAGATTGA (S	(SEQ ID NO.	6258)
16RB7 HP1488R1467	CAUCAUCAUATGTCAAATAGCATGTTGGAT (S	(SEQ ID NO.	6229)
16RB8_HP1489R1468	CAUCAUCAUAAGCATGAAAAAAAACAACCT (S	(SEO ID NO.	6260)
16RB9_HP1490R1469	CAUCAUCAUATGGGGAGGAATCAAGGAGCT (S	(SEQ ID NO.	6261)
16RB10_HP1491R1470	CAUCAUCAUCGATATGGAAATTAAAAACAT (S	SEQ ID NO.	6262)
16RB11_HP1492R1471	CAUCAUCAUGAGITITAAAAAAIGAIAGAA (S	(SEQ ID NO.	6263)
16RB12_HP1493R1472	CAUCAUCAUGCATGCAAAAGTTTGATTATG (S	SEQ ID NO.	6264)
16RC1_HP1494R1473	CAUCAUCAUATGAAACTTAAAAAAACCCTG (S	SEQ ID NO.	6265)
16RC2_HP1495R1474	CAUCAUCAUACAIGCAAGAAIICAGIIIGI (S	(SEQ ID NO.	(9979
16RC3_HP1496R1475	CAUCAUCAUATGTTAGAAGGCGTTATTAGA (S	(SEQ ID NO.	(2929
16RC4_HP1497R1476	CAUCAUCAUGTTATGACGCTTTTAGTAGGT (S	SEQ ID NO.	6268)
16RC5_HP1498R1477	CAUCAUCAUAGIGCGITIGITIAGAITIGI (S	(SEQ ID NO.	(6979

6270)	6271)	6272)	6273)	6274)	6275)	(9229)	6277)	6278)	6279)	6280)	6281)	6282)	6283)	6284)	6285)	(9879	6287)	6288)	6289)	6290)	6291)	6292)	6293)	6294)	6295)	(9679	6297)	6298)	6299)	6300)	6301)
(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.		(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEO ID NO.	SEC ID NO.	SEQ ID NO.	(SEG ID NO.
CAUCAUCAUAGGTTTTTGATGAGTTCTGTT	CAUCAUCAUTTATAATGTGTTCTAATTCTT	CAUCAUCAUGAGAGTGATGCTCAATTTTAT	CAUCAUCAUATGGATGCGATTTATCCTTAT	CAUCAUCAUAATTAAGGATTAAAAAAATGA	CAUCAUCAUATGGATAGAAAACTCTTAAGA	CAUCAUCAUATGAGACTTTATGAGAGTTTA	CAUCAUCAUGCAAGTTTGCAAGAAATTAAG	CAUCAUCAUAGTGTGGTGGCACACAAAATG	CAUCAUCAUATGCTTGAAACTTCTAGCCAT	CAUCAUCAUACGATTTTAAAAAATGGCTAG	CAUCAUCAUGAAAGTCTTATGAAAACTAAA	CAUCAUCAUATGAAAGCAATCTTTAGCCTC	CAUCAUCAUATGCTTAGAAATCAATTTCGT	CAUCAUCAVACTCATCATGGCTAAAGAAAC	CAUCAUCAUATGGAAAAAATCAGCGATCTT	CAUCAUCATCTATGAGAAAAAATCATA	CAUCAUCAUGGGCAGTGAATGGAAAAGTTA	CAUCAUCAUATGGATTATAAAAAATTAGAT	CAUCAUCAUATGATTCGTTTCGCTCACATC	CAUCAUCAUTIGCAAGAATGCAGACAATIT	CAUCAUCAUATGGGGTTAAAAATTATCAAT	CAUCAUCAUTAGGGGGTAGAGGTGAAAATC	CAUCAUCAUTTGCAAGAAACAGATAATTTA	CAUCAUCAUTIGATGAAATCTAAAATCACT	CAUCAUCAUAGGAAGTATTAAAGTGTGAAA	CAUCAUCAUATGAAACTGATTTCATGGAAT (CAUCAUCAUCATGAAAAAATCCCTTTGTCT (CAUCAUCAUATGCTTATTCCTTTTTATTTT (CAUCAUCAUGCCATGGATACCAACAACAAT (_	CAUCAUCAUA#GTTfGAAAAAATACGCAAG (
16RC6_HP1499R1478	16RC7_HP1500R1479	16RC8_HP1501R1480	16RC9_HP1502R1481	16RC10_HP1503R1482	16RC11_HP1504R1483	16RC12_HP1505R1484	16RD1_HP1506R1485	16RD2_HP1507R1486	16RD3_HP1508R1487	16RD4_HP1509R1488	16RD5_HP1510R1489	16RD6_HP1511R1490	16RD7_HP1512R1491	16RD8_HP1513R1492	16RD9_HP1514R1493	16RD10_HP1515R1494	16RD11_HP1516R1495	16RD12_HP1517R1496	16RE1_HP1518R1497	16RE2_HP1519R1498	16RE3_HP1520R1499	16RE4_HP1521R1500	16RES_HP1523R1501	16RE6_HP1524R1502	16RE7_HP1525R1503	16RE8_HP1526R1504	16RE9_HP1527R1505	16kE10_HP1528R1506	16RE11_HP1529R1507	16kB12_HP1530R1508	16RF1_HP1531R1509

i	b	4	
•	d	ř	
	•		

6302)	6303)	6304)	6305)	(306)	(2029	6308)	6309)	6310)	6311)	6312)	6313)	6314)	6315)	6316)	6317)	6318)	6319)	6320)	6321)	6322)	6323)	6324)	6325)	6326)	6327)	6328)	6329)	6330)	6331)	6332)	6333)
(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.
CAUCAUCAUATGTGTGGGATTGTAGGTTAT	CAUCAUCAUGATGTGGATCACCCAAGAAAC	CAUCAUCAUTTGCTTAACGCTATCAAGTTT	CAUCAUCAUGGAATGAGGAAAAACCATTAT	CAUCAUCAUTTTAATGAAAAAAATATTGTCG	CAUCAUCAUATGCATGCTTGAAAAAGTGTT	CAUCAUCAUGAGAGTTTAATGGCAGAGATA	CAUCAUCAUTTTTAATCATGGCAGATATT	CAUCAUCAUAATGATCCAATCCAGCCTTTA	CAUCAUCAUCAGATGGCAATCTTTGATAAC	CAUCAUCAUAGTGTTTTTAGACAGGCGTTT	CAUCAUCAUTIGAIGCCGCAAAACCAGCII	CAUCAUCAUATGAAAAATAGCCCTTTGAAT	CAUCAUCAUCATGAGGGCTTTACTTTTTT	CAUCAUCAUGTAGTGATGGATTTTATCAAT	CAUCAUCAUATGGATTGGGGTCGGTCGTT	CAUCAUCAUTTAGGAGGTTTTATGGAATTA	CAUCAUCAUGTGCCTTCTTTACTAGAAACT	CAUCAUCAUAATGGGACAAATTAAAGACAT	CAUCAUCAUGTCTATGAATCTCAAAAAAC	CAUCAUCAUTCTCAATGGATACCAAAAGAC	CAUCAUCAUATGGTAACCATGAAAGATTTA	CAUCAUCAUAGCCGAATAATGTCAGGAATT	CAUCAUCAUATGGATAATAGGAATATTGAT	CAUCAUCAUGTTCTATGCAAGCCATACACA	CAUCAUCAUCATGTTTTTATCTTCTTTGA	CAUCAUCAUTTTGAAAAAGGGGTTTTATTA	CAUCAUCAUATGACTACAGACAGAAATTTG	CAUCAUCAUGTTACGATATGTTAGTTACAA	CAUCAUCAUTTAATAAAGGGGTTTTTATGA	CAUCAUCAUGTATGAAAAATCTTCGCTATA	CAUCAUCAUATGCTCTCTTTAAAACAAGAT
16RF2_HP1532R1510	16RF3_HP1533R1511	16RF4_HP1534R1512	16RF5_HP1535R1513	16RF6_HP1536R1514	16RF7_HP1537R1515	16RF8_HP1539R1516	16RF9_HP1540R1517	16RF10_HP1541R1518	16RF11_HP1542R1519	16RF12_HP1543R1520	16RG1_HP1544R1521	16RG2_HP1545R1522	16RG3_HP1546R1523	16RG4_HP1547R1524	16RG5_HP1548R1525	16RG6_HP1549R1526	16RG7_HP1550R1527	16RG8_HP1551R1528	16RG9_HP1552R1529	16RG10_HP1553R1530	16RG11_HP1554R1531	16RG12_HP1555R1532	16RH1_HP1556R1533	16RH2_HP1557R1534	16RH3_HP1558R1535	16RH4_HP1559R1536	16RH5_HP1560R1537	16RH6_HP1563R1540	16RH7_HP1564R1541	16RH8_HP1565R1542	16RH9_HP1566R1543

	6364)	(SEQ ID NO.	CUACUACUACAAATTGACCCCTTGAATGTG CUACUACUACCACTTTTAATCAGTCGCTTCAC	17SC4_HP0143S1574 17SC5_HP0208S1575
	6363)	(SEQ ID NO.	CUACUACUATITACTATAACCATAACCCGC	17SC3_HP0120S1573
	6362)	(SEQ ID NO.	CUACUACUATTTAGCTTGAGCTTTAGAGCG	17SC2_HP0119S1572
-	6361)	(SEQ ID NO.	CUACUACUACCTTTTACTATAACCATAACC	17SC1_HP0118S1571
	6360)	(SEQ ID NO.	CUACUACUATTTTGAGAGATAACGATCGGC	17SB12_HP0107S1570
	6329)	(SEQ ID NO.	CUACUACUATITICACIGAAGCGITAAGCC	17SB11_HP0076S1569
	6358)	(SEQ ID NO.	CUACUACUÁCGATAGTATAATATGGTGGTG	17SB10_HP0058S1568
	6357)	(SEQ ID NO.	CUACUACUATTAATAATTGCGAATAAGCGC	17SB9_HP0009S1567
	6356)	(SEQ ID NO.	CUACUACUAATTCTGTTGAACTTGTCAATT	17SB8_HP1590S1566
	6355)	(SEQ ID NO.	CUACUACUAAAAGCTTAAATGGATTCTATT	17SB7_HP1588S1565
	6354)	(SEQ ID NO.	CUACUACUACTACTTTACCCACCACATAAC	17SB6_HP1587S1564
	6353)	(SEQ ID NO.	CUACUACUAGCTTATAGGGTAACCGTTCCG	17SB5_HP1586S1563
	6352)	(SEC) ID NO.	CUACUACUACCTTTTAGCGTTTGAGGGAAT	17SB4_HP1585S1562
	6351)	(SEQ ID NO.	CUACUACUATCCATTCACTCAAAACTTTTT	17SB3_HP1584S1561
	6350)	(SEQ ID NO.	CUACUACUAATCTTTAAGCCAAATATTTGA	17SB2_HP1583S1560
	6349)	(SEQ ID NO.	CUACUACUATTTTATCGCTTAATGAGTTGC	17SB1_HP1582S1559
	6348)	(SEQ ID NO.	CUACUACUAACCTTTGAGCTTTTTCATTGA	17SA12_HP1581S1558
	6347)	(SEQ ID NO.	CUACUACUATATCCCTTTACCATTGATAAG	17SA11_HP1580S1557
· - ·	6346)	(SEQ ID NO.	CUACUACUATAGCCTATGTTAGTTTTATT	17SA10_HP1579S1556
	6345)	(SEQ ID NO.	CUACUACUATICCAACAAATIAGAACTITT	17SA9_HP1578S1555
	6344)	₽	CUACUACUAAAACCAAATCCCTAATACTTA	17SA8_HP1577S1554
· ·	6343)	(SEQ ID NO.	CUACUACUATTTTAATCCTTTAATTTTTCC	17SA7_HP1576S1553
	6342)	(SEQ ID NO.	CUACUACUATTCCGATCACTTGGACATTTG	17SA6_HP1575S1552
	6341)	(SEQ ID NO.	CUACUACUATCATCTAATACCCTAAAGTCA	17SAS_HP1574S1551
	6340)	(SEQ ID NO.	CUACUACUAAGCCTTATTTAAGGGAAACT	17SA4_HP1573S1550
	6339)	(SEQ ID NO.	CUACUACUACCAAACCCATTAAAATTCCCT	17SA3_HP1572S1549
	6338)	(SEQ ID NO.	CUACUACUATTAATCATTCTCTCGTTAAAA	17SA2_HP1571S1548
	6337)	(SEQ ID NO.	CUACUACUATAAAACGCTATTAGAGGTAAA	17SA1_HP1570S1547
	6336)	(SEQ ID NO.	CAUCAUCAUCAAGATGAAGCGCTCAAGCTT	16RH12_HP1569R1546
	6335)	(SEQ ID NO.	CAUCAUCAUATGCGTTGGTGGTGTTTTTTG	16RH11_HP1568R1545
	6334)	(SEQ ID NO.	CAUCAUCAAAAAACCATGATTGTCATT	16RH10_HP1567R1544

	NO. 6368)					ġ.	Š.	ġ.	Ö.	ġ	ġ	9	Š.		_		Ö	9	ò.	Š.	Š.	9	Š.	S	ġ	9	9		ò.	ð.	D NO. 6397)	
(SEQ ID	(SECTIONO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID NO	(SEQ ID	(SEQ ID I	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID I	(SEQ IC	(SEQ IC	(SEQ	(SEQ	(SEQ		_	_		_	(SEQ ID	(SEQ ID	(SEQ ID	(SEQ ID	_		_	SEQ ID NO	
CUACUACUATTTTAAAACGCCCACAAACCC	CUACUACUATCTTCTTTGCTTCATGTGG	CUACUACUAATCCATTGCATTTGGGATATT	CUACUACUATTTGCACACAAGCCGCCCAAG	CUACUACUATACAGACTTGCAAAATAGCGC	CUACUACUATCATTGTCCTTAGTTTGTTGC	CUACUACUAAAAGGAGCGTATCGTCTGCTG	CUACUACUAGGCTTATTCTTATTGAGTATC	CUACUACUACCTAAATAATACTTACGCACC	CUACUACUACTATAGAGCCTTCTGTATTGC	CUACUACUACTCATCGCTGCTAAAGCTTGG	CUACUACUAGAGAGAAGTTATCATGCCAAC	CUACUACUATCTCGGTAATATTCGTATTGC	CUACUACUATTGCTGAATTGAGGCGGAATG	CUACUACUAATGCGTGATTTTATGCGTGCC	CUACUACUACTTTGCTTCATTAGGCGTTTG	CUACUACUATTTCGCATAGACCACGCTCCC	CUACUACUAGGCGTGCGCAGCGTATTATCG	CUACUACUACGCGCTTGTAACGATAATACG	CUACUACUATTTGGTTTTGCAAAGCGATTTC	CUACUACUATGCGCTTGAAGGGCGCTAATC	CUACUACUAACCTTGATTTTCTATATACGC	CUACUACUATITCIATATACGCCTTGATCG	CUACUACUATGCATGGATATTTCCTACCCC	CUACUACUAATGAATAACCCGGCGATAGTC	CUACUACUAAGAGGTTGAAAGGTGGGCTTG	CHACUAGUAGGCATGGCTTGCCTTATGTTT	CHACHAGUAGGATTTTGCAAGATTTCTTGC	CUACUACUATAGTGGGTTAAAGCGATAGCC	CUACUACUAAAACACTTCGTCCATGAGCAC	CUACUACUAATGCCTTAAAAGTTTAGCGCC	CUACUACUACATGCTGCCATAACAACAGC	
17SC6 HP0381S1576	17SC7 HP0451S1577	17SC8 HP0521S1578		175C10 HP0548S1580	178C11 HP0550S1581	175012 TT TT TT TT TT TT TT TT TT TT TT TT TT	178C12 III 001751583	1,501 mon 1581584	175D3 HD0722S1585	1750 TO TO TO TO TO TO TO TO TO TO TO TO TO	17SD HD0744S1587	17502 IF 0115255	LISDG_MEDIOSISS	1,5D/_MF0801,25C/1	LISCORUM OUCE	1/SDS_nFOGOESTS71	1/3D10_1150031232212 17SD11_HD0897S1593		172E1 HD0903S1595	17SE2 HP0904S1596	76513600H caser	1/2502020311 172504 UD009881598	1,252, III 2,522, I	COSTON COST	1/SEG_NETTOORICOS	I/SE/_HFII00SICOL	I/SEB_HFIZBUSIOUS	175E9_HP1353S1605 175E9_HP1353S1605	I SELOCIFICATION OF THE TOTAL OF THE TOTAL OF THE THE TOTAL OF THE TOT	1/3E11_nF138/31605	17SF1_HP1417S1607	

	6429)	(SEQ ID NO.	CAUCAUCAUAATGATTTCTCAAATGCTCAT	17KA8_HP1577R1554
. •	6428)	(SEC ID NO.	CAUCAUCAUGGIAIIAGAIGAAIAAAACCA CAIICAIICAIIAAACGAAGGAAGAATAA	17KA6_HP1575K1552
	6426)	(SEQ ID NO.	CAUCAUCTATGTTCAGCGGTCTAATCC	17RAS_HP1574R1551
	6425)	(SEQ ID NO.	CAUCAUCAUGGATAAAAGCATGTTTATAGA	17RA4_HP1573R1550
	6424)	Ω.	CAUCAUCAUGATGTCAAAAAAAATGAAGTG	17RA3_HP1572R1549
	6423.)	_	CAUCAUCAUAATGGGTTTGGCGTTGGAAAA	17RA2_HP1571R1548
	6422)	(SEQ ID NO.	CAUCAUCAUATGATTAAGTTATTGCTTTTA	17RA1_HP1570R1547
	6421)	(SEQ ID NO.	CUACUACUATGATCTTAATTTCTTCATCGG	17SH1_HP1517-2S1631
	6420)	(SEQ ID NO.	CUACUACUAAGCGAATTAGCGCACTTAATG	17SG12_HP1517-1S1630
	6419)	(SEQ ID NO.	CUACUACUAGTCGTTTCTTGGAAAGAGGCC	17SG11-HP1198-3S1629
	6418)	(SEQ ID NO.	CUACUACUACGCTCCAAGCTCCATTAAGCG	17SG10_HP1198-2S1628
	6417)	(SEQ ID NO.	CUACUACUAGCACGGTTGGCGTCATCATGC	17SG9_HP1198-1S1627
	6416)	(SEQ ID NO.	CUACUACUACCTCCTGTAACTCACATCAGC	17SG8_HP1157-2S1626
	6415)	(SEQ ID NO.	CUACUACUAGTTATTGTTAGGTGTCATCTC	17SG7-HP1157-1S1625
	6414)	(SEQ ID NO.	CUACUACUAGATTGATGATTGAGAGTAGGG	17SG6_HP922-3S1624
	6413)	(SEQ ID NO.	CUACUACUACGCTTTGAAAGGTTACATCCG	17SG5_HP922-2S1623
	6412)	(SEQ ID NO.	CUACUACUAGCGGTGTTTTGATTGTTGGTG	17SG4_HP922-1S1622
	6411)	(SEQ ID NO.	CUACUACUACCTCATTCCTAAATTGGAAGC	17SG3_HP887-2S1621
	6410)	(SEQ ID NO.	CUACUACUAAGIGCCAGITICCAAACGCAC	17SG2_HP887-1S1620
	6409)	(SEQ ID NO.	CUACUACUACGCATACAAGCCCACATCCAC	17SG1_HP610-2S1619
-	6408)	(SEO ID NO.	CUACUACUACGTACTAGAATGGAGCAATTG	17SF12_HP610-1S1618
	6407)	(SEQ ID NO.	CUACUACUATAATAGAGTCCCTTGTTCGCC	17SF11_HP609-2S1617
	6406)	(SEO ID NO.	CUACUACUAAATCGTGTCAGCTTTATCATC	17SF10_HP0609-1S1616
	6405)	(SEQ ID NO.	CUACUACUACTIGGCAGITICIGCGACATC	17SF9_HP0527-2S1615
	6404)	(SEQ ID NO.	CUACUACUAACAATCTAGAACCTGTTGTTC	17SF8_HP0527-1S1614
	6403)	(SEQ ID NO.	CUACUACUATTAATTTCGTTTGCTTGTGCC	17SF7_HP1589S1613
	6402)	(SEQ ID NO.	CUACUACUAGGITCAACCICIGCAICAIIC	17SF6_HP1562S1612
	6401)	(SEQ ID NO.	CUACUACUAAAAGGGCTCAACCTCTGCATC	17SF5_HP1561S1611
	6400)	(SEQ ID NO.	CUACUACCACGCATAAGCCAAGAACG	17SF4_HP1538S1610
	6399)	(SEQ ID NO.	CUACUACUACGTTTGGGTTTCCATTCTATC	17SF3_HP1522S1609
	6398)	(SEQ ID NO.	CUACUACUACTCGTGATGCCCGTGGCAGCA	17SF2_HP1427S1608

	•.		_																										
6430 6431	6432 6433	6434	6435	6436	6437)	6438)	6439)	6440)	6441)	6442)	6443)	6444)	6445)	6446)	6447)	6448)	6449)	6450)	6451)	6452)	6453)	6454)	6455)	6456)	6457)	6458)	6459)	6460)	6461)
	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.
CAUCAUCAUAAATTGATGCAACATGAAATC CAUCAUCAUAAAGTGCTAAAAAAATTATA	CAUCAUCAUGCTGCTATTTAATGGGCTATG CAUCAUAGTGTTGTGGGGTGCTATATT	CAUCAUCAUAGTCATGCGTTTTGGATTGAA	CAUCAUCAUCGATAAAATGGCTAAAAAGAA	CAUCAUCAUATGATTTTAAGCATTGAAAGT	CAUCAUCAUGAAAATCATGCTCCGTTCTCT	CAUCAUCATTGGGGTGGTTTTGTGTTTTT	CAUCAUCAUGCACTAAGAATGAATGAAGAC	CAUCAUCAUATGGCATACAAATATGATAGA	CAUCAUCAUATATAATATGGCATACAGATA	CAUCAUCAATCAAGCGGTAACGAACGC	CAUCAUCAUAGAGCTTTTAAAATCTGTTGG	CAUCAUCAUATGGCAAATCATAAGTCCGCA	CAUCAUCAUATGATGATTATCACCACAATG	CAUCAUCAUATAAGGTTGGCAAGAATACAG	CAUCAUCAUAAGAGTTTTAGTAATGCTTGC	CAUCAUCAUAAGGTTGGCAAGAATACAGAG	CAUCAUCAUATGATTAAACAAACCCTCATC	CAUCAUCAUAAGAGATTATCCCTATTGTCG	CAUCAUCAUACCCTTTCGCAAGCCCTAAAC	CAUCAUCAUTAAAGTTTTATCTAAAAACCG	CAUCAUCAUATGATACAAAGAGGATTGAGT	CAUCAUCAUATTGTAGCGATTGTTATTGTG	CAUCAUCAUAATTTGATGTTACCATCATAG	CAUCAUCADACGCGCTACGCAAAAGTTCGC	CAUCAUCAUTTTAAAAGAAAGTCAAAGGCG	CAUCAUCAUCCTATGGCTATAAAAGAATGG	CAUCAUCAUTGGATATTTTAAAAGCAGAGC	CAUCAUCAUGTCAAAAACACCGGCGAATTG	CAUCAUCAUCGGCTATCAAATCGGCGAAGC
17RA9_HP1578R1555 17RA10_HP1579R1556	17RA12_HP1580R1557 17RA12_HP1581R1558	17RB1_HP1582R1559	17RB2_HP1583R1560	17RB3_HP1584R1561	17RB4_HP1585R1562	17RB5_HP1586R1563	17RB6_HP1587R1564	17RB7_HP1588R1565	17RB8_HP1590R1566	17RB9_HP0009S1567	17RB10_HP0058S1568	17RB11_HP0076S1569	17RB12_HP0107S1570	17RC1_HP0118S1571	17RC2_HP0119S1572	17RC3_HP0120S1573	17RC4_HP0143S1574	17RC5_HP0208S1575	17RC6_HP0381S1576	17RC7_HP0451S1577	17RC8_HP0521S1578	17RC9_HP0544S1579	17RC10_HP0548S1580	17RC11_HP0550S1581	17RC12_HP0619S1582	17RD1_HP0713S1583	17RD2_HP0715S1584	17RD3_HP0722S1585	17RD4_HP0725S1586

																		1,														
	6462)	6463)	6464)	6465)	6466)	6467)	6468)	6469)	6470)	6471)	6472)	6473)	6474)	6475)	6476)	6477)	6478)	6479)	6480)	6481)	6482)	6483)	6484)	6485)	6486)	6487)	6488)	6489)	6490)	6491)	6492)	(2078
	(SEQ ID NO.		(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	Ω	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ ID NO.	(SEQ IĎ NÓ.	(SEQ ID NO.	
	CAUCAUCAUATCATGAGAAATTGAATGGCG	CAUCAUCAUCGCTTACTCCAAACTCTAGCG	CAUCAUCAUCGCGAAAGAACAGCATCACAC	CAUCAUCAUAAGCCGGCTAGAAAAAGAGCG	CAUCAUCAUTAAGAATTTAGAATTAAGCGC	CAUCAUCAUATGAGCTTGGAGCGTTTTGCC	CAUCAUCAGGACCAAAACCTGGTGCC	CAUCAUCAUAGCGTTGATCACCTCATTTCG	CAUCAUCAUGTGTTGAATCTGGGCAGTTCG	CAUCAUCAUAAAGTGGTTTTACCAGAGAGC	CAUCAUCAUATGAGGAAAAACCATTATCCA	CAUCAUCAUAACCATTATCCATTAAGGGGG	CAUCAUCAUTAAATTCCGCTTGTATCCCAC	CAUCAUCAUTTTAGTGTTTAGGGGATGGC	CAUCAUCAUTGAAGAGAGTTAGAGAACTTG	CAUCAUCAUAGATTTTAAACGCTCTGTATC	CAUCAUCAUTTGTTTCGTGCCAATACCGCC	CAUCAUCAUTTTACTAGAAGACGATTACC	CAUCAUCAUACGAAGCGCAATTTTATGAAG	CAUCAUCAUAAATTCCTTTGGCTTTTAGGG	CAUCAUCAUTGTTTCTCTTGTGTAACGCTC	CAUCAUCAUTGGCACACCATGAAGAACAAC	CAUCAUCAUCGTTATTTTCCCGGTTGCTTG	CAUCAUCAUAGITTAAGATTCTAATCATCC	CAUCAUCAUTTCTTTAGGCGTGCTTGTCGC	CAUCAUCAUTCTCTTATTCTTTAGGCGCGC	CAUCAUCAUAGTTCAACAGAATACCAAAGG	CAUCAUCAUAAGAAACCCAAACTCAAATGG	CAUCAUCAUGCGAGAAATTACTCACCCTG	CAUCAUCAUACAGATTTAAAGAATGAACGC	CAUCAUCAUTTAGTCATGCAGAGCAGACCG	からむかは さりつかり ひとれ を見る ないなりになりになり
:	_HP0744S158	17RD6_HP0790S1588	17RD7_HP0807S1589	17RD8_HP0814S1590	17RD9_HP0882S1591	17RD10_HP0884S1592	17RD11_HP0897S1593	17RD12_HP0898S1594	17RE1_HP0903S1595	17RE2_HP0904S1596	17RE3_HP0988S1597	17RE4_HP0998S1598	17RE5_HP1007S1599	17RE6_HP1180S1600	17RE7_HP1188S1601	17RE8_HP1280S1602	17RE9_HP1353S1603	17RE10_HP1365S1604	17RE11_HP1369S1605	17RE12_HP1372S1606	17RF1_HP1417R1607	17RF2_HP1427S1608	17RF3_HP1522S1609	17RF4_HP1538S1610	17RF5_HP1561S1611	17RF6_HP1562S1612	17RF7_HP1589S1613	17RF8_HP0527-1S1614	17RF9_HP0527-2S1615	17RF10_HP0609-1S1616	17RF11_HP609-2S1617	

Oligonucleotides	Sequence : (5'-3')	Reference	SEQ
		···	
570-1	-AUGAUGAUGACTTGAATTCGCGGCCGCATCGATG-	This study	6507
570-2	-UAGUAGUAGCTCGGGCAGCGTTGGGTCCTGGCCAC-	This	6508
7	and the state of t	study	
570-3	-CTTATCATCGATGCGGCCGCGAATTC-	This study	6209
570-4	-GIGGCCAGGACCCAACGCTGCCCGAG-	This study	6510
38bp-R	-CTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCC-	[Seifert,	6511
		1986]	
HP0061-1	-CGGGGTACCCAAATTCCAATCCTTAAACCCC-	[Tomb,	6512
HP0061-2	-CGCGGATCCCTTAAAATAGAAGACAAGCGTTCTAAC-	[Tomb.	6513
		1997]	
HP0130-1	-CGGGGTACCTAAAACTTCTCCCTGTCATTCACCAC-	[Tomb,	6514
		1997]	
HP0130-2	-CGCGGATCCAAGGCTAGAAAGTGGATGCAATCGTT-	[Tomb,	6515
	and a society of the	1997]	
HP0175-1	-CGGGGTACCGCTTCATTTTCTACAAGGCGGTGCG-	[Tomb,	6516
	The state of the s	1997]	1
HP0175-2	-CGCGGATCCTAGCCAATCGGGATACGATTGATCC-	[Tomb, 1997]	6717
HP0231-1		[Tomb,	6518
	CGGGGTACC TGTTGGGTGGCGT TAAGAGCTTGAAC-	1997]	

1	•	1	
1	Č	3	1
i		2	i

0230	Lomo,		
2633	19971 (Tomb	-CGGGGTACCTGACCATGAACACTTAATAACC.	HP0697-1
6535	[Tomb,	-CGCGGAICCITGGAAATTCCAGGGGTGAGTAAGGCT-	7-600714
6534	[Tomb, 1997]	-cocotaliliogcocoliliogacoco-	1-6600111
6533	[10mb, 1997]		LIDAGEO 1
6532	[Tomb, 1997]	CCCCATCCAACAACAAAAAAAAAAAAAAAAAAAAAAAAA	HP0650-2
1633	1997]		14P0650_1
6531	[Tomb,	-CGCGGATCCGAATTGGCTTATGAGGGGATTGTG-	HP0553-2
6530	[Tomb, 1997]	-CGGGGIACCACICCIAAGCAATACGC-	1-6660111
6259	[Tomb, 1997]	-CGCGGAICCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	2-61-0 III
9700	[10mb, 1997]		11B0410.2
6527	[Tomb, 1997]	-CACAGAI CCAAACICAICIAICAAAACCCGTCCGC-	7-4-CO III
6526	[Tomb, 1997]	-CGGGGGC.	110394-1
6525	[Tomb, 1997]	-cococa i central di central de la cococa del la cococa del la cococa del la cococa del la cococa de la cococa de la cococa de la cococa de la cococ	7-1/50 111
6524	[Tomb, 1997]	-CGGGGTEGGT CGCGCAATTCTTGAC-	11.03/1-1 2.772041
6523	[Tomb, 1997]	-cecesalceanceaecaccideicicicidaice	111 0530-2 HP0277 1
6522	[Tomb, 1997]	-CGGGTTGGT 1001001110000000000000000000000	HP0358-1
6521	[Tomb, 1997]	CGCCCTT CONTROL OF THE CONTROL OF TH	HP0358 1
6520	[Tomb, 1997]	-CGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	11.02/1-1 11.00271 2
6219	[Tomb, 1997]	-cococarceciiiaiaiigiciicaicecaigige-	1 120011
			14P0231_2

		1007	
0 20/0011		1777	6637
HP0697-2	-CGCGGATCCGCGTTTTGCGCTCCAGAGGAGAACTGG-	1 1 omb,	/500
		1/2/1	
HP0699-1	-CGGGGTACCCTGCATATCTTGTTCTAAAATAGGGG-	[Tomb, 1997]	6538
HP0699-2	-CGCGGATCCAAGTTGGGCGTTTCTATCCAAGCGCAC-	Tomb,	6239
		1,661	0730
HP0721-1	-CGGGGTACCICATGCAACTGCTTATGGAACGCC-	[Tomb, 1997]	6540
HP0721-2	-CGCGGATCCACTAAAAACACAGACAAAATGACCGTGGCG-	[Tomb,	6541
		1,661	3
HP0726-1	-CGGGGTACCGCGCTTTAGCGTATTCTACATCCCCC-	[Tomb, 1997]	6542
HP0726-2	-CGCGGATCCGTGTTTGTTAACCTCCCTATAGACACC-	[Tomb,	6543
•		1997]	
HP0739-1	-CGGGGTACCCCCCCACTTTCCCTCCAAAGCT-	[Tomb, 1997]	6544
HP0739-2	-CGCGGATCCGGCTTGAATTTAGGGTTTTTGAGG-	[Tomb,	6545
		1997]	
HP0746-1	-CGGGGTACCGCCCTCATCATAGTGGGTCGC-	[Tomb,	6546
		1997]	
HP0746-2	-CGCGGATCCGCCCTTGATAAAACGCATCTTGAAGGG-	[Tomb, 1997]	6547
HP0838-1	-CGGGGTACCTCGTTTAGTCATGTAAATATCGCCC-	[Tomb,	6548
		1997]	
HP0838-2	-CGCGGATCCTGTTCGGCTAAATGGATTGCTGCAAGG-	Tomb,	6249
7		1997	
HP0862-1	-CGGGGTACCGCCATTATTTACCGCCAGACA-	[Tomb, 1997]	6550
HP0862-2	-cccccarccaagcaattaagaggg-	Tomb,	6551
11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		1997]	
HP0928-1	-CGGGGTACCGATCGCGCTAATGCCTACAATCTT-	[Tomb,	6552
9. 7		[7997]	-
HP0928-2	-CGCGGATCCCTCATTGAAATTTATAGCAGACGC-	[Tomb, 1997]	6553

6554	6555	6556	6557	6558	6229	0959	6561	6562	6563	6564	6565	9959	6567	8959	6959	6570	6571
[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb, 1997]	[Tomb,
-CGGGGTACCGATAGGATTAAGCCCACAAATCCC-	-CGCGGATCCACAGAAGCCGAGCTGTGCAAATTCCAC-	-CGGGGTACCTGCTTTAATTTGACAAACAAAGC-	-CGCGGATCCTCTGCGTTGACGAGCAAACACATGAAAGGG-	-CGGGGTACCACCACGATCAGACTCAATTTAGCG-	-CGCGGATCCCATGAAATCATGAAGTATAAAAAACGC	-CGGGGTACCCGCATGACTCTTTCCATGCAATGCC-	-CGCGGATCCGAAACTAGAAGAAACCCAAGCA-	-CGGGGTACCGCCTTTCTTCAGCGACCACTTGAC-	-CGCGGATCCGGTAATCCTAATGTCAAAGCCGAAGCC-	-CGGGGTACCATCGCATAAACGGTGCAAATCCCC-	-CGCGGATCCACCGGGAATCTAGTTTATATGCC-	-CGGGGTACCTGATATAAAGGTTAGCCAAACGC-	-CGCGGATCCAATGACAGGACTAAATTCTATGGCCGT-	-CGGGGTACCATAAAATTATACGCTTTACCGCC-	-CGCGGATCCGGCAAGACCTACGTGAGAGTCACT-	-CGGGGTACCGTTTAGAGCGAATAAATTGTAGCGG-	-CGCGGATCCAGCGAGAATGCCAGAGGTTAGAAGAG-
HP0935-1	HP0935-2	HP0947-1	HP0947-2	HP0953-1	HP0953-2	HP0973-1	HP0973-2	HP1012-1	HP1012-2	HP1014-1	HP1014-2	HP1023-1	HP1023-2	HP1028-1	HP1028-2	HP1039-1	HP1039-2

1400				
Ž,	Gene name	Functional category (a)	Size	Inter.protein
			<u>e</u>	(၁)
1100du	hspA	Co-chaperone (groES)	367	HP0011
F-000E		Louis Assistant Control of the Contr		(HspA)
OZODÓ	ndou	HopD functions as a porin on the outer membrane of H.pylori	1101	HP0595
np0042	trbl, comb3	Predicted DNA transformation competence protein	702	HP0419
hp0045	wbcJ	Predicted GDP-fucose synthetase	933	RdxA
hp0061	dds	H. pylori specific predicted protein with no known function	570	HP0066
hp0063	dds	H. pylori specific predicted protein with no known function	1491	HP0064
hp0064	dds	H. pylori specific predicted protein with no known function	420	HP0063
hp0065	das	H. pylori specific predicted protein with no known function	354	HP006
9900dy	C L	Predicted ATP-binding protein	2496	HP0067
	ATPbinding			
hp0071	urel	Urea transporter	585	HP0288
hp0100	chp	Conserved hypothetical protein	1107	HP0823
hp0108	dds	H. pylori specific predicted protein with no known function	561	HP1541
hp0115	flaB	Flagellin B (flaB)	1545	HP0753 (Fils)
hp0132	sdaA	Predicted L-serine deaminase	1368	HP0338
hp0134	Dhs1, aroF	Pred. tyrosine-regulated 3-deoxy-D-arabino-heptulosonate7-	1350	HP1012
hp0156	chp	Conserved hypothetical periplasmic protein	603	HP0156
hp0172	тоеА	Predicted molybdopterin biosynthesis protein	1176	HP0507
hp0175	ppiase	Predicted peptidyl-prolyl cis-trans isomerase	897	HP0608
hp0224	msrA	Predicted peptide methionine sulfoxide reductase	1077	HP0377
0700				(DspC)
np0246	rig/	Predicted flagellar basal-body P-ring protein	585	HP0325 (FlgH)
npyz4/	деар	Predicted RNA helicase	1479	HP0247
npuzea	hpaim	Predicted adenine specific DNA methyltransferase	759	HP0486
hp0272	dds	H. pylori specific predicted protein with no known function	534	HP0762

	H. pylori specific predicted protein with no known function	700	
dsbC chp spp omp spp omp spp dapB virB11-1 chp spp flaA magIII spp ppa flaA magIII spp ppa flxA spp yxiC yxiE hyuB		38/	HP0950
chp chp spp omp spp dapB virB11-1 chp spp spp spp spp spp spp spp spp fixA spp ppa hydD fixA spp yxjD yxjE hydB	Predicted flagellar basal-body L-ring protein	714	HP1390
dsbC chp spp omp spp dapB dapB dapB chp spp flaA magIII spp ppa flaA frxA spp frxA spp frxA spp frxA spp	Conserved hypothetical protein	897	HP0510
spp omp spp dapB virB11-1 chp spp spp flaA maglII spp ppa hydD frxA spp yxjD yxjD yxjE hyuB	Predicted thiol:disulfide interchange protein	999	HP0224
spp omp spp dapB dapB virB11-1 chp spp spp spp spp ppa ppa ppa ppa ppa pp	Homology with putative S-adenosylmethionine-dependent methyltransferase	982	HP0042
app dapB dapB virB11-1 chp spp spp flaA. magIII spp ppa ppa ppa ppa ppa ppa ppa ppa ppa	H. pylori specific predicted protein with no known function	513	HP0482
spp dapB virB11-1 chp spp spp spp flaA magIII spp ppa hydD frxA spp yxjE yxjE spp	Predicted outer membrane protein	1212	HP0762
dapB virB11-1 chp spp spp spp flaA maglII spp pag hydD frxA spp yxjE hyuB	H. pylori specific predicted protein with no known function	633	HP0172
chp spp spp flaA magll! spp flxA spp frxA spp yxjE hydB	Predicted dihydrodipicolinate reductase	765	HP0347
spp spp spp fiaA, fiaA, spp ppa hydD frxA spp yxjE yxjE hyuB	Cag pathogenicity island encoded protein/ATPase protein	993	HP0525
spp laA flaA flaA maglII spp ppa hydD frxA spp yxjE hyuB	Homology with putative RNA methyltransferases	684	HP0553
Spp flaA flaA maglII spp ppa ppa hydD frxA spp yxjE hyuB spp	H. pylori specific predicted protein with no known function	975	HP0958
flaA. magll! spp ppa ppa hydD frxA spp yxjE hyuB	H. pylori specific predicted protein with no known function	1473	HP0870 (FigE)
maglil spp ppa hydD frxA spp yxjE hyuB spp	Flagellin A (flaA)	1533	HP0753,(FIIS)
spp ppa hydD frxA frxA spp yxjE hyuB	3-methyladenine DNA glycosylase	654	HP1402
ppa hydD frxA spp yxjE hyuB spp	H. pylori specific predicted protein with no known function	483	HP0175
hydD frxA spp yxjD yxjE hyuB spp	Inorganic pyrophosphatase (ppa)	522	HP0620
spp yxiD yxiE hyuB spp	Quinone-reactive Nii/Fe hydrogenase (hydD)	537	HP0285
spp yxjE yxjE hyuB spp	NAD(P)H-flayin oxidoreductase	654	HP0642
yxiE yxiE hyuB spp	H. pylori predicted coding region,HP0650	591	HP1245
yxjE hyuB spp	3-oxoadipate coA-transferase subunit A (yxjD))	669	HP0692
hyuB Spp	3-oxoadipate coA-transferase subunit B (yxjE)	624	HP0691
das	N-methylhydantoinase	2298	HP0697
444	H. pylori specific predicted protein with no known function	507	HP0696
Crip	H. pylori specific predicted protein with no known function	1983	HP0100
<u>"</u>	RNA polymerase sigma-54 factor (rpoN)	1245	HP0958
ф	Conserved hypothetical protein	726	HP0810
Flis	Flagejlar protein (filS),	381	HP115 (Flab)
H das	. pylori specific predicted, protein with no known function	558	HP0506
hp0800 moa£ Moly	Molybdopterin converting factor, subunit 2 (moa臣)	438	HP0801
moaD	Molybdopterin converting factor, subunit 1 (moaD))	225	HP0800
das	H. pylori specific predicted protein with no known function	621	HP0134

	- 22	Conserved hypothetical profein	200	
np0010	رايان	Excinitelesea ABC submit C (IVC)	1785	HP0821
11p0621 hp0822	dvio	Predicted homoserine dehydrogenase	1263	HP0822
11p0022 hp0833	SDD	H nylori specific predicted protein with no known function	879	HP1286
hp0862	ado	H pylori predicted coding region HP0862	672	HP/474
hn0874	ads	H. pylori specific predicted protein with no known function	873	HP0875
hp0875	Kat A	Catalase	1518	HP0874
hn0928	folE	GTP cyclohydrolase I (folE)	543	HP()928
hn0954	rdxA	Oxygen-insensitive NAD(P)H nitroreductase	633	HP()045
h00958	ads	H. pylori specific predicted protein with no known function	765	HP0714
hn0990*	ous	H. pylori specific predicted protein with no known function	699	HP()909
hn1012	DOOF	Professe	1332	HP0134
1101012 hp4044	hdhA	7-alpha-hydroxysteroid dehydrogenase (hdhA)	789	HP/1014
hp1032	Fili A	Alternative transcription initiation factor, sigma-F (fliA)	892	HP:1122
1101036 ho1035	APT TAB	Flacellar biosynthesis protein (flhF)	1380	HP0167
III) 1033 hn1074*	uds	H. pylori specific predicted protein with no known function	789	HP:1497
ho 1114	JuvrB InvrB	Excinuclease ABC subunit B (uvrB)	1977	HP()821
h01118	too	Gamma-clutamyltranspeptidase	1701	HP()822
hn1143	aus	H. pylori specific predicted protein with no known function	1302	HP0137
ho1160	cho	Conserved hypothetical	420	HP0712
hn1173	das	ed pr	552	HP()595
hn1230	aas	H, pylori specific predicted protein with no known function	543	HP 1529
504084#	hola		629	HP1247
hn12/5	dss	Single-strand DNA-binding protein	540	HP()661
ho 1247	uus	H. pylori specific predicted protein with no known function	1023	HP1231
hn1255	Sec	Protein translocation protein, low temperature (secG)	909	HP1072
hp1250	chn	Conserved hypothetical protein	618	HP 1259
1101403 hp1263	Cond	Predicted NADH-ubiquinone oxidoreductase chain D	1230	HP0276
110 1203	COS	Conserved hypothetical secreted protein	549	HP1492
1101500 hn1300	das	H. pylori specific predicted protein with no known function	909	HP1488
hp1228	nikB	1	444	HP1338
1101330 hp1270	acj	Predicted ATP-dependent protease	2505	HP1286
1101313 hp1200	TOO.	Ardinase	996	HP0108
1101333	5		1111	HD1413

hp1430	chp	Conserved hypothetical protein	2067	HP1072
hp1464	chp	Putative ABC transport system	816	HP0887
hp1489	dds	Weak homology with an outer-membrane protein of the type I	1533	HP0841
		secretion system		
hp1493	dds	H. pylori specific predicted protein with no known function	612	HP1025
hp1527	dds	H. pylori specific predicted protein with no known function	1440	HP1158
hp1529#	dnaA	Predicted chromosomal replication initiator protein	1374	HP1230

identified as Putative Essential Genes (PEGs) based on the inability to isolate kanamycin resistant transformants when the Table 5: List of the 96 selected ORFs of the genome of strain 26695 analyzed in this study. Grey lines indicate, ORFs known to be essential for which resistant transposon insertion occurred via integration of the plasmid through a single the Bold lines indicate ORFs that are true essential genes. ORF number with an asterisk (*) non ubiquitous ORFs, # genes crossing over (transformants were traces of the vector were demonstrated by DNA/DNA hybridization). «spp »: H. pylori ecombinant plasmid corresponding to the Tn3-Km disrupted cloned ORF was used to transform H. pylori strain HAS141 described characteristics specific predicted protein encoding gene; chp: conserved hypothetical protein encoding gene. to the sizes are according and categories Functional and b)

(c) - Interacting proteins have been screened through the two hybrid assay in yeast [Rain, 2001 #95]; protein-protein interactions were scored and classified in categories. The indicated interacting protein corresponds to that with the highest score for a given bait (http://pim.hybrigenics.com/pimrider/)

http://genolist.pasteur.fr/PyloriGene/ data base.

TABLE

																3		¥.	100								
			861	798	984	873	066	1536	759	1359	1251	648	2037	1119	1245	507	1029	459	918	1260	738	618	738	1584	486	363	267
																			-,,								
															1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1		A STATE STATE OF THE STATE OF T					Roman Carlon					
		-													1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1			The state of the state of				を できる ない			Contract of		*
Functional category			stein with no known function	redicted profein with no known function	stein with no known function	stein with no known function	stein with no known function	tein with no known function	redicted protein with no known function	stein with no known function	stein with no known function	otein with no known function	stein with no known function	stein with no known function	redicted protein with no known function	tein with no known function	H. nylori specific predicted protein with no known function	stein with no known function	stein with no known function	stein with no known function	stein with no known function	stein with no known function	stein with no known function	otein with no known function	ofein with no known function	otein with no known function	stein with no known function
		·	H. nylori specific predicted protein with no known function	H pylori specific predicted	H ovlori specific predicted protein with no known function	H. pylori specific predicted protein with no known function	H. pylori specific predicted protein with no known function	H. pylori specific predicted protein with no known function	H. pylori specific predicted I	H. pylori specific predicted protein with no known function	H. pylori specific predicted protein with no known function	H. pylori specific predicted protein with no known function	H. pylori specific predicted protein with no known function	H. pylori specific predicted protein with no known function	H pylori specific predicted	H pylori specific predicted protein with no known function	H nylori specific predicted pro	H. pylori specific predicted protein with no known function	H. pylori specific predicted protein with no known function	H. pylori specific predicted protein with no known function	H nylori specific predicted protein with no known function	H. pylori specific predicted protein with no known function	H oviori specific predicted protein with no known function	H pylori specific predicted protein with no known function	H pylori specific predicted protein with no known function	H pylori specific predicted protein with no known function	H. pylori specific predicted protein with no known function
Gene name			aus-	200	das	gas	aas	aus	SDD	aas	ads	oos	dds	aas	ous	das	das	ous	ous	aas	uus	dan	1	das	dde	dde	dds
ÓRF N°			HD0430	LE0034	HP0271	HP0292	HP0304	HP0358	HP0394	HP0508	HP0563	HP0565	HP0578	HP0580	HP0659	HP0607	HPORGO	HP0721	HP0726	HP0746	HP0771	HDOB38	HD0842	T DOODE	11,000	HP0047	HP0953

HP0971	dds	H. pylori specific predicted protein with no known function	1242
HP0973	das	H. pylori specific predicted protein with no known function	1062
HP1022	dds	H. pylori specific predicted protein with no known function	837
HP1023	dds	H. pylori specific predicted protein with no known function	1251
HP1028	dds	H. pylori specific predicted protein with no known function	498
HP1039	dds	H. pylorl specific predicted protein with no known function	1290
HP1053	dds	H. pylori specific predicted protein with no known function	654
HP1054	dds	H. pylori specific predicted protein with no known function	1269
HP1085	dds	H. pylori specific predicted protein with no known function	516
HP1106	dds	H. pylori specific predicted protein with no known function	1308
HP1265	dds	H. pylori specific predicted protein with no known function	286
HP1327	dds	H. pylori specific predicted protein with no known function	1239
HP1336	dds	H. pylori specific predicted protein with no known function	762
HP1440	dds	H. pylori specific predicted protein with no known function	780
HP1454	dds	H. pylori specific predicted protein with no known function	912
HP1568	dds	H. pylori specific predicted protein with no known function	552
HP1580	dds	H. pylori specific predicted protein with no known function	663

ORFs identified as Putative Essential Genes (PEGs) based on the inability to isolate kanamycin resistant transformants Table 6: List of the 42 selected ORFs of the H. pylori genome, strain 26695, analyzed in this study. Grey lines indicate when the recombinant plasmid corresponding to the Tn3-Km disrupted cloned ORF was used to transform H. pylori strain HAS141. Bold lines indicate ORFs that are true essential genes. "pp ": H. pylori specific predicted protein encoding gene.

Amino Acid Sequence	LSGFNPLNSPLVASSSLSL KEAYYLEKLSLKKGFKIH YKMTKDSLNLLEKSDLC VLFGGFSNACLNENERW ILESISHSKRPYALLRPLQ DTRDLQENCLFASYEIHT EAAILALILRGILEQTSQL KGHVLEKIDVGYLSSEA NMSEBELQBLIALIVKAK KRALVLNREITKHANNAF LYTLLSELQNYLEILHPC YDSSATTAFYDFKDQEW LLETAFKEGILPFKSQLQS KDLELLERISEANGSFVY VSYKSLETPKLSFSKQFK IANKIEHSKAGFQISNQT LECELEENPHLKGLIAIL EGGLEENPHLKGLIAIL EGGLEENPHLKGLIAIL EGGLEENPHLKGLIAIL EGGLEENPHLKGLIAIL EGGLEENPHLKGLIAIL
SEQ ID No. Amino acid SEQ	0659
Nucleic acid Sequence	TTGAGCGGCTTTAACCCCTTAAATTCTCCC TTGAGCGGCTTTAACCCCTTAGAAA GAAGACTCTTCTCTT
SEQ ID No. Nucleic Acid SEQ	6289
Bait name	HP1265

C	٠	ú
Č	•	S
١	Ī	5
7	7	•

٠ -	02/00007																		- 4/4		11/1	
		EPESKVEALEGRKQ ESSLDKKIRQELKNK	DLKNKELKNKKEEK KNTEEKKETKAKRK	PRAEVHHGDTKNPT OKTTPPKIK FNAK GV	QNQGVQSNAPKLEEK	DI I SÇI LEKKGASPSS ÇFNSIFGNPNDAANN	TLEDKVVGGISLLVNG	SKAQARDRLIAERIK	NQEIERLKIHVDDDKL	DQEMAMMAQQQGMD LDHFKQMLMAEGHYK	LYRDQLKEHLEMQEL	LRNILLTNVDTSSETKM REVVNKHKFOERIPTEIF	TVRYTSTNQEDLERAM	ADPNLEIPGVSKANEKI	EMKTLNPQIAQVFISHE OGSFTPVMNGGGGOFI	TFYIKEKKGKNEVSFSQAK	QFIAQKLVEESKDKILE	EHFEKLRVKSRIVMIRE				
									-		-					-						
		6592		· · · · ·															· · · · · ·			
	A TG CG	AA AA	AA	AA Sec		¥ SG	AA .	AT.	Y.	,	4A	Ç.	4.TG	د ت	AI T	. 9	<u>ي</u>	ΤΑ	21	Ħ	8	2
	AGATCGCTAATAAGATTGAGCATTCTAAA GCGGGGTTTCAAATCTCCAATCAAACGCTA GAATGCGAGTTGGAAGAAACCCCCATTTG AAGGGTTTGATTGCGATTTTAGAAGGGGCG TTTTTTGACGCTTACCTTATATTTTAGATTTTTTTTTT	GAGCCGGAATCTAAAGTGGAAGCCTTAGAA GGGAGGAAGCAAGAGTCTTCTTTGGATAAA	GAAGAATAAGGAT GAAAAATAAAAAAA	GAAGAAAGAAAACACCGAAGAAAAAAAAAAAAAAAAAA	ATACCAAAAATCCC	ACICAAAAATAAGGCCICCTAAAATCAAA GAGAACGCTAAAGGAGTTCAAAATCAAGGC	AAAACTTGAAGAA	AAAGGAGCAAGCCTAGAACTCTTGAAAAA AAGGGAGCAAGCCCTAGCTCTCAATTCAAT	AATGACGCTGCTA	ACAATACCCTTGAAGATAAGGTCGTAGGG GGCATTTCTTTGCTTGTTAATGGTTCGCCT	ATCACGCTGTATCAAATCCAAGAAGAGCAA	GAAAAATCTAAAGTGAGCAAAGCTCAAGCA AGGGATCGTTTGATCGCTGAACCCATTAAA	CTTAAAAATCCATG	TAGATGACGACAAGCTAGACCAAGAAATG	GCGATGATGGCGCAACAACAAGGCATGGAT TTGGATCATTTCAAACAAATGCTTATGGCT	GAGGGACATTATAAACTCTATAGGGATCAG	CITAAGGAGCATITGGAAATGCAAGAATTG	TTGCGTAATATCTTACTCACGAATGTGGATA	GCAATTCAGTATC	CCCACTGAAATAGAAACCGTGCGCTACACT	TCCACCATCAAGAGGATTTAGAAAGGGCG	A I GUCUGA I CC I AA I I I GGAAA I I CCAGGO
	AGATCGCTAATAAGATTGAGCAT GCGGGGTTTCAAATCTCCAATCA GAATGCGAGTTAGAAGAAAACCC AAGGGTTTGATTGCGATTTTAGAA TTTTTTGACGCTTACCCTTATATCA	ATCTAAAGTG SCAAGAGTCT	CAAGAATTG.	3AAAAACACC	TCATGGGGA		AACGCGCCA,	AGCCCTAGC	3GTAATCCTA.	TIGAAGATA/ TIGCTIGITA/		AAAGTGAGC		ACAAGCTAG	GCGCAACAA	TATAAACTCI	CATTTGGAAA	ATCTTACTCA(CACAAGGAG	ATAGAAACC	CAAGAGGATT	CCIAAIIIGO
	AGATCGCTAATAAGATT GCGGGGTTTCAAATCTC GAATGCGAGTTAGAAGA AAGGTTTGATTGCGAT TTTTTTGACGCTTACCCT	GGGAGGAA	AAAATCCGCCAAGAATT	GAAGAAAA	AGAAGTCCATCATGGGG	ACI CAAAAAT AACGCC GAGAACGCTAAAAGGAGT	GTTCAAAGCAACGCGCC	AAGGGAGC	TCCATTTTTGGTAATCCT	ACAATACCTTGAAGAT GGCATTTCTTTGCTTGTT	ATCACGCTG	GAAAAATCTAAAAGTGAG	AACCAAGAAATTGAGCG	TAGATGACG	GCGATGATGGCGCAACA TTGGATCATTTCAAACA	GAGGGACAT	CTTAAGGAG	TTGCGTAAT	TACAACAAACACAAGGA	CCCACTGAA	TCCACCAAT	Algocooal
																٠						
		16291																				
		HP0659					-															

0 02/066501	·
	MLETYALKNGAVFISD AHFLPKSPHLIHTLKEL LSAKPPQVFFMGDIFHV LVGYLPLDKEQQKIIDL IHALSEISQVFYFEGNHD FSMRFVFNSKVMVFER QNQPVLFQYDNKRFLL AHGDLFITKAYEFYITQ LTSTWARFFLTFLNLLS FKTLYPLFKKLIYQKPV RLWELEPKELQSFIEKR LKAYQNYIKDLNIGSID GIIEGHFHLKSGAKIPLN TPIYCPLPSFYYEQSLFKV SSSVLEPSQNKDA
	6594
GTGAGTAAGGCTAAAAAAAATAGAGAT GAAAACCTTAAAACCCTCAAATCGCTCAAGTC TTTATTTCGCATGAGCAAGGCTCTTTTACGCC CGTTATGAATGGGGGTGGGGGGCAGTTC ATCACCTTTTATATCAAGGGAAAAAAGGGT AAAAACGAAGTTTCAGTCAGGCCAAG CAATTCATCGCCCAAAATTAGTGGAAGAA TCTAAAGATAGAGGTTAAGATTAGAAGGATTTTAGAAAATTAGAAGA	TATGCACTTAAAAATGGGGCTGTTT GCATTTTTTGCCCAAAGCCCTCAT TTTAAAGAACTTTTAAGCGCCAAAC TTTTCATGGGCGATATTTTCCATGTT TTGCATGGGCGATATTTTCCATGTT TTGCATGGGCAACCATGTTTTTCCA TATTGAAGGCAACCATGATTTTTCCA TTTTACATCCAAAATGGTTTTTGA TTTTACATCACGCAGTTTTATTCATTACA TTTTACATCACGCAGCTCACTTCCA TTTTACATCACGCAGCTCACTTCCA TTTTACATCACGCAGCTCCATTCCA TTTTACATCACGCAGCTCCATTCCA TTTTACATCACGCAGCTCATTATTA TTACATCATCAAAAGCGCCTAAAAG TTTTTAACATTTTTTTAAAATTTATTA TTAACGCCTTTTTTTAAAAAACTCAA TTTTAAAAGATCTTAAAAAACTCAAA ATATTAAAGAGGCCTAAAAG TATTAAAAGATCTTAACATTTATT CCTTTTTATTAAAAAACCTCCAAA ATATTAAAAGACCTTTTTATTATT CCTTTTAATTCCAAAATTATTATT AGCGCTTTTTATTACAAAATA ATCCCCTTTAATTACAAAATA AGCGTTTTAATAAAAACAAATA AGCGTTTTAATAAAAAATA
	HP0394 6593

Bait	Prey Name	SIDNucleic	SID Nucleic Acid Sequence	SID	SID Amino acid	
ORF		Acid SEO ID		Amino	Sequence	
		No		Acid SEQ	-	
				ID No.		
HP1265	HP0025	96592	CGACCCCAACGCTATCAATAACGCAAGG	9659	DPNAINNARGNLNAS	
			GGCAATTTGAACGCTAGTGCGAAGAATT		AKNLINDKKNSPAYQ	
			TGATCAATGATAAAAGAATTCCCCGGC		AVLLALNAAAGLWQ	
			GTATCAAGCGGTGCTTTTAGCCTTGAATG		VMSYSISVCGPGSDK	
			CGCCAGCGGGTTGTGGCAAGTCATGAGC		NKNGGVQTFENVPSN	
			TATTCGATCAGCGTTTGTGGCCCTGGCTCT		GGTTIACDSFYEPGKW	
			GACAAAAAAAATGGGGGCGTCCAAA		SGISTENYAKINKAYQ	
			CCTTTGAAAATGTGCCGTCAAATGGGGGG		IIQKAFGASGQDIPALS	
			ACTACCATTGCTTGCGATTCATTTTTATGA		DTKELNFEIKGKKNDS	
			ACCAGGAAAGTGGAGCGGTATATCCACTG		VQPGERWKFPWTNGK	
			AAAATTACGCAAAATCAATAAAGCCTAT		FVSVKWVNGKYEEIK	
•			CAAATCATCCAAAAGGCTTTTGGAGCAAG		EDIKVSNNAQELLKQA	
			CGGGCAAGATATTCCTGCCTTAAGCGACA		STILTTLNEACPWLSN	
			CCAAAGAACTTAATTTTGAAATTAAAGGGA		GGAGNVAGGNSLWA	
			AAAAAATGATAGCGTCCAGCCAGGAGAA		GIDKGDGSACGIFKNE	
			AGATGGAAATTCCCATGGACTAATGGAAAA	`	ISAIQDMIKNAEIAVEQ	
			TTTGTTTCAGTCAAGTGGGTGAATGGGAAG		SKIVTANAQNQHNLD	
			TATGAAGAAATTAAAGAAGACATCAAAGT		TGKAFNPYKDANFAQ	
		-	GTCAAATAACGCTCAAGAGCTTTTAAAACA		SMFANARAQAEILNRA	
			GGCTAGCACTATTTTAACCACTCTTAATGA		QAVVKDFERIPAAFVK	
			AGCATGCCCATGGTTGAGTAATGGTGGTGC		DSLGVCHEKGSDGNLR	
			AGGCAATGTGGCCGGTGGCAATAGTTTATGG		GTPSGTVTSNTWGAG	
			GCCGGAATAGATAAAGGCGACGGGAGCGCAT		CAYVGETVTNLKNSIA	
			GCGGGATTTTAAAAATGAAATCAGCGCCATT		HFGDQAERIHNARNLA	
			CAAGACATGATCAAAACGCTGAAATAGCCG		YTLANFSGQYKKLGEH	
			AGAGCAATCCAAAATCGTTACCGCCAACGCG		YDSITAALSSLPDAQSL	

8

QNVVSKKTNPNSPQGIQ	SSSMTFSTQSMDNSQN LNGLNSNGKLSVYGT TFTNEAKDGKFIFNAG QAVFENTNFNGGSYQ FSGDSLNFSNNNQFNS GSFEISAKNASFNNAN FNNSASFNFNNSNATT SFVGDFTNANSNLQIA GNAVFGNSTNGSQNT ANFNNTGSVNISGNA TFDNVVFNGPTNTSV KGQVTLNNITLKNLN APLSFGDGT
	8659
CAAAACCAGCACCAACCTAGACACTGGGAAAG CATTCAACCCTATAAAGACGCCAACTTCGCC CAAGCATGTTCGCTAACGCTAGAGCGCAAG CGAAGCATTTTAAACCGCTAGAGCGCCAAG CGGAGATTTTAAACCGCTCCAAGCGCTTC GAAGGACTTTGAAAGAATCCCTGCAGCGTTC GTGAAAGACTCTTTAGGATTCTCAACGTGGCCCC ATCTGGCACGGTTACTTCTAACACTTTGGGGAGC CGGCTGCGCGTTACTTCTAACACTTTGGCGAC ATCTGGCACGGTTACTTCTAACACTTTTGGCGAC ATCTGGCACGGTTACTTCTAACACTTTTGGCGAC ATCTAAAAACTGCGAATCTCTATGCGCAATCTC CGCTACACTTTAGCGAATTTCAGCGCAATC CGCTACACTTTAGCGAATTTCAGCGCAATC CTAAAAGCTAGGCGAACCTTTGACAAAAGCTAGCCAATC TTTACAAAATGTGGTGACAAAAGGCTAACC CTAACAGCCCGCAAGCCTTTACTAACAGGCAATC CTAACAGCCCCCAACCTTCTCAAGTGCAAT ACTAGACTCCAACATCCATTCTCAAGTGCAAT	TTCAAGCTCTATGACTTTTTCCACGCAAAGCA TGGATAATTCGCAGAATTTGAATGGCTAAA TTCTAACGCAAACTTTCGGTGTATGGCACCA CTTTCACTAACGAAGCTAAAGATGGCACCA CTTTCACTAACGAAGCTAAAGATGGCACCA ATTTCAATGCAGGGCAAGCGGTTTTTGAAA CACCAACTTTAATGGAGGGAGTTTTTGAAAA CACCAACTTCATTGAATTTTTCAAACACACCA GCGGCGATAGCTTCGTTTCAATACCCTAACTTTAAC AAAACGCTTCGTTCAATTTCAATACTTAAC CAGTTCAATTGCAAATTGCCGGGAACGC CTAATTCAAATTTGCAAATGGCTCTCTAAATA TTTTGGGAACTCTACTAATGGCTCTTCAAATA CCGCTAATTTAATAATACCGGCTCTTTTAATA TTTCAGGGAATGCAACCTTTGATAATA TTTCAGGGAATGCAACCTTTGATAATA TTTCAGGGAATGCAACCTTTGATAATA TTTCAGGGAATGCAACCTTTGATAATA CCGCTAATTTTAATAATACCGGCTCTGTTAATA TTTCAGGGAATGCAACCTTTGATAATA CCGCTAATTTTAAATAATACGGCTCTGTTAAAA TTTCAGGGAATGCAACCTTTGATAATAA CCGCTAATTTTAATAAATACGGCTCTGTTAAAA TTTCAGGGAATGCAACCTTTGATAATAACCTTTAAAAAAAA
	6597
	HP0289
	HP1265

	-			Y LIALLY CALL		
	, 21 6761	2027		ATTACI		3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
HP1265	HP)317 (omp	6299		CTCCCGGCGTATCAAGCCGTGTTTTAG	0099	SPAYQAVFLAINAAV
	6			CGATCAACGCGGCGGTAGGGTTGTGGAAT		GLWNTIGYAVMCGN
				ACCATCGGCTATGCGGTCATGTGCGGGAA		GNGTESGPGSVIFNDQ
				CGGGAACGCCACAGAGAGTGGGCCTGGCA		PGQDSTQITCNRFEST
				GCGTGATCTTTAATGACCAACCAGGACAGG		GPGKSMSIDEFKKLNE
				ATTCCACGCAAATTACTTGCAACCGCTTTG		AYQIIQQALKNQSGFP
				AATCAACTGGGCCTGGTAAAAGCATGTCTA		ELGGNGTKVSVNYNY
				TTGATGAATTCAAAAACTCAATGAAGCCT		ECRQTADINGGVYQF
•				ATCAAATCATCCAGCAAGCTTTAAAAAATCA		CKAKNGSSSSSNGGN
				AAGTGGGTTTCCTGAATTAGGCGGGAACGGC		GSSTQTTATTTQDGV
				ACAAAAGTGAGTGTTAATTACAATTACGAATG		TITTTYNNNKATVKFD
-				CAGACAAACTGCTGATATCAACGGCGGTGTG		ITNNAEQLLNQAANIM
				TATCAGTTCTGCAAGGCTAAAAATGGTAGTA		QVLNTQCPLVRSTNNE
	-	· · ·		GTAGCAGTAGTAATGGCGGTAATGGCAGTAG		NTPGGGQPWGLSTSGN
	-			CACGCAAACAACGGGACAACCACGCAAGAC		ACSIFQQEFSQVTSMIK
		-		GGCGTAACGATCACCACTACCTATAATAA		NAQEIIAQSKIVSENAQ
				CAAAGCCACCGTCAAATTTGACATCACCAATA		NONNLDTGKPFNPYTD
				ACGCTGAACAGCTGTTAAATCAAGCGGCAAAC		ASFAQSMLKNAQAQA
				ATCATGCAAGTCCTTAATACGCAATGCCCTTT		EMFNLSEQVKKNLEV
•	-			AGTGCGTTCCACGAATAACGAAAACACTCCA		MKNNNNNNEKLAGFG
				GGGGGTGGTCAACCATGGGGTTTAAGCACATC		KEEVMTNFVSAFLAS
				CGGGAATGCGTGCAGCATCTTCCAACAAGAAT		CKDGGT
	_			TTAGCCAGGTTACTAGCATGATCAAAAACGCC		
				CAAGAATAATCGCGCAAAGCAAAATCGTTAG		
				TGAAAACGCGCAAAATCAAAACAACTTGGATA		
-				CTGGAAAACCATTCAACCCTTACACGGACGCCA		
				GCTTTGCGCAAAGCATGCTCAAAAACGCTCAAG		
-				CGCAAGCAGATGTTCAATTTGAGCGAACAAG		
	-			TGAAAAGAACITGGAAGTCATGAAAAACAACA		
				ATAATGTTAACGAGAAATTAGCAGGATTTGGGAA		
-				### AGAAGIAA IGACCAA I I I I GI I AGCGCCI I I I		
		,,,,,		100CAAGCIGCAAAGAIGGIGGCACA		
HP1265	HP0609	6601	_	CATTGTCAATAATGGTAATTTGAATGTAAC	6602	OTDECCENT VANNIT
				TOGAGGCTTTAACCTTAAGGCCAATAACAT		WDK GSVNGGGNFGV

					STATE OF STA
			TACTTGGGATAAAGGCTCTGTGAATGGAGG		DNADSNGAT IISGV /
			GGGGAATITIGGCGTGGATAGCCCGATAG		INITIAL IN THE INCOME.
			CAATGGCGCAACCACCATTAGCGGAGTAAC		AGNSCILENNIFNS
			TTTCAATAATAACGGCACTTTGATTTATAAA		NINAKAONLIFNNNSF
			GGGGGTGAAAATAGCGCCGGAAATTCTTTA		NGGSYSFNDTKNTTF
			ACCCTAGAAAACAACACTTTCAATTCCTACA	=	KGTNTLINSDPFSRLK
			ATATCAACGCAAAAGCGCAAAACCTAATTTT	<u> </u>	GSVSIENNSVFNIERD
			TAACAACACTCGTTTAATGGCGGTAGCTAT	-	LTDKTTYTLLSGNSFK
			TCGTTTAATGACACTAAAACACCCCCTTTA		YNNÖALAGQCFFKK
			AAGGCACAAACACGCTCATTAACAGCGATCC		FMEFNPLWWRTRDSI
			TTTTAGCCGCCTTAAAGGATCAGTTTCTATTG		KSG
			AAAATAATAGTGTTTTTAATATTGAAAGGGA	• .	
			TTTGACCGATAAAACCACTTACACGCTTTTAA		
		-	GCGGAAATAGTATCAAATACAATAACCAAGC		
			TTTAGCGGGCAATGCTTTTCAAAAATTTA		
			TGGAATTTAATCCATTATGGTGGCGAACAAGG		
			GACTCTATTAAGAGCGGA		
HP1265	HP0780	6603	GGCGGTGAAAAAATCGTTGTGAGTTGGT 6604		AVKKIVVSWCVALAF
			GTGTGGCGTTGGCTTTTTAAGCGCGGAT		SADSAQANKAISNA
			TCAGCACAAGCCAATAAAGCGATCAGTA		DLIKEIRDLKKIISAQN
			ATGCGGATTTGATTAAAGAGATAAGGGA		TEINNLRKVQEVLSG
			TTTAAAAAAATCATCAGCGCGAAAAC	<u> </u>	QLGDMRKDILSTRDY
			ACTGAGATTAACAACTTAAGAAAAGTGC	<u> </u>	CISLRPYIYNWR
· · ·			AAGAAGTGTTGTCTGGGCAATTAGGGGA		•
			CATGCGTAAGGATATTAAGCACTAGA		
			GATTATTGCATTAGCTTAAGGCCTTATAT	_	
			CTATAATTGGCGC		
HP1265	HP0792	9099	ATGATTAACACGATGTTTTGCGCGACCATGCAAAG 6606	<u> </u>	MINTMFCATMQRG
			GGGAGTGGCGGAAATCGTGGCTGTGGAAGCGACT		VAEIVAVEATFTRA
			TTCACAAGGGCTTTGCCGGCGTTTGTGATTTCAGG		LPAFVISGLANSSIQE
			GTTAGCTAATAGCTCTATCCAAGAAGCCAAACAG		AKQRVQSALQNNDFT
			CGGGTTCAATCGGCTTTACAAAATAACGATTTCAC		FPPLKITINLSPSDLPK.
			TTTCCCGCCTTTAAAATCACCATCAACCTTTCCCC		SGSHFDLPIALLIALQ
		-	CTCAGATTTGCCTAAATCCGGGAGTCATTTTGATTT) 	KQELAFKEWFAFGE
		-	GCCTATCGCTCTTTTAATCGCTTTGCAAAAACAAGA		GLDGKIKPNPNIFPM
-			GTTGGCTTTTAAAGAGTGGTTTGCTTTTGGGGAGTT		LLDIAIKHPHAKIIAP

٥	c
Č	5
ū	7

				AGGGCTTGATGGCAAGATCAAACCCAATCCTAACAT		KANEELFSLIPNLQCF
				THECCCATGCTTTTAGACATTGCCATTAAACACCCC		FVGHFKEALEILQNPE
				CATGCTAAGATCATTGCGCCTAAGGCCAATGAAGAG		TKADTHTKKLPFKTI
				CTTTTTCGCTTATCCCTAATTTGCAATGCTTTTTTGT		ELNDKEYYFSDAYA
				GGGGCATTTTAAAGAAGCGTTAGAAATCTTGCAAAA		LDFKEVKGQAVAKE
				CCCTGAAACCAAAGCAGACACCACACGAAAAACT		AALIASAGFHNLILEG
				ACCCTTTAAAACGATAGAATTGAACGATAAAGAGTAT	•	SPGCGKSMIINRMRY
				TATITITCAGACGCCTATGCCTTAGAITITTAAAGAAG		ILPPLSLNEILEATKL
				TAAGGGCCAAGCTGTCGCTAAAGAGGCCGCTTTGAT		RILSEQDSAYYPL
.•				CGCTAGCGCTGGGTTTCATAACTTGATTTTAGAGGGA		•
				AGTCCAGGGTGTGGGAAAAGCATGATCATTAATCGC		
				ATGCGTTATATCTTGCCTCCATTAAGCCTGAATGAAA		
				TCCTAGAAGGGACAAATTACGCATTTTAAGCGAGCA		
				AGACAGTGCCTATTACCCCTTA		
HP1265	HP1157	2099		CAACGCTCAAGGCCAAAATATCAGCGCC 66	8099	NAQGONISAYDCMTA
			•	TATGATTGCATGACTGCTACCGGAAGCC		TGSLSSNASSGISCSA
				TTTCTAGCAATGCTTCTAGCGGGATTTCA		TSSTSSTNSFDNSLVA
	-			TGCTCAGCCACAAGCTCCACAAGTTCCAC		TSKVQTINGKEQIGV
				AAATAGCTTTGACAATTCTTTAGTCGCTA		NSFNLVSQVWSVYN
-	·.			CCTCCAAAGTCCAAACCATCAACGGCA		SLKTSEENLOKNANI
				AAGAGCAGATCGGCGTGAATTCTTTT		LCANGTÓSGTSSCNS
	-			AACCTTGTCTCTCAAGTGTGGAGCGTTTA		SSGGLSISGNAQLQN
				TAATTCTTTAAAAACTTCAGAAGAAAT		ILSPTSGTTTNTQAKS
				TTGCAAAAAACGCCAATATTTTATGCG		NAPKLKAMVVVNNE
		-	÷	CTAATGGGACGCAATCTGGGACAAGCTC		EEAKTANLAQSSGTT
				ATGCAATAGCTCTTCAGGGGGTTTGAGCA		TQSPNSTVMGALNT
				TCAGCGGGAACGCCCAATTGCAAAATATT		VLQNVSNFQQSIQNA
				TTAAGCCCTACTAGTGGGACTACCACTAAT		FQNQESNIQAWANAI
				ACTCAAGCTAAAAGCAACGCTCCCAAACTA		YNTNGSÓSÓEMTPN
				AAAGCGATGGTGGTGAATAATGAAGA		NNQDLRIQLRANFYQ
				AGAAGCTAAAACGGCCAATTTAGCCCAAA		LINTÍNQÓVPTDMNA
				GCAGCGGGACAACCACAATCTCCTAACA		LINQSQQTQQTSGSA
	•			GCACGGTGATGGGAGCTTTAAACACCGTGTT		SNINACASGMSGSNG
-				GCAAAATGTCAGCAATTTCCAACAAAGCATT		NWCYÓÓWSĎSKAYY
				CAAAACGCTTTTCAAAACCAAGAAAGTAATA		SGLQSALGYŐTQATT
				TCCAAGCTTGGGCGAATGCGATTTATAACACT		OSGSNGGNSITYNVO

QITLTSNGLLNQIIT	6610 LLNQDDDLKAKEQ ALYDLGALYARIKD FKNAHLYNLQYLQ DHAELDKASVVRA RDEKALFSMEGNTQ EKIAHYDKIIQNFPN SNEALKALELKAQL LFENKRYAEVLSM QKNLPKDSPLIQKTL NVLAKTPLENHRC EEALKYLSQITTFE FSPKEEIQAFDCLY FASIKEKAQIIALN AFKTAKAPSEKLI WLYRLGRNYYRL GDFKNSTLASKD ALILAQSLNKKEFY DIAFVLFSDYMQNN EKELALHLYAFLEK HFKGDKRMALVYF KLLENEKDPKSVKIY
AATGGGAGTCAGTCGCAAGAGATGACACCTA ACAATAACCAAGATTTACGCATCCAATTGAGG GCGAATTTTTACCAGTCCATCCATTGAGG GCGAATTTTTACCAGTCCATCAATTGAGG GCGAAGTGCCTACAGACCATGAATGCTTTAAT TAATCAAAGCCAACAAACCAACAGCG GAATGATGGAATAATAACGCATGCGCGAGT GGAATGGAAT	GCTCCTCAATCAAGATGATGATCTG AAAGCTAAAGAGCAAGCGCTTTATG AAAGCTTAAAAACGCCCACCTTTAC AAGGACTTTAAAAACGCCCACCTTTAC AATCTGCAATATTTGCAGGACCATGCG GAACTGGATAAAAGCTTCTGTCGTTAGG GCGCGCATGAAAAAAAAT TTCCCTATGAAAAAACCTTTAAAAAT TTCCCTAATTCTAAAAAAAT TTCCCTAATTGAAAAAAT TTCCTAAATTTTGCAAAAAAT TTCCCTAAATTCTAAAAAAAT TTCCTAAAACCCCATTTGCTAAAGG CTTTTAGAAAAAAATTTGCCTAAAGG CTTTTTTTTTAGAAAAAATTTTTTAT CCCCAAATCCAAAAAAAAAA
	6099
	HP1274(pfiA)
÷	HP1265

				CTACCGCTTAGGGGATTTTAAAAATTC CACTCTGGCCTCTAAAGACGCTTTAAT				
				TCTCGCTCAAAGCTTGAATAAAAAGA ATTTTATGATATTGCTTTTGTTTTTTTTTT	•			
				CAGATTACATGCAAACAATGAAAAG AATTGGCTCTCCATTTGTATGCGTTTTT	· ·			
	-			AGAAAAGCATTTCAAAGGCGATAAAC				
•			٠.	GCA1GGCGC1AG111AAA11GC1 AGAAAATGAAAAAGATCCTAAAAGCG			•	,
				TCAAAATTTATGCCACAAGCTTGCTCAA				
HP1265	HP1379(Ion)	1199		CAATGACGATCCTAACGCATCGCTG	199	6612	NDDPNRIADLIAAA	
				ATTTAATCGCAGCGCCTTGCATTTAA	-		LHLKKDQAYSLFA	
		,		AAAAAGATCAAGCGTATTCTCTTTTTG			NNNTEQRILDLIDIV	
				CCAACAACACCGAACAGCGTTTGT			IEETKTQKLQKEIKS	
		- · · · · · · · · · · · · · · · · · · ·		TGGATTTGATATTGTGATAGAAGA			KVHQKMEQTNKEY	
				GACTAAAACCCAAAACTCCAAAAGA			FLKEQLKQIQKELG	
				AATCAAATCCAAAGTCCATCAAAAAT			TDKQRDEDLNQYY	
				OCAGCARACCAATAAGAATATTIOTIA AAAGAGCAGCTCAAACAAATCCAAAAA	-,		KEESIKFLKEEAF KEIKKOIDPI SPTHA	
				GAGCTTGGCACAGACAGCGAGATG			DSSDSATLONYIETM	
				AAGATTTAAACCAATACTACCAAAAACT			LDVPFGQYGKKALD	
				AGAAAGCATCAAGCCTTTTTTAAAAGAA			IKHVREQLDKDHYS	
				GAAGCGTTTAAGGAGATTAAAAAGCAAA			LKRPKERIVEYFATM	
	·			TTGACCGGCTGAGCCGAACCCATGCGGAC			QLLEMRRKKKPEK	
				AGCTCGGATAGCGCGACTTTACAAAATTAT		_	KDKTKGTILCFYGPP	
				ATTGAAACCATGCTGGATGTGCCTTTTGGG			GVGKTSLANSIAKAI	
_				CAATACGGGAAAAAGCGCITGACATTAA			ERPLVRIALGGLEDV	
	•			GCATGTGAGAGAACAACTAGACAAGGATC			NELRGHRRTYIGSMP	
_				ATTATTCCTTAAAAGGCCTAAAGAGCGCA		-	GRIVQGLIEAKKMNP	
				TIGIAGAATACTITIGCCACCATGCAGCTTT				
				A A A A A A A A A A A A A A A A A A A				
				TATGCTTTTATGGGCCTCCTGGCGTGGGTA				
				AAACAAGCTTAGCTAATTCCATCGCTAAA				
7				GCGATAGAGCGCCCTTTAGTTCGGATCGCT				

۰	-	-
٠	-	-
١	1	3

	ENQIQISKENTKLQ IAKFLPQVSFFGSY IMKQNNSVFEDMI PSWFVGVAGRMPI LSPTGRIQKYQASK LAELQVSSEQIQAK KNMELLVNKTYKE TLSYLKEYKSLLSS VELAKENLKLQEQA FLQGLSTNAQVIDA RNTLSSIVVEQKSV AYKYIVSLANLMA LSDHIDLFYEFVY	LADSLNQRSNEIT QVISLIDDIAEQTN LLALNAAIEAARA GEHGRGFAVVADE VRKLAEKTQKATK EIAVVVKSMQQE ANDIQTNTHDIN SIVSSIKGDVEELK STVKNNMIVAQA AKYTIYNINNRV FCGLAKLDHVVF KNNLYGMVFGLN
	6614	6616
TTAGGGGGATTAGAAGATGTGAATGAATT AAGAGGCACAGACGCACTTATATAGGCT CAATGCCTGGGCGCATTGTCCAAGGCTT	AGAAATCAGATTCAAATCTCTAAA GAAAACCAGATTCAAATCTCTAAA GAAACCACGAAATTACAGATCGCTA AATTCTTGCCCCAAGTGAGTTTTTTT GGCTCTTATATTATGAAGCAAAACAA TTCGGTGTTTGAAGACATGATCCCTAG TTCGTTTTTTTCTCCCCACGGGCGCA TTCAAAATACCAAGCGAGCAAATTA GCGAGTTGCAAGTGAGTAGCGAAAT TATTAGTGAATAAAAAAAAAA	GCTAGCGACTCTCCAACCAACGG AGCAATGAAATCACCAACGG TTTGATTGATGATATTGCAGACACAA TTTGATTGATGATGCAGACACAA ATTGAGCGCGCGAGCGGGCGAGCA AAAAGGCGTTTGCGGTGGTGGCTGAT GAGAGAAACTCGCTGAAAAAACCC AAAAAGCCACTAAAGAAATCGCTGTTGT CGTTAAAAGCATGCAACAAGAAGCGAA CGATATTCAAAACCCAATACCCACGATATT AATTCAATTGTAAAACCCAATACCCACGTAAA
AA	6613	HP0599 (hylB) 6615 GC AC TT TT TT CC GC GC CC
	HP1489	НР0659 НР0

C	٧
₹	⋜

			ACAACGAAATAACCGCTAATCAAACG		SITOEKNOATSEITEAK
			CAAGCGCTAACTAACATTAACGAAGCA		KSAFNELLETLKPKFS
			AAAGAAACGCTAACAATCAAATAACC		GLFAGAYYIRNVIIFK
			GAAAATAAAACCCAAGCGATAACTAAC		ADGRRKSRI
			ATTAACGAAGCGAGAGAAGTGCTACA		
			ACGCAAATTACCACCAATAAGCAAGAA		
	-		GTTTTAAACAGCATCACGCAAGAGAAG		
			AATCAAGCCACAAGCGAGATTACTGAA		
		٠	GCGAAAAAGAGCGCATTTAACGAACTT		
			TTAGAGACCCTAAAGCCGAAGTTTAGC		
			GGCTTGTTTGCGGGGCTTACTATATTC		
			GCAATGTGATTATTCAAGGCGGATGG		
			GAGAAGAAAGTCAAGGATT		
HP0394	HP0257(cag7)	6621	TGCCACTATTAACGCCACTAATG	6622	ATINATNVDA
			TTGATGCGGACAAATAGCTAGCG		DKIASDNPIYA
			ATAATCCTATTTATGCTTCCATAG		SIEPDIAKQYE
			AGCCTGATATTGCCAAGCAATACG	•	TEKTIKDKNL
			AAACAGAAAAACCATTAAGGATA		EAKLAKALGG
			AGAATTTAGAAGCTAAATTAGCT		NKKDDDKEKS
			AAGGCITTAGGTGGCAATAAAA		KKSTAEAKAE
			AGATGACGATAAAGAAAAAGTA		NNKIDKDVAE
			AAAAATCCACAGCAGAAGCTAAA		TAKNISEIALK
			GCAGAAAACAATAAGATAGACAAA		NKKEKSGEFV
			GATGTCGCAGAACTGCCAAGAAT		DENGNPIDDKK
	·		ATCAGTGAAATCGCTCTTAAGAACA		KAEKQDETSPVK
			AAAAAGAAAGAGTGGGGAATTTG		QAFIGKSDPTFVLA
			TAGATGAAATGGTAATCCCATTGA		QYTPIEITLTSKVD
			TGACAAAAGAAAGCAGAAAAAC		ATLTGIVSGVVAK
			AAGATGAAACAAGCCCTGTCAAAC		DVWNM
		•	AGGCCTTTATAGGCAAGAGTGATCC		
			CACATITIGITITIAGCGCAATACACC		
			CCCATTGAAATCACTCTGACTTCTAA		
			AGTAGATGCCACTCTCACAGGTATA		
			GTGAGTGGGGTTGTAGCCAAAGATG		
HP0394	HP0693	6623	CCTTTAAGCGTTGCCACCCAAAATGA	6624	IAKNVKGVDYRLL

7	5	3	Ì	•
٠				•
۱	1			۱

9636	•
	,
CTGGGG ATCAGT AATTTA GGAGGG GATCC CGTGGCAT AGGGGGA AGGGGGA AGGGGGA AGGGGGA AGGGGGA AGGGGGA AGGGGGA AGGGGGG	AAAC
AAATCTATCCAAAATAAGCGCTGGGG TGATTGAAAAAGCTATCCTATC	CGGTCAAGAGCGTGGCTAAAAC GCTTTCTTTAGCCCTAGACAACCAG
AAATCTATCCAAA TGATTGAAAAAGG CAGACGATTTTTA ATCATTATAGGGA GTTACCCTTTTTAA ACCAAAGAACA ATTTTCCTTTTTTAA ATCTTTTGATTTAA ATCTTTTTTTTTT	CGGTCAAG
6635	-
HP0394 HP0717(dnaX)	

RALMCEEGPKAVPCD TCIQCQSALNNHHIDI IEMDGASNRGIDDVR NLIEQTRYKPSFGRYK IFIIDEVHMFTTEAFNA LLKTLEEPPSHVKFLL ATTDALKLPATILSRT QHFRFKKIPENSVISH LKTILEKEQVSYETSA LEKLAHSGQGSLRD TITLLEQAINYCDNAI TESKVAEMLGAIDRS VLEDFFQSLINQDEAR LKERYAILENYFTESV LEEMMLFLKAKLLSP DFYSILLIERFFKIIMS	SLSLLKEGANASFVL
CGTTTGGCTAACGCTTATTTATTCAG CGGGTTAAGAGGCTCAGGGAAAACC AGCTCTTCTAGGATTTTTGCTAGGGC TTTAATGTGTGAAGAGGCCCAAAG GCTGTGCCTTGCGATACTTGCATCCA ATGCCAGAGCGCTTTAAACACCACC ACATAGATATTATAGAAATGGATGGG GCGTCTAATAGGGGGATTGATGATGT CCGTAATCTCATAGAGAGCGTTAAAA ACATAGAGCTTTGGGGCTATAAA ATCTTTATCATTGTGATGAGCCTCCTA GCCATGTGAAGCGTTTAACGCGCT ACAACCCAGGCGTTTAAAA ATCTTTAAAGGCGTTTAAACGCGC TTTTAAAGGCTTTAGAAGTGCTCCTA GCCATGTGAAATTCCTTTTAACGGACAA CAGACGCCTTGAAACTGCCCCCACCAACCCAGCCTTTTAAAAGACTTTAGAAGTGTTTAACGGACAA CAGACGCCTTGAAACTGCCCACCAACCACCAACCCCACCCA	TAAAAAATCCCTGAAATTCCGTTAT TTCTCATTTAAAAACCATTTTAGAAA AGAACAAGTGAGTTATGAAACAAGCG CGTTAGAAAACTGGCTCACAG CGGCAAGGGAGCCTAAGGGAT ACGATCATTTTAGAACAAGC CATCAATTATTGCATAACGCTAT CACAAAAGCAAGGTGGCTGAAAT GTTAGAAAGCGATTGACAGGT TTTAGAAAGCGATTTTTTCCAAAGCCTA AAAGAGCGTTATTGCATTTTAGAAA ATTATGAAAGCGAAATTATTTT TTTGAAAGCGAAATTATTCATCC TTTGAAAGCGAAATTATTCATCC TTTTGAAAGCGAAATTATTCATCC TTTTGAAAGCGCAAATTATTCAACCCTTTTTAAAAAGCCGTTTTTAATTCTATCC TTTTTTTTTT

١	£	7
Ľ	_	
•	_	_
١		

												-	<u></u>												_		· · · ·		 -				
	NLKADNNTEFKEENO	DTKENOPNDLFSLPL	PTQTTINGIKEFVEEP	VIETEKKETSQNEPIQ	EKKERIFKNFFSRIGF	DKSIAPTMLFEEVRD	ASVIYHLEKKLGDYI	FYVACFFFGTTALLII	LLTILLPLKQKEPYL	VQFSNNKENFALVQ	KADSSITANKALIRS	LVGAYVLNRESITHI	EQHEKMRONTIKEÓ	SSNEVWYEFEKLIAH	YDSIYTNPLLTRKVK	IANIYLDKĎLAYIDIE	VSLYHSGELESLKRYK	VVMSFEFKKQEINFD	SMSLNPTGFMVTSY	DVTEIAIVNYPTAKA	IGLFLAS												
																															_	_	
	6638	_																															
		-								,				<i>f</i>																			
A	CA	AA	AA	ည	ATT	GTG	AAC	AGA	AAA	GATA	TTTT	STTA	LAGGC	GTTT	CTTA	3000	TTAG	VAAA	GATA	CICIT	ATGT	TCATA	GTCAA	TCCAA	VAAACT	TACAC	GTAAA	AAAGAT	TCAGCT	AGAGCTT	SAGTTTT	AATTTIG	AGGCTT
GTTATTGA	GACAACAA	AGAAAATC	ACCAGCCI	TGCCATTG	TCAATGGA	AAGAGCCT	AAAAAGA.	CCAATCCA	AATTTTAA	TAGGCTTT	TACAATGC	BATGCAAG	BAAAAT	TGTAGCGT	CGGCATTC	ATTCTGTT	AGCCGTAT	AATAAAG/	AAAAGGCA	CAATAAAG	GGGAGCGI	AGCATTAC	AAAAATGC	AGCAAAGT	SAATTTGA/	ACAGCAT	CAAGAAA/	FACTTAGAT	CATTGAAC	GAATTAG	GTGGTGAT	AAGAAATC	AATCCTAC ATGATGTA
AGTITTGTGCTGTTGTTATTGAA AATGAAATTCAAA	AAATCTTAAAGCAGACAACAACA	CAGAATTTAAAGAAGAAAATCAA	GACACTAAAGAAAACCAGCCTAA	CGATTTGTTTTCTTTGCCATTGCCC	ACTCAAACCACCATCAATGGAATT	AAAGAATTTGTAGAAGAGCCTGTG	ATAGAAACAGAGAAAAAAAAA	ATCCCAAAATGAGCCAATCCAAGA	AAAAAAGAAAGAATTTTAAAAA	CITITICICCAGAATAGGCITIGATA	AAAGTATTGCCCCTACAATGCTTTTI	GAAGAAGTGAGAGATGCAAGCGTTA	TCTATCATTTAGAGAAAAAATTAGGC	GATTATATCTTTTATGTAGCGTGTTT	CITCITTGGCACAACGGCATTGCITA	ITATCITACTGACTATTCTGTTGCCC	ITAAAACAAAAAGAGCCGTATITAG	TGCAATTTTCTAACAATAAAGAAAA	TITTGCTTTAGTTCAAAAGGCAGATA	GCAGCATTACAGCCAATAAAGCTCTT	ATTCGTTCATTAGTGGGAGCGTATGT	GCTAAACAGGGAAAGCATTACTCATA	TTGAGCAACATGAAAAATGCGTCAA	AACACCATTAAAGAGCAAAGTTCCAA	TGAAGTATGGTATGAATTTGAAAAACT	CATCGCTCATTATGACAGCATTTACAC	TAATCCTTTACTCACAAGAAAGTAAA	GATTGCAAATATTTACTTAGATAAAGAT	TTAGCCTATATTGACATTGAAGTGAGCT	TGTATCATAGTGGAGAATTAGAGAGCTT	GAAGCGCTATAAAGTGGTGATGAGTTTT	GAATITAAAAAACAAGAAATCAATTITG	ACTCCATGTCTTTAAATCCTACAGGCTT TATGGTTACAAGTTATGATGTAACTGAA
AATGA	AAATC	CAGA	GACAC	CGATT	ACTCA	AAAG	ATAGA	ATCCC	AAAA	CTTT	AAAGI	GAAGA	TCTAT	GATTA	CTTCT	TTATC	TTAAA	TGCAA	TTTTG	GCAGC	ATTCG	GCTAA	TTGAG	AACAC	TGAAG	CATCG	TAATC	GATTG	TTAGC	TGTAT	GAAGC	GAATT	ACTCC
																					-												
	6637	_	-,					_										_															
	HP0439					÷								-	•						-			٠								ı	
	HP0394																•									_	-						

	6640 FDENTTKLFLWILT	ATIALVVLTLIYAK I.RIVKRIDEI.VI.KIN	AFSRGDKDLRAKID	VGDRNDEISQVGRG	INLFVENARLIMEEIK	GISTLNKTSMDKLVQ	I I CE I CKSMIK DSS I I	MNASIEQSQGLRKR	LIETQGLVKESKDAI	GDLFSQITESAHTEE	ELSS										6642 DSLNQRSNEITQVI	SLIDDIAEQTNLLA	LNAAIEAARAGEHG	KGFAVADEVKAL	AEKTOKATKEIAVV	VKSMQQEANDIQIN	THDINSIVSSIKGDV	EELKSTVKNNMIVA	QAAKYTIYNINNRV	FCGLAKLDHVVFKN	NLYGMVF
ATTGCGATTGTGAATTACCCAACCGCTA AAGCGATTGGGCTTTTTCTTGCTTCA	TTTTGATGAAACACCACGAAATT	ATTCCTTTGGATACTGACAGCGAC	CATATACGCTAAATTAAGGATCGT	GAAACGCATTGATGAACTGGTCCT	TAAAATCAACGCTTTTAGCCGTGG	GGATAAGGATTTGAGAGCCAAAAT	TGATGTGGGTGATCGCAACGATGA A A TCTCGCA A GTGGGGCCGTGGGGAT	CAATTTGTTTGTGGAAAACGCCCGC	TTGATTATGGAAGATTAAAGGG	ATTTCCACCTCAATAAACTTCAA	TGGATAAATTAGTCCAAATCACGCA	AGAAACCCAAAAGAGCATGAAAGA	TTCCTCAACCACCTAAATTCCGTGA	AAAATAAAGCCACTGATATAGCGA	GCATGATGAATGCTTCCATAGAGCA	ATCTCAAGGGTTAAGGAAGCGTTTG	ATTGAAACGCAAGGGCTGGTCAAAG	AGAGCAAGGATGCGATCGGGGATTT	ATTTTCTCAAATCACAGAGAGCGCGC	ACACTGAAGAGGAACTCTCTAGC	GGACTCTCCAACCAACGGAGCAAT	GAAATCACTCAAGTCATTTCTTTGAT	TGATGATATTGCAGAACAAACCAATC	TATTAGCCCTAAATGCCGCTATTGAG	GCCGCGCGAGCGAGCATGGGAG	AGGGTTTGCGGTGGTGGCTGATGAGG	TGAGAAACTCGCTGAAAAAACCCAA	AAAGCCACTAAAGAAATCGCTGTTGT	CGTTAAAAGCATGCAACAAGAAGCGA	ACGATATTCAAACCAATACCCACGAT	ATTAATTCTATTGTAAGCTCTATTAA
·	HP103(tlpB) 6639					·															HP0394 Hp0599(hylB) 6641								•		

٠	>	C
٠	-	-
١	1	;

·		I CA I KDADKNH I SS NNNTHTYYVTYNLG GTLYNFROIFSPDSIV	LQSVYYGANNLYYT NSVNIHDNVFNLKN	INDDKADTIFYLNGL	GGKNSALVFNATTP	W ANGOIF KOINS I V K FGGYEGVNWGKTG	YITGTFTADRVYITG	ATLNFVGATEINIAGA	TFKNLKTTSQNSYMT	FMALGDSSGSAKINV	FTGNGVFDSVNFNK	AYYKFQGTENSYNF	KNTNFLAGNFKFQG KTTHFKSVI SDASVT	FDGTNNTFTEDKFN	NGSFNFSHAEQTDA	FINNNSFNGGSFSFN	VENENNTEXXXETT	DTFNVNNQFKINGT	QTTFTFNKGVVFNM	QGLLSSLSVGTTYQ LL
	6644	· · · · ·			·													-		
ACCGTAAAAATAACATGATTGTTGC GCAAGCGCAAAATACACCCATCTACA ATATCAATAACCGGGTGTTTTGCGGTT TGGCCAAACTTGATCATGTGGTCTTTA AAAACAATCTTTATGGCATGGTTTTTGG	CGCTTACACGCTCTTTAGCATGAA AAATGGCTCTATCACCTATAATGA	IGICAATAACITATGGAATATCAT CAGGCTTAAAAACACGCAAGCCAC AAAAGACGCTGATAAAAATCATACA	AGTTCAAATAACAACCCCACACTTA CTATGTAACCTACAATTTAGGCGGCA	CGCTTTATAATTTCAGACAAATTTTTA GCCCTGATTCTATTGTTTTGCAATCTG	TCTATTATGGCGCGAACAATCTTTACT	ACACCAATAGCGTGAATATCATGAT AATGTTTTTAATTTAA	TGATGATAAAGCTGACACGATTTTCTA CCTCAATGGCTTAAACCTTGGAATTA	CACTAATGCGAGATTCACTCAAACCTA		1GGCGGGAAAACAGCGCTTTAGT CTTTAACGCTACGACCCCTTGGGGCT	AATGGCAGCATCCCTAAATCTAACA	GCACGGTGCGTTTTGGGGGGTATGA	GGGAGTCAATTGGGGGAAAACGGGC DATATTACTGGCACTTTCACAGCCGA	TAGGGTTTATATCACCGGTAACATGA	TGACTGGTAACGGCGCTCAAACCGG	TGGGGGGGCGACTTTGAATTTTGTGG	GCGCGACTGAAATAATCGCTGGA	TTCACAAAACTCTTACATGACTTTTA	TGGCATTAGGGGATAGCTCTGGGAGC	GCTAAGATCAATGTTTCTCAATCTGAT TTTTACGATTGGACGGTGGGGGGTAT
	6643	• .			,					•	. •							<u></u> -	· ·	
	HP0609				-							•								
	HP0394																			

5

	GATTTTACCGGTAATGGCGTTTTTGATA	
	GCGTGAATTTCAACAAGGCTTATTACA	
	AATTTCAAGGCACTGAAATTCTTACAA	
	TTTTAAAAACACGAACTTTTTAGCAGGG	
	AATTTTAAGTTTCAGGGCAAGACCACCA	
	TTGAAAAATCCGTTTTAAGCGACGCTTCT	
	TACACTITIGATGGCACGAATAACACCTT	
	TACTGAAGACAAGTTTAATAATGGCTCG	
	TTTAAŤTTTAGTCATGCAGACAG	
	ACGCTTTTAATAACAACTCGTTTAATGGC	
	GGTTCGTTTAGTTTTAACGCCAAGCAAGT	
	AAATTTTAGTGGGAACTCGTTCAATGGGG	
	GCGTGTTTAATTTCAATAACCCCTAAA	
	GTCAGTTTCACTGATGACACTTTTAATGT	
-	GAATAACCAATTCAAAATAAATGGTACT	
	CAAACAACTTTCACTTTCAATAAGGGCGT	
	TGTTTTCAACATGCAAGGGCTTTTGAGCA	
	GTTTAAGCGTAGGCACGACTTATCAATTG	
	CTTA	

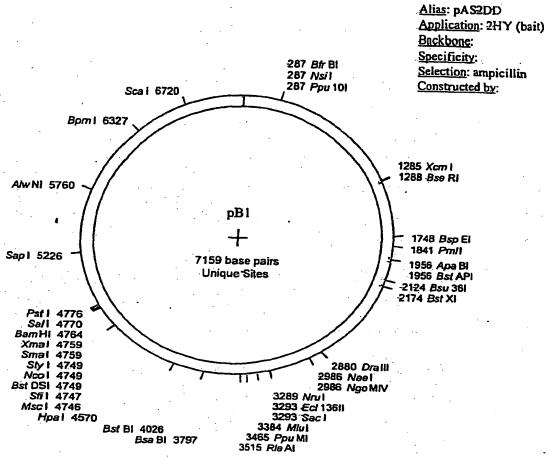
CLAIMS

What is claimed is:

- 1. A complex of protein-protein interactions in *Helicobacter pylori* as defined in Table 1 and Table 8.
- 2. A complex of polynucleotides in *Helicobacter pylori* encoding for the polypeptides defined in Table 1 and Table 8.
- 3. A recombinant host cell expressing the interacting polypeptides in *Helicobacter pylori* defined in Table 1 and Table 8.
- 4. A method for selecting a modulating compound in *Helicobacter pylori* comprising:
 - (a) cultivating a recombinant host cell on a selective medium containing a modulating compound and a reporter gene the expression of which is toxic for said recombinant host cell wherein said recombinant host cell is transformed with two vectors:
 - (i) wherein said first vector comprises a polynucleotide encoding a first hybrid polypeptide and a DNA bonding domain;
 - (ii) wherein said second vector comprises a polynucleotide encoding a second hybrid polypeptide and an activating domain that activates said toxic reporter gene when the first and second hybrid polypeptides interact;
 - (b) selecting said modulating compound which inhibits the growth of said recombinant host cell.
- 5. A modulating compound obtained from the method of Claim 4.
- 6. A SID® polypeptide in *Helicobacter pylori* comprising the even SEQ ID Nos. 2 to 3256 in column 3 of Table 2, even SEQ ID Nos. 6590 to 6594 in Table 7 and even SEQ ID Nos. 6596 to 6644 in Table 8.
- 7. A SID® polynucleotide in *Helicobacter pylori* comprising the uneven SEQ ID Nos. 1 to 3255 in column 2 of Table 2, uneven SEQ ID Nos. 6589 to 6593 in Table 7 and uneven SEQ ID Nos. 6595 to 6643 in Table 8.
- 8. A vector comprising the SID® polynucleotide in *Helicobacter pylori* comprising the uneven SEQ ID Nos. 1 to 3255 in column 2 of Table 2,

- uneven SEQ ID Nos. 6589 to 6593 in Table 7 and uneven SEQ ID Nos. 6595 to 6643 in Table 8.
- 9. A fragment of said SID® polypeptide according to Claim 6.
- 10. A variant of said SID® polypeptide according to Claim 6.
- 11. A fragment of said SID® polynucleotide according to Claim 7.
- 12. A variant of said SID® polynucleotide according to Claim 7.
- 13. A vector comprising the SID® polypeptide according to Claim 11.
- 14. A recombinant host cell containing the vectors according to Claim 8.
- 15. A pharmaceutical composition comprising a modulating compound of claim 5 and a pharmaceutically acceptable carrier.
- 16. A pharmaceutical composition comprising a SID® polypeptide of claim 6, and a pharmaceutically acceptable carrier.
- 17. A pharmaceutical composition comprising the recombinant host cells of claim 14 and a pharmaceutically acceptable carrier.
- 18. A protein chip comprising the polypeptides of claim 6.





Oligo 160

gagagtagtaacaaaggtc AAAGACAGTTGACTGTATCGCCG GAA TTT AT

Sfi I Sma I BamH I Sal I Pst I

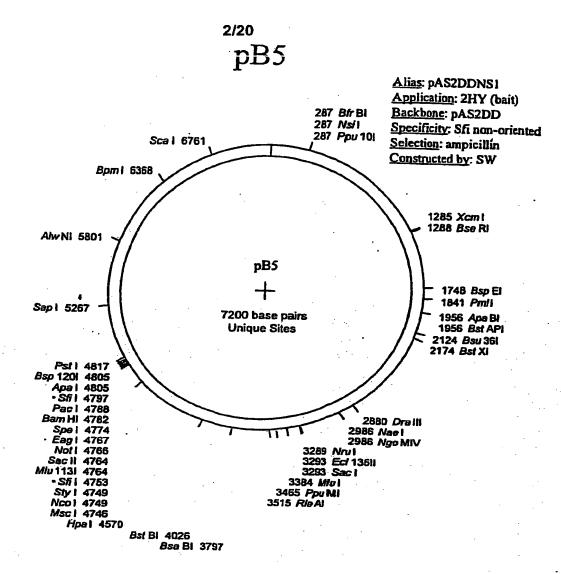
G GCC ATG GAG GCC CCG GGG ATC CGT CGA CCT GCA GCC

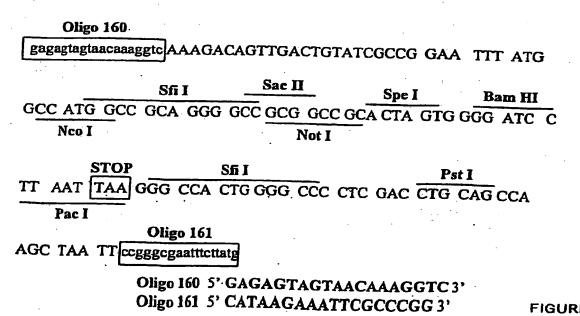
Nco I

Oligo 161

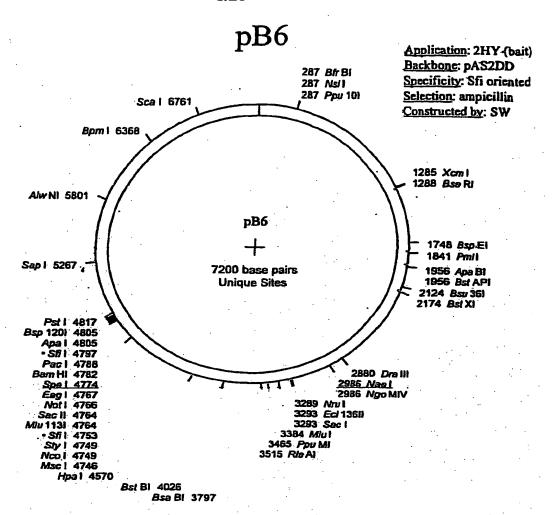
AAG CTA ATT ccgggcgaatttcttatg

Oligo 160 5' GAGAGTAGTAACAAAGGTC 3' Oligo 161 5' CATAAGAAATTCGCCCGG 3'





BNSDOCID: <WO__ _02066501A2_l_>



Oligo 160

gagagtagtaacaaaggtc AAAGACAGTTGACTGTATCGCCG GAATTT ATG

Sfi I Sac II Spe I Bam HI

GCC ATG GCC GGA CGG GCC GCA CTA GTG GGG ATC C

Not I Not I

TT AAT TAA GGG CCA CTG GGG CCC CTC GAC CTG CAG CCA

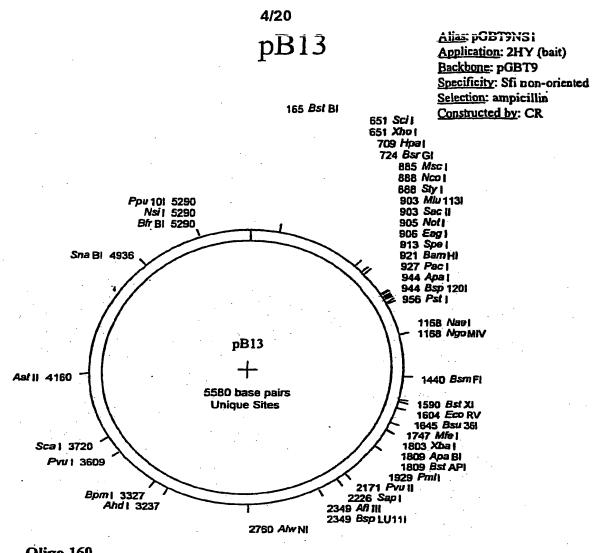
Oligo 161

AGC TAA TT ccgggcgaatticttatg

Oligo 160 5' GAGAGTAGTAACAAAGGTC3' Oligo 161 5' CATAAGAAATTCGCCCGG3'

FIGURE 3

SUBSTITUTE*SHEET (RULE-26)



Oligo 160

gagagtagtaacaaaggtc AAAGACAGTTGACTGTATCGCCG GAA TTT ATG

 Sfi I
 Sac II
 Spe I
 Bam HI

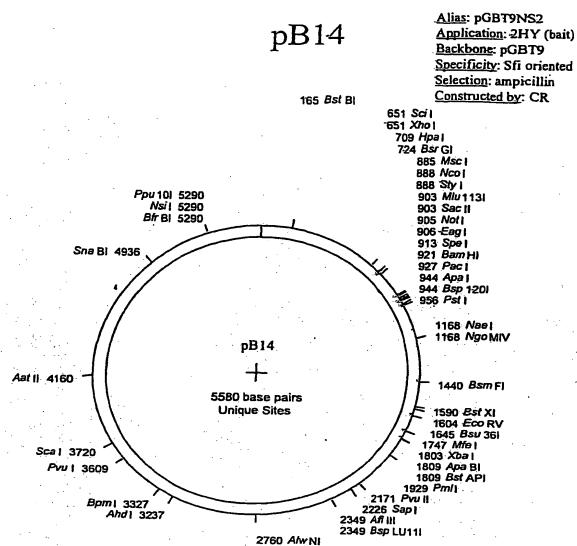
 GCC ATG GCC GCA GGG GCC GCG GCA CTA GTG GGG ATC C
 Not I
 Not I

TT AAT TAA GGG CCA CTG GGG CCC CTC GAC CTG CAG CCA

Pac I

Oligo 161
AGC TAA TT ccgggcgaatttcttatg

Oligo 160 5' GAGAGTAGTAACAAAGGTC 3' Oligo 161 5' CATAAGAAATTCGCCCGG 3'



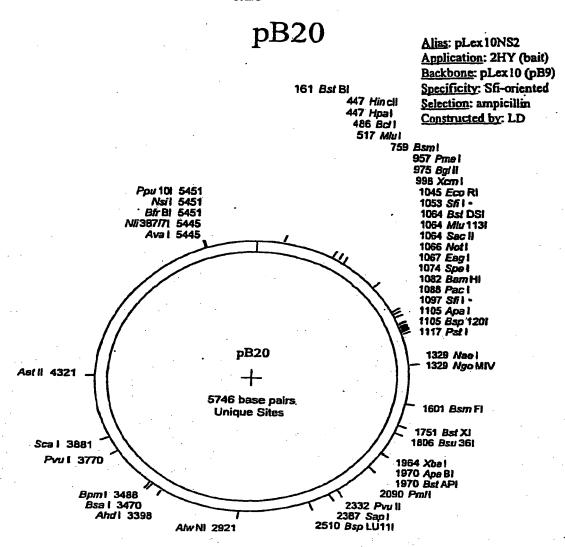
Oligo 160
gagagtagtaacaaaggtc AAAGACAGTTGACTGTATCGCCG GAA TTT ATG

STOP Sfi Apa I

TT AAT TAA GGG CCA CTG GGG CCC CTC GAC CTG CAG CCA

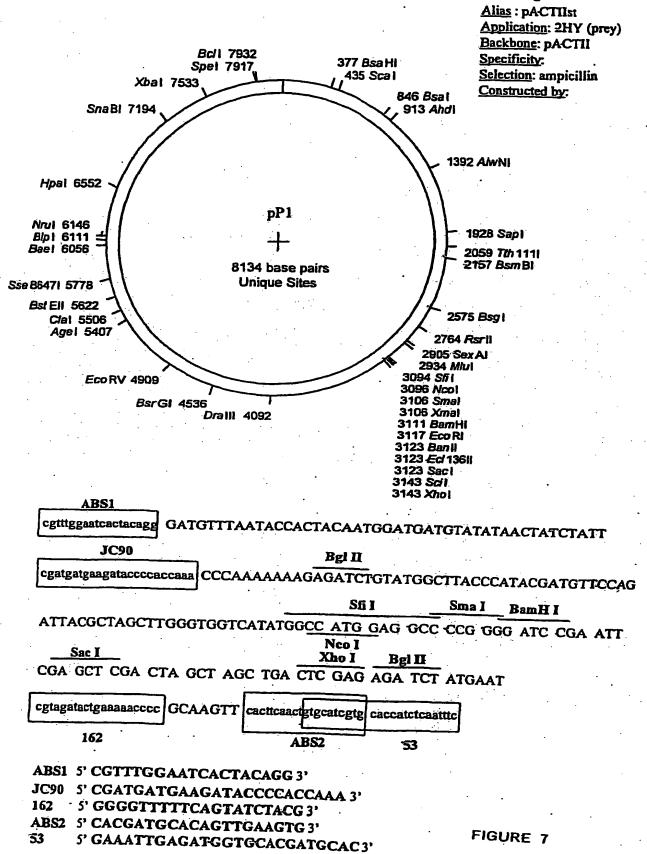
Pac I

Oligo 161
AGC TAA TT ccgggcgaatttcttatg

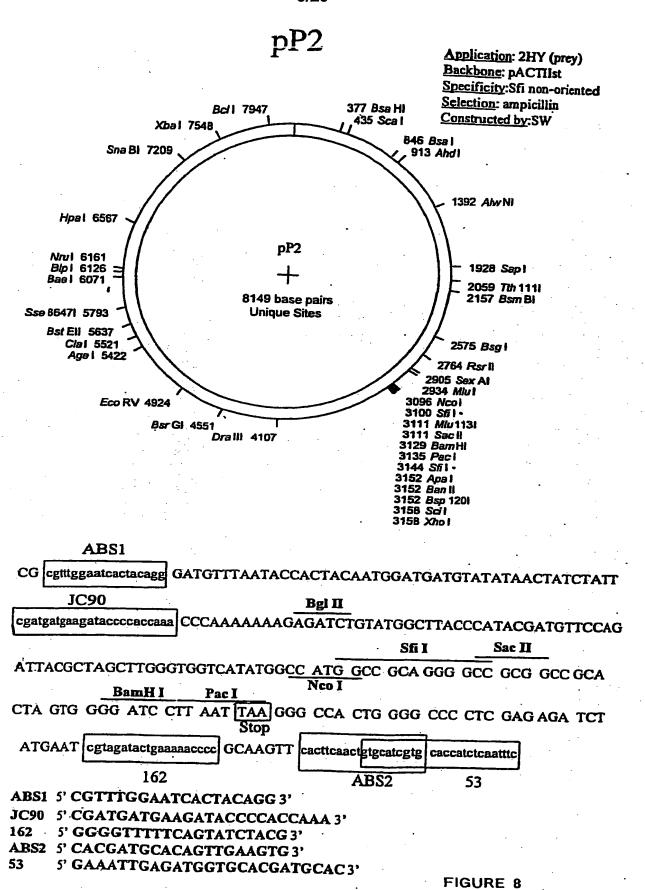


EcoR I			Sfi	I			Not I		Spe I	[
GAA TTC	GGG	GCC	GGA	CGG	GCC	GCG	GCC	GCA	CTA	GTG
BamH			STOP			Sac II				•
GGG ATC	CIT	AAT			CCA	CTG	GGG	CCC	CTC	GAC
		Pac]				Sfi I	-			One
CTG CAG	}				•					
Pst I	•						FIGUR	E 6		



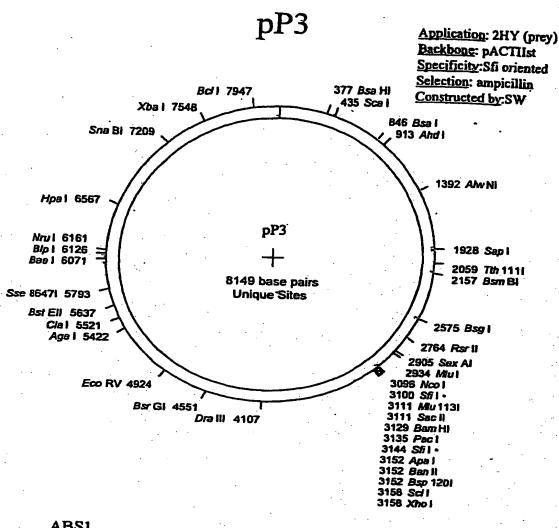


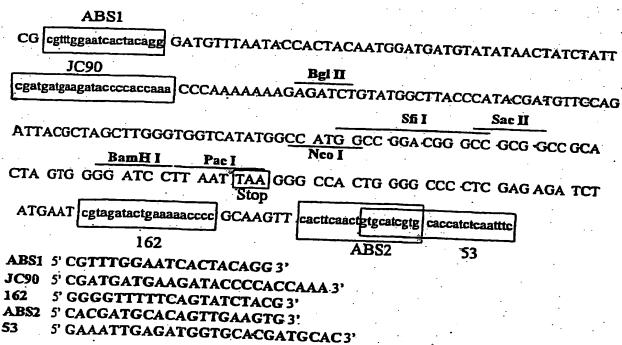
SUBSTITUTE SHEET (RULE 26)

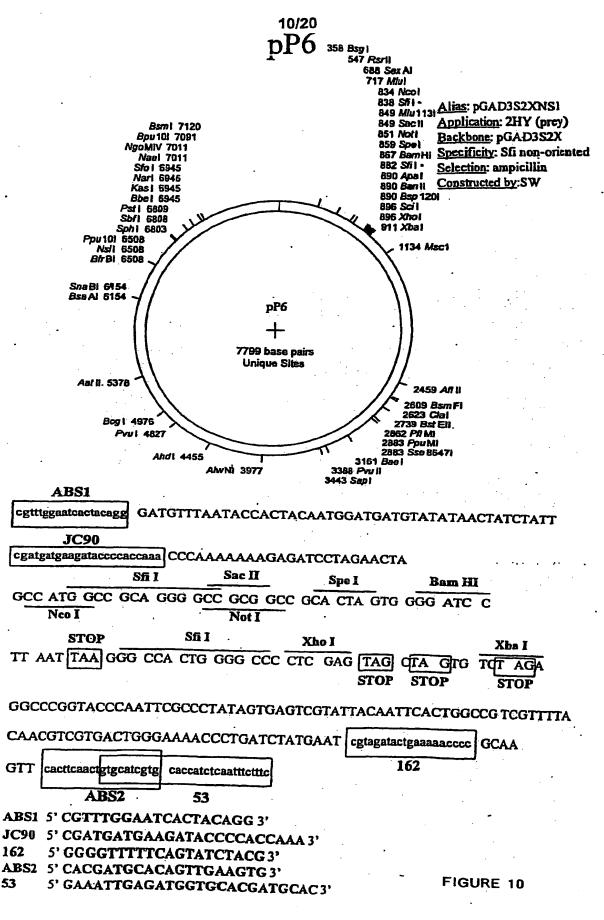


SUBSTITUTE SHEET (RULE 26)

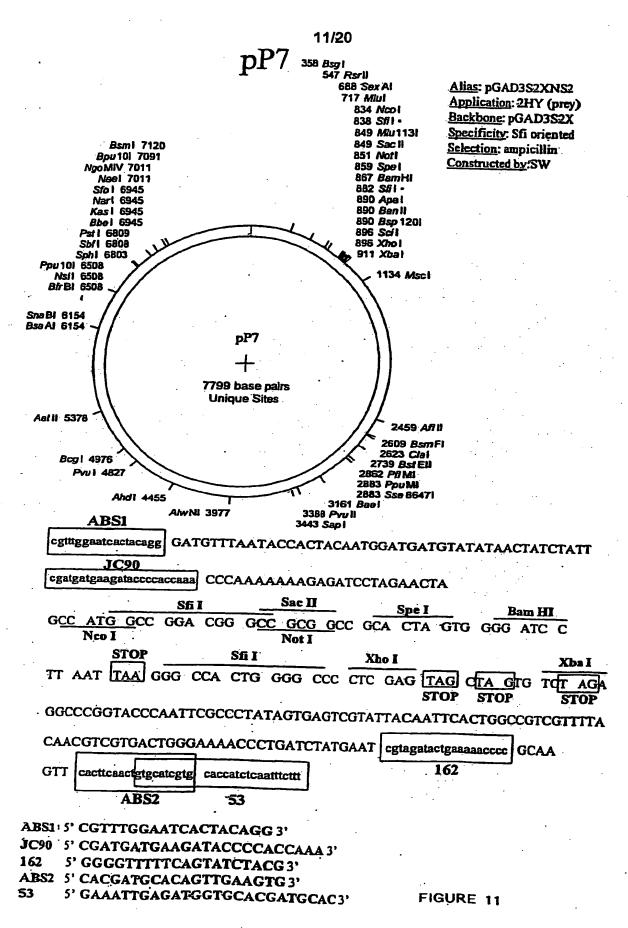








SUBSTITUTE SHEET (RULE 26)



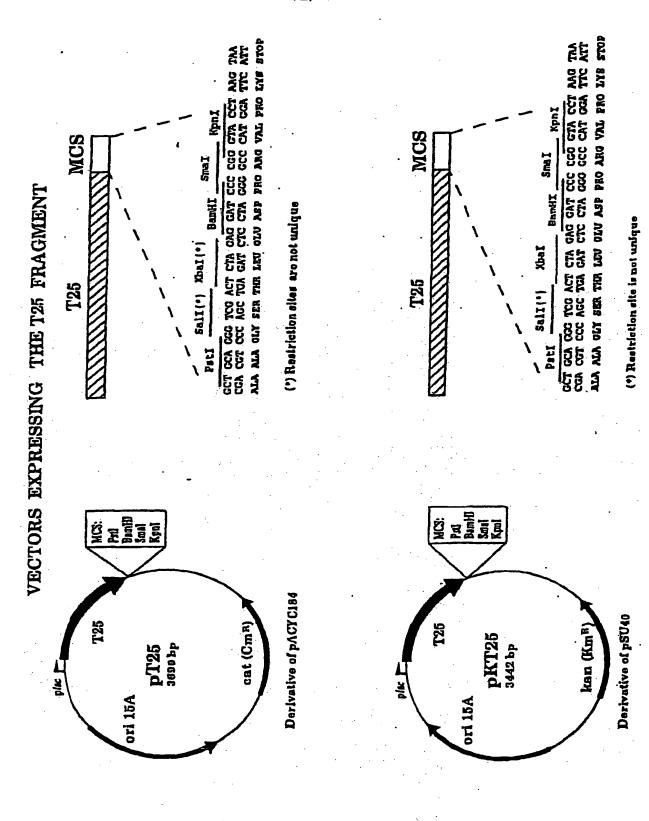
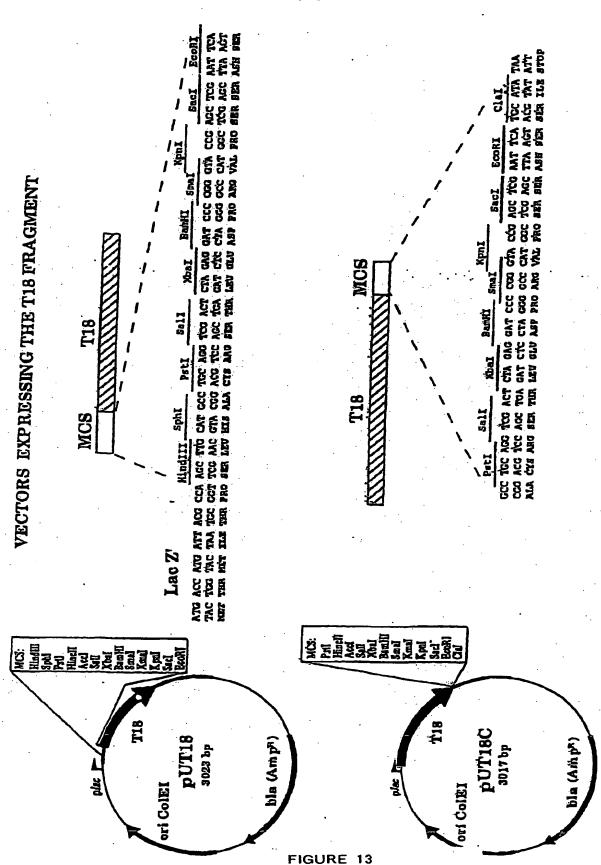
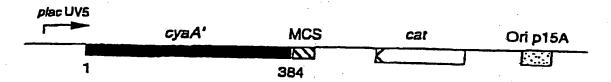


FIGURE 12

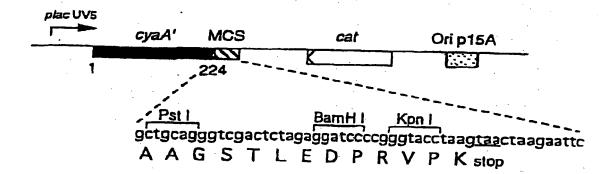




pCmAHL1



pT25



pT18

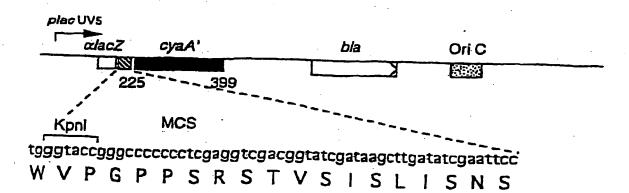
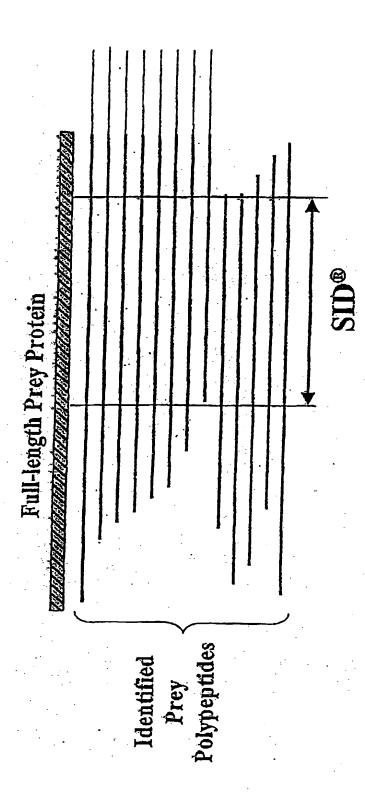
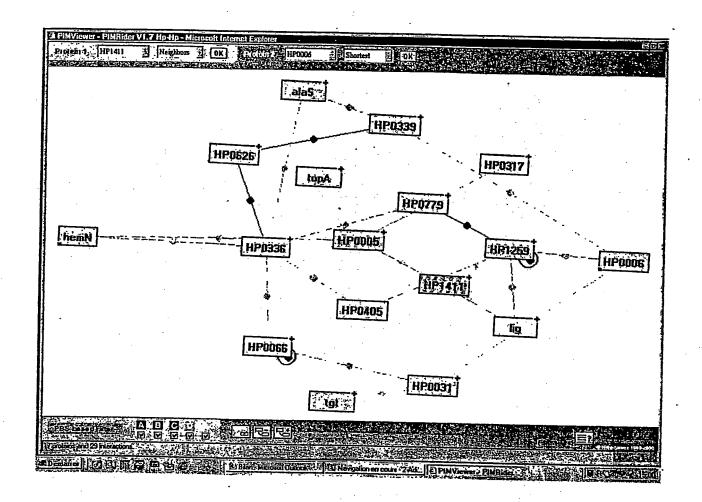


FIGURE 14



Schematic representation of SID® determination

FIGURE 15



Exemple of Protein Interaction Map

FIGURE 16

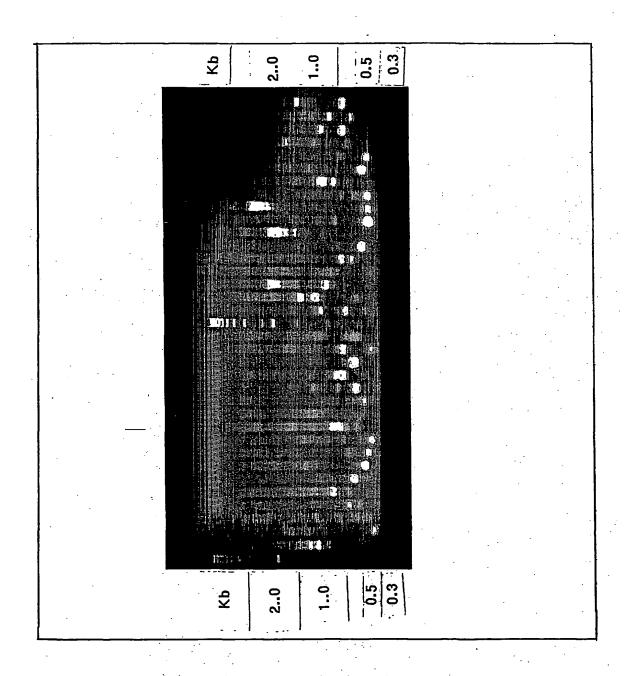
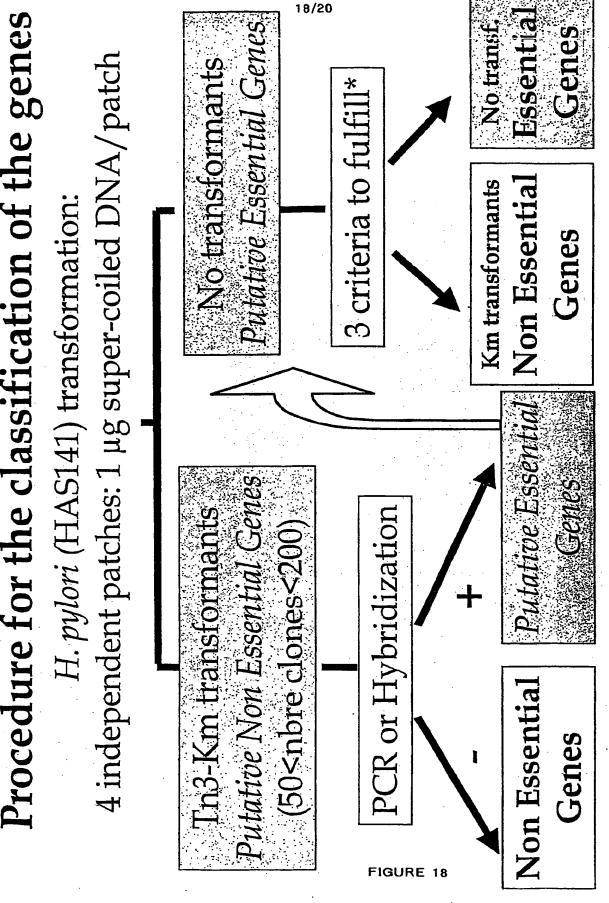
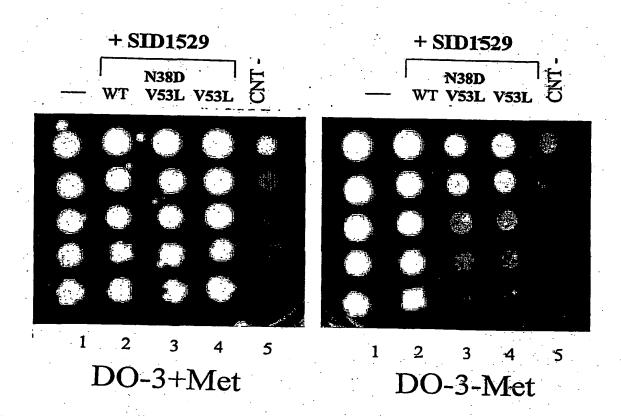


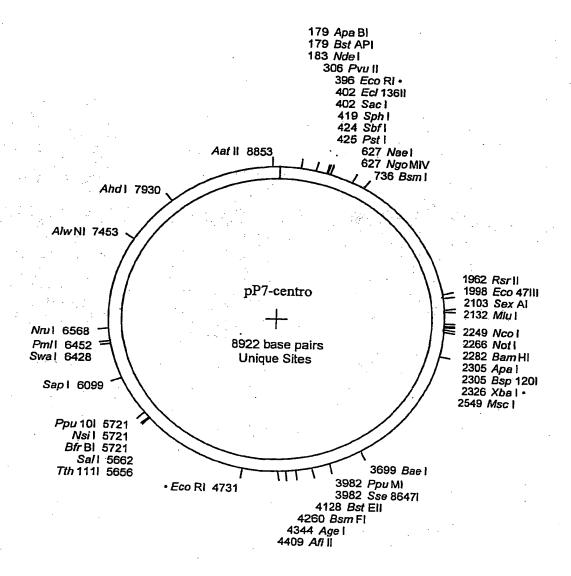
FIGURE 17

Procedure for the classification of the genes





pP7-centro



ATGGCCGgAcGGCCGCGCCGCACTAGTGGGGATCCTTAATTAAGGG
NotI BamHI
CCACTGGGGCCCCTCGAGTAGCTAGTGTCTAGAGGCCCGGTACCCAATT

(19) World Intellectual Property Organization International Bureau



\ (0.010 0.011.00 1) | 0.011 0.011 0.011 0.011 0.011 0.011 0.011 0.011 0.011 0.011 0.011 0.011 0.011 0.011 0.0

(43) International Publication Date 29 August 2002 (29.08.2002)

PCT

(10) International Publication Number WO 02/066501 A3

- (51) International Patent Classification⁷: C07K 14/205, C12N 15/31, G01N 33/68, C12N 15/63, A61K 39/106, 35/74
- (21) International Application Number: PCT/EP01/15428
- (22) International Filing Date:

28 December 2001 (28.12.2001)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data: 60/259,302

2 January 2001 (02.01.2001) US

2.01.2001) 176

- (71) Applicants (for all designated States except US): HYBRI-GENICS [FR/FR]; 3/5 Impasse Reille, F-75014 Paris (FR). INSTITUT PASTEUR [FR/FR]; 25-28, rue du Dr Roux, F-75724 Paris Cedex 15 (FR).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): LEGRAIN, Pierre [FR/FR]; 5, rue Mizon, F-75015 Paris (FR). RAIN, Jean-Christophe [FR/FR]; 32, Jardin Boeldieu, F-92800 Puteaux (FR). COLLAND, Frédéric [FR/FR]; 16, rue du Manoir, F-95380 Puiseux en France (FR). DE REUSE, Hilde [BE/FR]; 49, rue Rouelle, F-75015 Paris (FR). LABIGNE, Agnès [FR/FR]; 29, rue du Bois Michel Pierre, Appt 106, F-91440 Bures sur Yvette (FR).

- (74) Agent: ERNEST GUTMANN YVES PLASSERAUD S.A.; 3, rue Chauveau-Lagarde, F-75008 Paris (FR).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

- with international search report
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments
- (88) Date of publication of the international search report: 20 November 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

11 A

(54) Title: PROTEIN-PROTEIN INTERACTIONS IN HELICOBACTER PYLORI

(57) Abstract: The present invention relates to protein-protein interactions of *Helicobacter pylori*. More specifically, the present invention relates to complexes of polypeptides or polynucleotides encoding the polypeptides, fragments of the polypeptides, anti-bodies to the complexes, Selected Interacting Domains (SID®) which are identified due to the protein-protein interactions, methods for screening drugs for agents which modulate the interaction of proteins and pharmaceutical compositions that are capable of modulating the protein-protein interactions.



International Application No PCT/EP 01/15428

A. CLASSIFICATION OF SUBJECT MATTER IPC 7 C07K14/205 C12N15/31 A61K35/74

[2N15/31 G01N33/68

C12N15/63

A61K39/106

Relevant to claim No.

1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Category *

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

Citation of document, with indication, where appropriate, of the relevant passages

WO 00 66722 A (SELIG LUC ; HYBRIGENICS S A

EPO-Internal, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

	(FR); LEGRAIN PIERRE (FR); RA 9 November 2000 (2000-11-09) cited in the application the whole document	IN JEAN CH)	
Α	LEGRAIN P ET AL: "Genome-wid interaction maps using two-hy FEBS LETTERS, ELSEVIER SCIENC AMSTERDAM, NL, vol. 480, no. 1, 25 August 2000 (2000-08-25), XP004337490 ISSN: 0014-5793 cited in the application	brid systems" E PUBLISHERS,	
	the whole document	•	
		-/	
Special cat "A" docume conside "E" earlier d filling d "L" docume which i citation "O" docume other n "P" docume later th	nt which may throw doubts on priority claim(s) or s cited to establish the publication date of another or or ther special reason (as specified) int referring to an oral disclosure, use, exhibition or	"T" later document published after the interr or priority date and not in conflict with the cited to understand the principle or the cinvention "X" document of particular relevance; the class cannot be considered novel or cannot be involve an inventive step when the document of particular relevance; the class cannot be considered to involve an inventive document is combined with one or more ments, such combination being obvious in the art. "8" document member of the same patent father than the control of the same patent father than the control of the same patent father than the control of the same patent father than the control of the same patent father than the control of the same patent father than the control of the same patent father than the control of the same patent father than the control of the same patent father than the control of the control of the same patent father than the control of the con	national filing date the application but the application but the application but the application but the application but the application but the considered to the application alone timed invention the application application to a person skilled the application but t
Date of the c			
20	9 June 2003	- 9.	09. 2003
Name and m	halling address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Hix, R.	
OF DETACAD	10 (second sheet) (July 1992)		

Form PCT/ISA/210 (second sheet) (July 1992)



International Application No PCT/EP 01/15428

		PCI/EP 01	./13460
C.(Continua	tion) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages		Relevant to claim No.
A.	CHALKER ALISON F ET AL: "Systematic identification of selective essential genes in Helicobacter pylori by genome prioritization and allelic replacement mutagenesis." JOURNAL OF BACTERIOLOGY, vol. 183, no. 4, 2001, pages 1259-1268,		
	XP002245013 ISSN: 0021-9193 cited in the application the whole document		
	TOMB J-F ET AL: "THE COMPLETE GENOME SEQUENCE OF THE GASTRIC PATHOGEN HELICOBACTER PYLORI"		
	NATURE, MACMILLAN JOURNALS LTD. LONDON, GB, vol. 388, no. 6642, 7 August 1997 (1997-08-07), pages 539-547,TABEL, XP002062106 ISSN: 0028-0836 cited in the application		
a .	the whole document WO 99 42612 A (FROMONT MICHELINE ; LEGRAIN PIERRE (FR); PASTEUR INSTITUT (FR); RAI) 26 August 1999 (1999-08-26) cited in the application the whole document		
	the whole document		
	l .		I

INTERNATIONAL SEARCH REPORT

International application No. PCT/EP 01/15428

Box I Observations where certain claims were found unse	earchable (Continuation of item 1 of first sheet)
This International Search Report has not been established in respect of	centain claims under Article 17(2)(a) for the following reasons:
1. Claims Nos.: because they relate to subject matter not required to be search	the symmetric managements
2. X Claims Nos.: 1-3, 6-18 because they relate to parts of the International Application the	at do not comply with the prescribed requirements to such
because they relate to parts of the International Application in an extent that no meaningful International Search can be carrised See FURTHER INFORMATION sheet PCT/IS	led out, specifically.
SEC LANINER THEOWNSTON SHEEL LOLLE	
o Claims Nos :	
Claims Nos.: because they are dependent claims and are not drafted in acc	cordance with the second and third sentences of Rule 6.4(a).
Box II Observations where unity of Invention is lacking (C	Continuation of item 2 of first sheet)
This International Searching Authority found multiple inventions in this	international application, as follows:
see additional sheet	
SEC GRATTIONAL SHEET	
As all required additional search fees were timely paid by the searchable claims.	applicant, this International Search Report covers all
2. As all searchable claims could be searched without effort just	stifying an additional fee, this Authority did not invite payment
of any additional fee.	
As only some of the required additional search fees were time.	nely paid by the applicant, this International Search Report
covers only those claims for which fees were paid, specifical	iny ciantis inos
	applicant Consequently this International Search Report is
4. X No required additional search fees were timely paid by the a restricted to the invention first mentioned in the claims; it is	covered by claims Nos.:
none	
·	
Remark on Protest The ac	dditional search fees were accompanied by the applicant's protest.
No pro	otest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1 : claims 1-3

A complex of protein-protein interactions in Helicobacter pylori as defined in Table 1 and Table 8, polynucleotides encoding therefor, recombinant host cells expressing said interacting polypeptides.

NB. Invention 1 involves a vast number of separate inventions however due to the nature of Tables 1 and 8, it is not possible to subdivide the inventions further.

Invention 2: claims 4, 5 and 15

A method of selecting a modulating compound in Helicobacter pylori according to claim 4, a modulating compound obtained therefrom and pharmaceutical composition comprising said modulating compound.

Inventions 3-3257: claims 6 to 14 and 16 to18 (partially):

A Selected Interacting Domain (SID) polypeptide in Helicobacter pylori comprising the even Nos. 2 to 3256 in column 3 of Table 2, a SID polypucleotide in Helicobacter pylori comprising the uneven SEQ ID NOs 1 to 3255 in column 2 of Table 2, a fragment or variant of said SID polypeptide or SID polypucleotide, a vector and host cell comprising said SID polypeptide, a pharmaceutical composition comprising said SID polypeptide or said recombinant host cells and a protein chip comprising said polypeptides.

Inventions 3258-3262: claims 6 to 14 and 16 to 18 (partially):

A Selected Interacting Domain (SID) polypeptide in Helicobacter pylori comprising the even Nos. 6590 to 6594 in Table 7, a SID polynucleotide in Helicobacter pylori comprising the uneven SEQ ID NOs 6589 to 6593 in Table 7, a fragment or variant of said SID polypeptide or SID polynucleotide, a vector and host cell comprising said SID polypeptide, a pharmaceutical composition comprising said SID polypeptide or said recombinant host cells and a protein chip comprising said polypeptides.

Inventions: 3263-3312: claims 6 to 14 and 16 to 18 (partially):

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-3, 6-18

Present claims 1-3, 6-18 relate to an extremely large number of possible products. In fact, the claims contain so many options, variables, possible permutations and provisos particularly in the light of the protein-protein interactions defined in Table 1 and Table 8, that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure. if the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination before the EPO (see EPO Guideline C-VI, 8.5), should the problems which led to the Article 17(2) declaration be overcome.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No PCT/EP 01/15428

Patent document cited in search report	•	Publication date		Patent family member(s)	Publication date	
WO 0066722	A	09-11-2000	CA EP WO JP US	2371596 A1 1173560 A1 0066722 A1 2002542821 T 2003017478 A1	09-11-2000 23-01-2002 09-11-2000 17-12-2002 23-01-2003	t.
WO 9942612	A	26-08-1999	US EP WO US US	6187535 B1 1055000 A1 9942612 A1 2003134268 A1 6531284 B1	13-02-2001 29-11-2000 26-08-1999 17-07-2003 11-03-2003	-

Form PCT/ISA/210 (patent family annex) (July 1992)

644

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

A Selected Interacting Domain (SID) polypeptide in Helicobacter pylori comprising the even Nos. 6596 to 6644 Table 8, a SID polynucleotide in Helicobacter pylori comprising the uneven SEQ ID NOs 6595 to 6643 in Table 8, a fragment or variant of said SID polypeptide or SID polynucleotide, a vector and host cell comprising said SID polypeptide, a pharmaceutical composition comprising said SID polypeptide or said recombinant host cells and a protein chip comprising said polypeptides.

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:
BLACK BORDERS
☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
☐ FADED TEXT OR DRAWING
☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
☐ SKEWED/SLANTED IMAGES
COLOR OR BLACK AND WHITE PHOTOGRAPHS
GRAY SCALE DOCUMENTS.
☐ LINES OR MARKS ON ORIGINAL DOCUMENT
☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
□ OTHER:

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.

THIS PROK BLANK USERO